ICOFAAS 2024

6TH INTERNATIONAL CONFERENCE
ON FOOD, AGRICULTURE AND ANIMAL SCIENCES
19-22 DECEMBER 2024
ERZURUM, TÜRKİYE
(FACE TO FACE AND ONLINE)

6TH INTERNATIONAL CONFERENCE ON FOOD AGRICULTURE AND ANIMAL SCIENCES PROCEEDING BOOK

ISSUED: 30/12/2024

ISBN: 978-625-99950-2-1

2024

INTERNATIONAL CONFERENCE ON FOOD, AGRICULTURE AND ANIMAL SCIENCES

DATE-PLACE

ICOFAAS 2024
ERZURUM, TÜRKİYE
DECEMBER 19-22, 2024

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REF: *Akademik Teşvik*

İlgili makama;

6th International Conference on Food, Agriculture and Animal Sciences (ICOFAAS 2024) kongresi 19-22 Aralık 2024 tarihleri arasında Atatürk Üniversitesi'nde 26 farklı ülkenin (Türkiye:75, Diğer Ülkelerden:124) akademisyen/araştırmacılarının katılımıyla gerçekleştirilmiştir. Kongre 16 Ocak 2020 Akademik Teşvik Ödeneği Yönetmeliğine getirilen "Tebliğlerin sunulduğu yurt içinde veya yurt dışındaki etkinliğin uluslararası olarak nitelendirilmesi için Türkiye dışından en az beş farklı ülkeden sözlü tebliğ sunan konuşmacının katılım sağlaması ve tebliğlerin yarıdan fazlasının Türkiye dışından katılımcılar tarafından sunulması esastır." değişikliğine uygun düzenlenmiştir.

Bilgilerinize arz edilir,

Saygılarımla

ICOFAAS

Assist. Prof. Dr. Fazıl HACIMÜFTÜOĞLU
Chair of ICOFAAS 2024

Dear Conference Participants,

Welcome to 6th International Conference on Food, Agriculture and Animal Sciences.

On behalf of the Organizing Committee, I am very happy to open 6th International Conference on Food, Agriculture and Animal Sciences. I believe that this event, which is the fruit of an intensive and devoted teamwork, will have an invaluable contribution to the scientific world. At the end of busy schedule of nearly one year, we have now achieved to organize this conference.

The aim of the International Conference on Food, Agriculture and Animal Sciences is to bring together experts and young researchers from all over the world working in Food, Agriculture and Animal Sciences to present their researches, exchange new ideas, discuss challenging issues, foster future collaborations and interact with each other. In this sense, we are happy to bring together world mathematicians and exchange information with them.

The main objective of our conference is to discuss recent results in Food, Agriculture and Animal Sciences and applications and their relationship with other disciplines. We expect the participation of many prominent researchers from different countries who will present high quality papers. The conference brings together about over 199 participants from 26 countries (Algeria (41), Argentina (1), Azerbaijan (8), Belgium (4), Brazil (1), Bulgaria (2), China (8), Greece (1), India (1), Indonesia (3), Iran (6), Iraq (1), Jordan (2), Korea (2), Kyrgyzstan (1), Lithuania (4), Malaysia (3), Moldova (1), Morocco (7), Pakistan (6), Russia (6), Serbia (2), Spain (1), Sri Lanka (6), Tunisia (6), Türkiye (75)), out of which 137 are contributing to the meeting with oral presentations and with 14 poster presentations, including eight keynote talks.

It is also a purpose of the conference to promote collaborative and networking opportunities among senior scholars and graduate students in order to advance new perspectives. The papers presented in this conference will be considered in the journals listed on the conference websites.

I'd like to express my gratitude to all our authors, members of scientific committee, keynote speakers and contributing reviewers. I believe we will see the best papers of scholars in this event. My sincere thanks go to Prof. Dr. Ahmet HACIMÜFTÜOĞLU, the rector of Atatürk University, sets the goal of being also a top-ranking university in scientific sense, for supporting and motivating us in every respect. Special thanks are also due to the organizing committee members, for completing all preparations that are necessary to organize this conference. I express my gratitude to the members of technical committee of the conference for the design and proofreading of the articles.

We wish everyone a fruitful conference and pleasant memories in our online event.

Thank you.

Assist. Prof. Dr. Fazıl HACIMÜFTÜOĞLU
Chair of ICAFOAS 2024

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KEYNOTE SPEAKERS

Exosomes Drived from Edible Plants Used in Regenerative Medicine

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ABSTRACT: Regenerative medicine is an exciting emerging discipline that aims to develop new therapeutics to repair and regenerate damaged and diseased organs. Stem cells, gene therapy, biomaterials, engineered tissue, and therapeutics containing biologically active compounds are widely used in regenerative medicine. In recent years, extracellular vesicles particularly exosomes have received great attention in the field of tissue repair and regeneration. Exosomes are well known for playing a leading role in intercellular communication. They transport lipids, proteins, nucleic acids and other biomolecules from one cell to another. As natural or engineered carriers, exosomes can be highly suitable for drug delivery. More recently, plant exosomes have received much attention due to their ability to serve as therapeutic delivery systems for drugs and regenerative medicine applications. It has become important to investigate plant-based exosomes as a cutting-edge platform for the treatment of diseases such as autoimmune, infectious diseases, inflammatory, neurological and cancer. Previously, in vitro and some preclinical studies have shown that plant derived exosomes have great potential for use in regenerative by promoting recipient cell proliferation, inhibiting apoptosis, facilitating angiogenesis and nerve regeneration, and preserving stem cell phenotypes.

Current studies at Yeditepe University have focused on several types of exosomes derived from different biological sources including mamalian stem cells, plants and microorganisms. Our in vitro and in vivo studies have well documented the importance of plant-derived exosomes in their cell-free therapeutic potential in cartilage and bone tissue regeneration, neuroregeneration, wound healing, hair growth, antiviral therapy, and cancer treatment.

Keywords: Regenerative Medicine, Exosomes, Drug Delivery, Biomarkers, Extracellular Vesicules

Research and Application Progress of Natural Products for Animal industry

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ABSTRACT: The consumption of antibiotics by human and animal industry is very huge in the world, resulted in the big problem of bacterial resistance and drug residues, the frequency and probability of "superbacteria" occurrence is increased significantly, that threat to human and livestock health. Although developed countries, such as the Europe union, the United States American, as well as our country, have successively issued a series of policy to decrease the consumption of antibiotics, the use of antibiotics in some countries developing country, such as Africa and Southeast Asia, still is insufficient supervision and excessive used, and the long-term threat of bacterial resistance still exists. Therefore, to search the effective natural products to reduce the use of antibiotics is vital important in currently. Now, Chinese herbal medicine, probiotics, antimicrobial peptides, acidifiers, enzyme, and animal used marine drugs, all showed an excellent antibacterial, anti-inflammatory, immunity enhancement and growth-promoting functions. A green, antibiotics-free breeding technology in animal industry is of tendency in future. This presentation reviewed the current situation of antibiotic used in China, as well as the antibiotics replacement products, focused on the function, mechanism, problems in used, and possible methods for deal with this problem. Whilst, the recently progress of marine drugs development in my lab, especially focused on the prevention and therapy of stress, inflammatory bowel disease, and the mechanism of them alleviated the disease by in vivo and in vitro model.

Keywords: Animal Industry, Natural Products, Superbacteria, in Vivo Model, in Vitro Model

Edible Insects: Trend or Necessity for the Food Industry?

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ABSTRACT: Entomophagy has deep historical roots and is practiced by over two billion people globally. Insects offer a sustainable solution to global food security challenges, providing high-quality protein, essential amino acids, beneficial fats, fibre, and some micronutrients (magnesium, copper, iron, zinc etc.). Compared to traditional livestock farming, insect farming requires significantly fewer resources, including land, water, and feed, while producing lower greenhouse gas emissions. Despite these advantages, entomophagy faces cultural resistance in regions like Europe and concerns about safety, including chemical, biological, and allergenic risks. These risks stem largely from improper postharvest handling and require robust food control measures. This research focus on the nutritional, environmental, and socioeconomic benefits of edible insects while addressing the barriers to their acceptance.

Keywords: Edible Insects, Entomophagy, Insect Protein, Insect National Value

INTRODUCTION

Entomophagy, the consumption of insects as food, has deep historical roots and has been practiced by humans since prehistoric times (Costa-Neto & Dunkel, 2016; Pali-Schöll et al., 2019; Papastavropoulou et al., 2021). Prehistoric evidence suggests insects were a significant part of early human diets. Archaeological findings indicate that insects were consumed across various ancient cultures, including those in the Near East and China (Liceaga, 2022; Van Huis, 2017). The global food system faces mounting challenges due to increasing population growth and the rising demand for animal protein. Traditional methods of food production, such as livestock farming, are unsustainable in the long term, as they contribute significantly to environmental degradation. Insect farming presents a viable and sustainable alternative to conventional protein sources. Insects are nutrient-dense, providing high-quality protein and essential micronutrients, and their farming requires significantly fewer resources, such as water, land, and feed, compared to livestock (Papastavropoulou et al., 2021; Papastavropoulou et al., 2023). Overall, historical and archaeological evidence points to a longstanding tradition of insect consumption, indicating their importance as a food source across time and geography. Thus, entomophagy represents a sustainable solution to global food security challenges.

Currently, more than two billion people in 113 countries include insects in their diets. This practice is particularly prevalent in Asia, Africa, and the Americas, where insects have historically been a staple food source due to their nutritional value and availability. the consumption of insects as food was recorded in 29 countries in Asia, 11 countries in Europe, 23 countries in Americas, 36 countries in Africa, and 14 countries in Oceania (Figure 1) (Papastavropoulou et al., 2021; Papastavropoulou et al., 2023; Suthar et al., 2020). Entomophagy is prevalent in subtropical and tropical regions due to greater insect diversity and abundance, allowing year-round availability and easier mass harvesting. However, it is also widespread in temperate-zone countries like China, Japan, and Mexico (Papastavropoulou et al., 2023; Van Huis, 2017).

Figure 1. Global patterns of insect consumption

The most commonly consumed edible insects belong to various orders, with beetles (31%), butterflies (18%), and ants, wasps, and bees (14%) being the most prevalent. Other widely consumed species include crickets, honeycomb moths, grasshoppers, mealworms, houseflies, and black soldier flies. 88% of edible insects are terrestrial, with the remaining 12% being aquatic. Different insect species are consumed at various life cycle stages, depending on the order (Papastavropoulou et al., 2023; Van Huis, 2017). Here are some examples of commonly consumed edible insect species categorized by type (Raheem et al., 2019):

- Crickets (*Acheta domesticus, Gryllodes sigillatus, Gryllus assimilis, G. Bimaculatus, G. locorojo*)
- Caterpillars (*Galleria mellonella*)
- Grasshopers (*Ruspolia differens*, *Locusta migratoria*)
- Warms (*Tenebrio molitor, Zophobas atratus, Alphitobius diaperinus*)
- Flies (*Musca domestica, Hermetia illucens*)

While 80% of the global population consumes insects, entomophagy remains limited in regions like Europe, where it constitutes only 2% of food intake. Cultural, psychological, and social factors contribute to the negative perception of insects in Western societies, where they are often regarded as associated with disgust and primitiveness (Papastavropoulou et al., 2023; Raheem et al., 2019).

Edible insects are commonly prepared using traditional methods such as drying, roasting, and frying, and are increasingly processed into non-recognizable forms like powders and protein hydrolysates for the food industry. Figure 2 show the different way of insect's consumption. However, employing different processing technologies such as drying, can affect the nutritional composition of insects, with variations in protein solubility and lipid oxidation (Liceaga, 2022; Papastavropoulou et al., 2021).

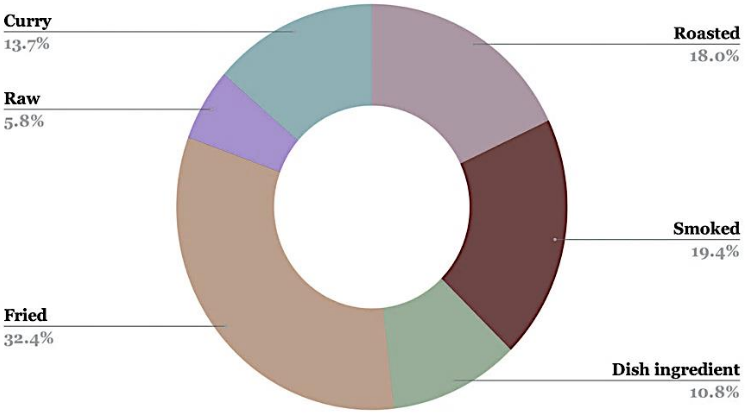

Figure 2. Ways of insect consumption

The increase in world population raises concerns about food availability, particularly animal protein. Agricultural land, freshwater, and current animal protein sources are expected to be insufficient to meet the growing demand. Additionally, increasing animal protein production is linked to environmental challenges. Thus, using alternative, highly nutritious, and sustainable food sources, such as insects, offer significant nutritional value, environmental benefits, and socioeconomic advantages (Liceaga, 2022; Papastavropoulou et al., 2023).

Insect farming offers several environmental advantages over traditional livestock farming (Figure 3). It requires less water, as insects can obtain moisture from their food and are more drought-resistant than cattle. Additionally, insect farming uses significantly less land to produce the same amount of protein, with up to ten times less land needed compared to pigs and cattle. Insects also produce fewer greenhouse gases, with methane emissions being much lower than those from pigs. Moreover, insect farming generates less ammonia. Another benefit is the potential reduction in pesticide use, as many edible insects are pests themselves, and harvesting them for food could reduce the need for chemical insecticides (Liceaga, 2022; Nadeau et al., 2015; Papastavropoulou et al., 2023; Tang et al., 2019).

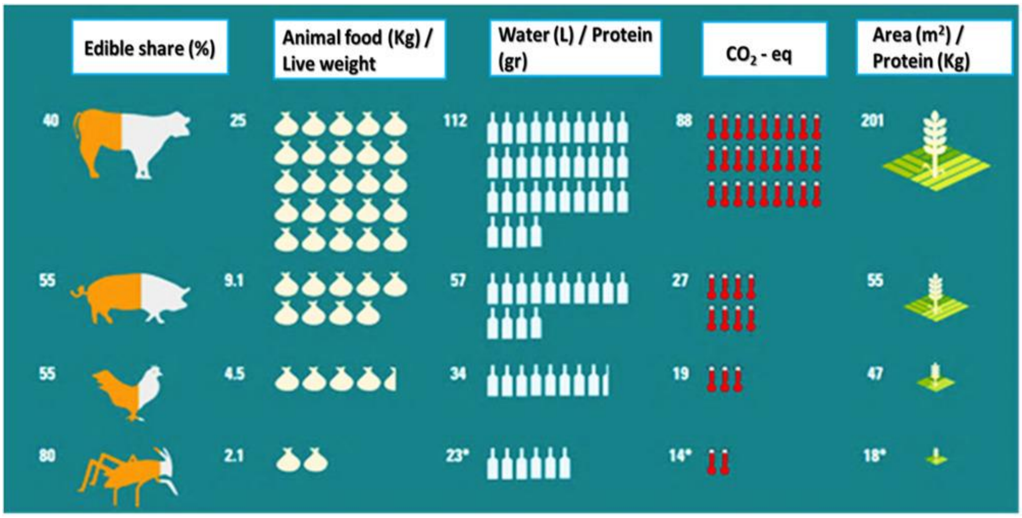

Figure 3. Resource requirements for protein production from livestock and insects.

Edible insects are a rich source of protein, fat, carbohydrates, vitamins, and trace elements, with their nutritional value varying depending on the insect type, development stage, and diet. They are high in protein, with some species containing 35% to 61% protein by weight, and they provide essential amino acids that meet human dietary needs. Insects also contain beneficial fats, including polyunsaturated fatty acids, which are comparable to those found in fish and poultry, and are beneficial for heart health. Additionally, insects are a good source of fibre, mainly in the form of chitin, which has various medicinal properties. They also offer important trace elements like iron, zinc, calcium, and magnesium, which are often more abundant in insects than in traditional animal proteins. In this regard, Papastavropoulou et al. (2021) highlights the nutritional benefits of mealworms and cricket flour, as a sustainable food source. Mealworm and cricket flour were presented as excellent sources of protein, lipids, carbohydrates, dietary fibre, and micronutrients (Table 1). They provide essential fatty acids such as omega-3 and contain essential amino acids (such as threonine, leucine, isoleucine, lysine, histidine, and methionine) required for human nutritional. Mealworm and cricket flour samples are also rich in key minerals like magnesium, copper, iron, and zinc.

Table 1. Nutritional values of the mealworms and cricket (Papastavropoulou et al., 2021)

	Mealworms (raw)	Mealworms (dry weight)	Cricket flour (raw)	Cricket flour (dry weight)
Water content (g/100g)	75.8	--	10.0	--
Ash (g/100g)	1.16	5.24	4.98	5.53
Protein (g/100g)	10.2	57.8	65.3	72.6
Fat (g/100g)	5.66	23.8	15.1	16.8
Dietary fibers (g/100g)	1.20	5.33	1.46	1.62
Carbohydrates (g/100g)	7.18	--	--	5.13
Total Energy Value				
KJ/100g	505	2087	1747	1941
Kcal/100g	120	496	416	462

While edible insects offer significant benefits for human nutrition and environmental sustainability, concerns about their safety remain a major barrier to widespread acceptance, particularly in developed countries. Potential risks are categorized as chemical, biological, and allergenic. Improper postharvest handling, production, processing, and storage are key concerns for the safety of the produced insects. So, effective food control measures are essential to minimize these risks.

Conclusion

Edible insects present a sustainable and nutrient-rich alternative to conventional protein sources, addressing global food security challenges. They offer high-quality protein, essential amino acids, beneficial fats, fiber, and vital micronutrients, while requiring fewer resources and producing lower environmental impact than traditional livestock farming. Despite their historical and cultural significance in many regions, the adoption of entomophagy is hindered by cultural perceptions and safety concerns, particularly in developed countries. To unlock their potential, we need to raise public awareness and address safety risks by improving postharvest handling and food safety measures, making insects a practical global food option.

Funding

The authors thank the National and Kapodistrian University of Athens, Special Account for Research Grants, Grant No. 14053

Statement of Conflict of Interest

The authors declare that they are no conflict of interest.

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Herbicide Resistance Challenges and Management Approaches

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ABSTRACT: Herbicide resistance in weeds must be minimized, because it is a major limiting factor to food security globally. Weed scientists and evolutionary biologists have to join together towards more integrated understanding of resistance. This approach is likely to simplify the design of innovative solutions to the herbicide resistance challenges. Chemical herbicides exert a high selection pressure on weed fitness, and the diversity of weed community's changes over time in response to both herbicides and other strategies imposed on them. Repeatedly and intensively, the use of herbicides with the same mode of action may swiftly result in population shifts to tolerant, difficult to suppress and ultimately the development of herbicide-resistant weeds, particularly in absence of using herbicides with different modes of action. The hypotheses and proposals put forward here require field verification, which may prove them to be incorrect.

Keywords: Weed Fitness, Herbicide Resistance, Selection, Mode of Action, Diversity

INTRODUCTION

Herbicides are applied widely as a weed management tool in cropping systems throughout the world. One consequence of the extensive use of herbicides has been the appearance of herbicide resistance in weed species (Heap, 1999). It has been more than 50 years since Harper discovered resistance to herbicides (Harper, 1956). More recently, resistance to herbicides has been identified in more than 180 weed species (Heap, 2007). Over the years there have been numerous publications on weed resistance to herbicides (Gressel, 2000; Powles and Shaner, 2001; Tranel and Wright, 2002; Delye, 2005; Powles and Yu, 2010).

The first occurrence of resistance was observed in wild carrot (Daucus carota L.), which developed resistance to the auxin analog class of herbicides after the herbicide had been used for several season (Switzer, 1957; Whitehead and Switzer, 1967). Since then, 362 weed cases of resistance have been reported in 198 species (Heap, 2011). More than one-third of these resistant weeds have been detected in intensive arable crops (Heap, 2011; Vencill et al., 2012). Ongoing herbicide selection in a wide cropping area on multiple populations of genetically diverse weeds has led, and will continue to lead to further herbicide resistance development (Powles and Yu, 2010).

Some factors influence herbicide resistance development, including the intensity of selection and the frequency of herbicide resistance genes. The first is easy to determine, but there is little information linked to the initial herbicide resistance development in weeds (Jasieniuk et al., 1996). For instance, Lolium rigidum is a major annual grass weed of cropping systems. For instant, Herbicide resistance first emerged in L. rigidum in 1980 (Heap and Knight, 1982) and is now widespread across the more intensive cropping systems (Preston et al., 1999). In some areas more than 40% of cropland is infested with herbicide resistant L. rigidum (Nietschke et al., 1996). Multiple herbicide resistant populations of L. rigidum are simultaneously resistant to more than 12 herbicides representing seven modes of action (MoA) (Preston et al., 1996). Overall, all weeds that growers manage in agricultural fields have the capacity to become resistant to whatever tactic is used to control them (DuPont, 2008). In this paper, we summarize the main challenges of herbicide resistance research to develop an integrated and sustainable weed management strategy.

Assessment of Herbicide Resistance Status

The development of herbicide resistance in weeds is an evolutionary process. Genetically, weed species are extremely diverse; the genetic variation within weed species includes the inherent capability to resist some chemicals. Nevertheless, the frequency of this genetic variation in a weed population is low. During 2001–2005, 12% of scientific papers published in weed research journals were on herbicide resistant weeds (Neve, 2007). Obviously, herbicide resistance is an important issue of weed science. Herbicide resistance evaluations might be divided into three categories: those that confirm and characterize resistance traits (characterisation); those that examine the biological characteristics of resistance (biological); and those related to resistance management (management). It is not surprising that many of the earliest herbicide resistance studies intended to prove resistance and to illustrate the physiological and genetic basis of resistance traits in weeds (Powles and Holtum, 1994). Consequently, one may conclude that scientists have become fixated with investigating resistance and less inclined to undertake research that synthesizes this information in order to achieve a more comprehensive understanding of the population biology of resistance (Neve et al., 2004). On the other hand, farmers' have responded in various ways to herbicide resistance (Farmassist, 2006; Preston et al., 2006).

From the beginning of 2012, 372 unique, herbicide-resistant biotypes have been reported in all over the world. The United States have 139, Australia has 60, Canada has 52, France and Spain each of them have 33, Brazil has 25, Germany has 26, the United Kingdom has 24, and there are from 1 to 19 in most other countries with intensive cropping systems. Each of these biotypes is resistant to at least one herbicide mode of action, and numerous MOAs have chosen for a number of resistant weeds. For instant, about more than 100 weed species are resistant to the acetolactate synthase (ALS) inhibiting herbicides (e.g., chlorimuron, pyrithiobac, imazaquin) (Vencill et al., 2012). The main herbicide groups in which herbicide resistance has developed to date are the ACCase inhibitors, s-triazines and ALS inhibitors (Heap, 2006). Similar developments are occurring in the group of glycines, specifically glyphosate. Glyphosate resistance is particularly significant as it is a globally used highly effective herbicide, and due to its use to control weeds in genetically modified crops (Powles and Preston, 2006). Since 1996, glyphosate-resistant crops have had a significant efficacy on agriculture, especially in the US, Brazil, Argentina, and Canada (Brookes and Barfoot, 2011). In the United States, some species, including Palmer amaranth (Amaranthus palmeri), common waterhemp (Amaranthus rudis), common ragweed (Ambrosia artemisiifolia), horseweed (Conyza canadensis), Italian ryegrass (Lolium multiflorum), rigid ryegrass (Lolium rigidum), and johnsongrass (Sorghum halepense), have developed resistance to glyphosate (Heap, 2009). Recently, many weed species have developed resistance to herbicides globally, especially in United States, where 156 weeds species have become resistant to a range of herbicide formulations (Fig 1)

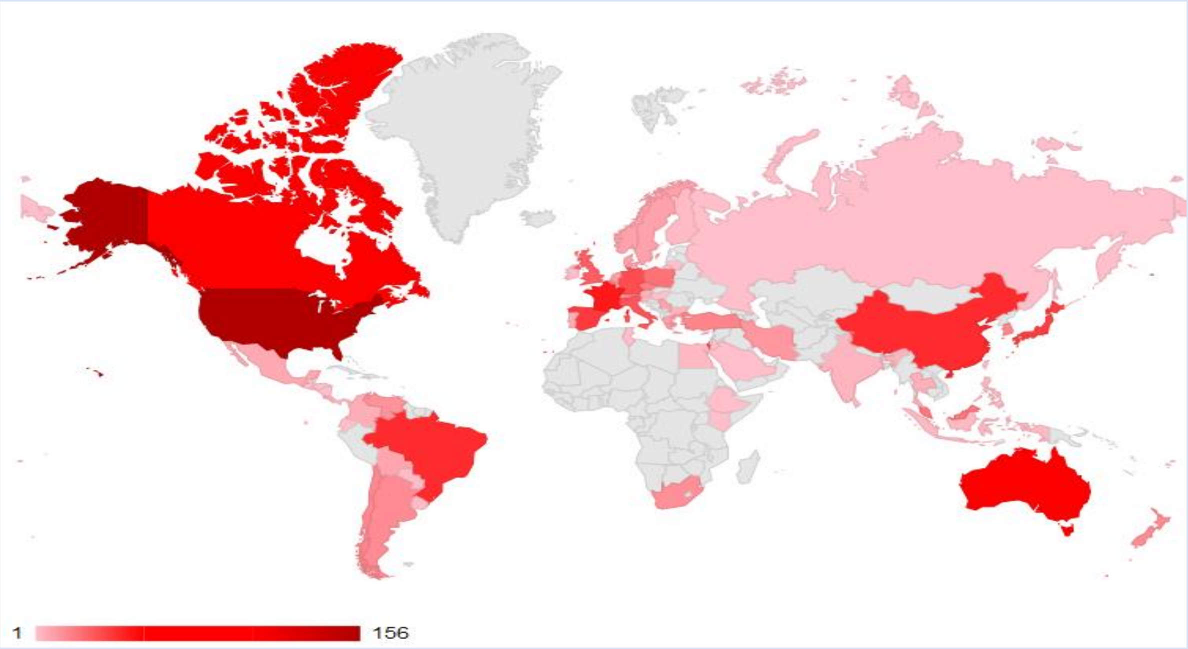

Figure 1. The number of unique herbicide resistance all over the world (www.weedscience.org).

Numbers of herbicide resistant weed species are displayed in graduated colours, the United States has the highest number of herbicide resistant weed species (156 species)

Consequences of Overreliance on a Single Mode of Action

Although many factors contribute to the frequency of herbicide resistance events in weed communities, reviewing the reported incidents strongly suggests that the single most significant factor leading to the development of resistance is overreliance on one group of herbicides, all with the same mode of action, without using other weed management tools (Heap, 2011). Rigid ryegrass and Italian ryegrass populations were identified where glyphosate had been applied for at least fourteen consecutive years (Perez-Jones et al., 2005; Simarmata et al., 2005). Glyphosate-resistant horseweed and common ragweed had developed after continuous use of glyphosate on soybean (Glycine max) for three and six years, respectively (Pollard et al., 2004; VanGessel, 2001). Additionally, glyphosate resistance in Palmer amaranth was detected after only four to six years of consecutive glyphosate application (Culpeppper et al., 2006; Legleiter and Bradley, 2008). Herbicide resistance development is not limited to glyphosate. Herbicide resistance has been reported for, but is not limited to, 2,4-D resistance in wild carrot (Switzer, 1957; Whitehead and Switzer, 1967), common groundsel (Senecio vulgaris) resistance to atrazine (Ryan, 1970), and barnyardgrass (Echinochloa crus galli) resistance to propanil (Carey et al., 1995). Hence, a large number of weed species both dicots and monocots are highly resistant to different herbicide groups with the various MoAs (Table 1).

The incidence of resistance in a weed population that was not previously exposed to the target herbicide is rare (Gressel and Levy, 2006; Gressel and Segel, 1990). The number of resistant individuals will swiftly increase with repeated use of the same herbicide or those with similar MoA. Beckie (2006) indicated that significant levels of resistance to ALS-inhibitor herbicides evolved in weed communities with as few as five applications. Combining recommended dose of various herbicide MoAs sequentially, or annually, greatly reduces the likelihood of individual plants resistant to a specific MoA to survive. In the majority of weed species, individual's naturally tolerant to more than one herbicide MoA will be rare (Vila-Aiub et al., 2009).

Table 1. Herbicide resistant weeds by mode of action. (www.weedscience.org)

No	Herbicide Group	HRAC Group	Example Herbicide	Dicots	Monocots	Total
1	ALS inhibitors	B	Chlorsulfuron	97	62	159
2	Photosystem II inhibitors	C1	Atrazine	50	23	73
3	ACCase inhibitors	A	Sethoxydim	0	48	48
4	EPSP synthase inhibitors	G	Glyphosate	18	17	35
5	Synthetic Auxins	O	2,4-D	24	8	32
6	PSI Electron Diverter	D	Paraquat	22	9	31
7	PSII inhibitor (Ureas and amides)	C2	Chlorotoluron	10	18	28
8	Microtubule inhibitors	K1	Trifluralin	2	10	12
9	PPO inhibitors	E	Oxyfluorfen	9	1	10
10	Lipid Inhibitors	N	Triallate	0	10	10
11	Long chain fatty acid inhibitors	K3	Butachlor	0	5	5
12	PSII inhibitors (Nitriles)	C3	Bromoxynil	3	1	4
13	Carotenoid biosynthesis inhibitors	F1	Diflufenican	3	1	4
14	Carotenoid biosynthesis (unknown target)	F3	Amitrole	1	3	4

15	Cellulose inhibitors	L	Dichlobenil	0	3	3
16	Antimicrotubule mitotic disrupter	Z	Flamprop-methyl	0	3	3
17	HPPD inhibitors	F2	Isoxaflutole	2	0	2
18	DOXP inhibitors	F4	Clomazone	0	2	2
19	Glutamine synthase inhibitors	H	Glufosinate-ammonium	0	2	2
20	Mitosis inhibitors	K2	Propham	0	1	1
21	Unknown	Z	Endothall	0	1	1
22	Cell elongation inhibitors	Z	Difenzoquat	0	1	1
23	Nucleic acid inhibitors	Z	MSMA	1	0	1

*This table lists weeds species resistant to each site of action. Many species have evolved resistance to more than one site of action.

The Impact of Efficient Herbicide Dosage

In most countries, herbicides are the dominant technology for weed control that infests cropping systems. Consequently, where herbicides have been used intensively, there are many examples of the development of herbicide resistance (Heap, 2010; Powles and Yu, 2010). From an evolutionary perspective, many factors affect the dynamics of herbicide resistance under herbicide selection pressure. Notwithstanding the reported predominance of single gene Mendelian inheritance of resistance traits, Gressel *et al.* (2006) have argued that reduced herbicide rates favors the development of quantitative resistance (Gardner *et al.*, 1998; Gressel, 2002). One vital element in herbicide resistance development is the intensity of herbicide pressure, the major determinant of which is the herbicide application rate. Therefore, herbicides, when used at the proper plant growth stage and at the registered label-rate, cause very high mortality. In contrast with herbicides applied at lower rates, where weed mortality is reduced. For instance, herbicide use rates in Australia are often about 50% of that in other parts of the world (Bayer, 2010)

On 28% of the crop lands in Canada weeds are managed with reduced herbicide rates (Beckie, 2006). In addition to rate-cutting, environmental variability under field conditions and decay rates for residual soil herbicides can result in lower than label rates of herbicides being used on target weed populations (reviewed by Zargar *et al*., 2012; Zhang *et al*., 2000). Thus, if herbicide treatment occurs to bigger plants that are well past the optimum plant growth stage for control, this effectively constitutes a cutting herbicide rates (Wauchope et al. 1997). Several studies on a range of crops and environmental conditions by Zhang *et al*. (2000) illustrated substantial variation in weed management efficacy from applying different herbicide rates (Zargar and Pakina, 2014). The same research indicated that weed control efficacy tended to be lower and more variable at reduced rates than recommended rates, but remained within the 60-

100% range in over 90% of the cases. In many cases, weed control was over 70% at rates between 30 and 60% of the recommended rate (Zhang *et al*., 2000). Similar effects as below label rate applications to weeds are generated after spraying plants that were larger than those recommended on the label; where inadequate coverage of weeds was achieved because of size or density, or low effective rates were caused by imprecise sprayer calibration or inaccurate mixing.

Herbicide Resistance Costs

The cost in herbicide-resistant weeds has ecological and agronomic implications. In many developed countries, herbicide resistance results in higher short term costs to manage weed communities because herbicides are the primary means of weed management, particularly in the absence of new herbicide formulations. Recent studies have described the added costs related to the management of herbicide resistance weeds. It is usually expected that mutations conferring resistance to a novel stress will incur a fitness cost in the original stress free environment (Coustau *et al*., 2000). Also, it is well established that target site triazine resistance incurs a substantial fitness cost in the absence of herbicide selection (Gronwald, 1994). Efforts to find out the costs related to herbicide resistance to other herbicide MoAs has been more equivocal, but, many of the published studies misinterpreted or mis-measured fitness costs.

On the other hand, resistance fitness and susceptible types have to be compared with a common genetic background. Researchers who compare resistance from various locations make little mention about resistance cost, because the genetic background is not controlled and differences in growth and other fitness-determining factors can be due to population differences that have nothing to do with the presence or absence of herbicide resistant weeds. Fitness itself should be compared from germination to germination (life cycle) in various environments, under competitive situations. Recently, some studies have been more observant in addressing these provisions (Roux *et al*., 2004; Vila-Aiub *et al*., 2005) and have indicated a significant cost of resistance. Therefore, it might be assumed that costs expressed for laboratory-derived mutants can be quite different from those which evolve the field.

The economic costs of herbicide-resistant weeds are a concern (Mueller *et al*., 2005; Boerbrom, 2006). Hence, two aspects will be illustrated: (a) if the resistance takes a long period of time to develop, the cost of prevention will be high. In this case, prevention is always the best. (b) if the herbicide to be replaced is cheaper than the new control strategy, it is more economical to prevent the resistance; it is more economically to prevent the resistance. Many researchers have revealed that herbicide resistance in important crop weeds results in economic losses (Pannell *et al*., 2004; Doole *et al*., 2009) this has been observed globally, especially in developed part of the world such as Australia and the United States.

Resistance Management Approaches

Although there is a significant cost to manage herbicide resistant weeds, growers are often hesitant to implement proactive measures to reduce the risk of resistance development in their fields. A key element that negatively affects producer adoption of practices that will mitigate herbicide resistance development is the expectation that there will be new herbicides available in the future (Foresman and Glasgow, 2008; Llewellyn *et al*., 2002, 2007). Studies are essential to develop integrated weed strategies as alternatives to the dominant and often exclusive method of managing weeds with herbicides in field crops. Recent studies highlighted the need to investigate resistance research within an evolutionary context. The application of evolutionary principles to agricultural settings is not new, but it is essential to understand and manage the effect of herbicide selection with a system perspective (Thrall *et al*., 2011).

Our deep understanding of the molecular, biochemical and physiological bases of herbicide resistance at the genetic level has failed to shed light on the interpretation of the evolutionary aspects of herbicide resistance (Neve, 2007). Vila-Aiub (2013) has re-emphasized how a greater understanding of the processes that cause resistance development could be gained by studies that assess the adaptive value of selected herbicide resistance. The ability of resistant weeds to persist and reproduce depends on the fitness level of the resistance gene (Maynard Smith, 1998). A focus to distinguish the effects of the environmental stresses on the fitness of resistant weeds under current cropping conditions could identify those factors that broadly reduce heritability of resistance alleles over time (Vila-Aiub *et al*., 2013).

Finnoff *et al*. (2007) indicated how managers who are cautious risk averse are less likely to adopt preventive measures because prevention only reduces the risk, rather than eliminating it. This perception is likely true for growers comparing the value of prevention control against the cost of herbicide resistance. However, in an illustration of more than 1000 corn, cotton, and soybean growers in the United States, Frisvold *et al*. (2009) determined that using multiple herbicides with different MOAs was one of the least-adopted methods for herbicide resistance management, despite this practice being frequently identified by scientists as an effective means to reduce the risk of resistance development. The reason is that using diverse MoAs can increase short term weed control costs (Hurley *et al*. 2009), whiles the benefits of delaying resistance, accrue in the future and are more uncertain. In this regard, using different herbicide formulations with the different MoAs (Fig 2) is logically recommendation to control herbicide resistant weeds.

Some growers believe that mitigating herbicide weed-resistant is beyond their control, depending more on their neighbor's behavior (Llewellyn, 2006; Wilson *et al.,* 2008). Growers may also believe that industry will develop new formulations of herbicides, decreasing the benefits of resistance management (Llewellyn *et al*., 2002, 2007). Alternatively, when using different MoAs provides short term returns comparable to current weed control strategies, farmers will be less certain about new, unfamiliar practices. Resistance management methods are naturally adopted reactively when a resistant weed species has become problematic and should be suppressed. Introduction of new herbicide resistance crop varieties can provide options for managing weed resistance to other herbicide MoAs, but desirable resistance management strategies must be adopted to avoid resistance emerging to the new herbicide as well.

The future commercialization and adoption of transgenic crops with additional resistance traits for auxinic herbicides such as 2, 4-D may provide some diversity in herbicide control tactics (Wright *et al*., 2010). To date, herbicide application causes strong selection pressure for weed resistance and any effort to manage resistance only through herbicide diversity is likely to be inadequate (Norsworthy *et al*., 2012).

Although the most favorable practice is to proactively use annual herbicide rotations and sequential applications before resistance evolves, that requires growers using multiple herbicides with different MoAs even if weed densities are low (Powles *et al*., 1997). More commonly, growers prefer to use one herbicide that still provides good control on susceptible weeds while adding a second herbicide to control resistant weeds. Jacquemin *et al*. (2009) indicated that applying mixtures to weed populations after resistance has evolved could be effective if the resistance mechanism imposes a significant fitness penalty via negative cross resistance. However, that scenario is not common. More research is required on the use of combined herbicide practices on already-resistant weed species, as well as on the potential for such methods to select for cross resistance (Preston, 2004).

Conclusion

Herbicides resistance development is globally a serious agronomic problem in many agro-ecosystems. The major research attempts in this area have to be towards the development of economically viable practices to prevent and manage herbicide resistant weeds. Herbicide-resistant crops have given growers economic and environmental benefits, involving time savings and reduced production costs as well as enhancing the opportunity to perform conservation-tillage approaches. Repeated herbicides application with the same MoA in herbicide-resistant crops has led to wide-spread herbicide resistance. The vast spectrum herbicides are also an answer to control weeds that had started to develop resistance to other herbicide MoAs. The majority of weeds studies have focussed on predicting the probability of resistance development and the rate at which it will develop. Resistance prevention needs adopting an integrated weed management approach, since no single control practice can effectively and desirably eliminate resistant-weeds.

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Slow Down to Speed Up: Spain Strategies for Boosting Crop Production

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ABSTRACT: Climate change and the anticipated increase in the global population pose significant challenges to food security, making the need for more efficient fertilizers increasingly urgent. Urea is the most widely used nitrogen fertilizer worldwide. However, the presence of extracellular ureases in the soil accelerates the hydrolysis of urea into ammonia and carbon dioxide, a process that, when occurring on the soil surface, undermines fertilizer efficiency and contributes to environmental pollution. Urease inhibitors can help control this premature urea decomposition, extending the fertilizer's effectiveness and allowing plants to uptake nitrogen more efficiently. Another approach to improving fertilizer efficiency is the use of biostimulants—substances or microorganisms applied to plants to enhance nutrient uptake, improve tolerance to abiotic stress, and/or boost crop quality. This presentation will focus on these two strategies that can address these challenges more effectively: the development of fertilizer formulations that incorporate urease inhibitors and/or biostimulants.

Keywords: Spain, Climate change, Crop Production, Fertilizers

Isolation and Mode of Action of Bacteriocins from Lactic Acid Bacteria

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ABSTRACT: In recent years, the demand for “natural” products has increased, as customers prefer this type of product over those with added chemical preservatives. The critical issues associated with natural products are how to maintain their safety and quality as well as how to prolong their shelf life. Our lab previsouly screen and isolated severals bacteriocins from lactic acid bacteria, which was found to exert antibacterial activity on both Gram-positive and Gram-negative bacteria, including multidrug-resistant strains. An innovative method, biochromatography (cell membranes chromatography) coupled with reversed-phase high-performance liquid chromatography (RP-HPLC), was developed for the efficient screening and purification of the bacteriocins found in the cell-free suspension of lactic acid bacteria. Additionally, bacteriocins were also able to inhibit the formation of biofilms. As the concentration of plantaricin YKX (one of previously isolated bacteriocins) reached 3/4 MIC, the percentage of biofilm formation inhibition was over 50%. Finally, the effect of bacteriocins on the AI-2/LuxS QS system were investigated. Molecular docking predicted that the binding energy of AI-2 and plantaricin YKX was -4.7 kcal/mol and the binding energy of bacteriocin and luxS protein was -183.701 kcal/mol. The expression of the luxS gene increased significantly after being cocultured with bacteriocin.

Keywords: Bacteria, Bacteriocins, Lactic Acid

Productivity Parameters of European Grape Clones in the Agro-Ecological Conditions of ATU Gagauzia

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ABSTRACT: Regenerative medicine is an exciting emerging discipline that aims to develop new therapeutics to repair and regenerate damaged and diseased organs. Stem cells, gene therapy, biomaterials, engineered tissue, and therapeutics containing biologically active compounds are widely used in regenerative medicine. In recent years, extracellular vesicles particularly exosomes have received great attention in the field of tissue repair and regeneration. Exosomes are well known for playing a leading role in intercellular communication. They transport lipids, proteins, nucleic acids and other biomolecules from one cell to another. As natural or engineered carriers, exosomes can be highly suitable for drug delivery. More recently, plant exosomes have received much attention due to their ability to serve as therapeutic delivery systems for drugs and regenerative medicine applications. It has become important to investigate plant-based exosomes as a cutting-edge platform for the treatment of diseases such as autoimmune, infectious diseases, inflammatory, neurological and cancer. Previously, in vitro and some preclinical studies have shown that plant derived exosomes have great potential for use in regenerative by promoting recipient cell proliferation, inhibiting apoptosis, facilitating angiogenesis and nerve regeneration, and preserving stem cell phenotypes.

Current studies at Yeditepe University have focused on several types of exosomes derived from different biological sources including mamalian stem cells, plants and microorganisms. Our in vitro and in vivo studies have well documented the importance of plant-derived exosomes in their cell-free therapeutic potential in cartilage and bone tissue regeneration, neuroregeneration, wound healing, hair growth, antiviral therapy, and cancer treatment.

Keywords: Regenerative Medicine, Exosomes, Drug Delivery, Biomarkers, Extracellular Vesicules

Enhancing Underutilized Products for Prebiotics Production

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ABSTRACT: Fructo-oligosaccharides (FOS) are well-known for their prebiotic properties and nutritional benefits. These compounds are widely used in food and beverage products, such as dairy, bakery items, and infant formula, to improve functionality. Consequently, global demand for FOS has been steadily increasing.

FOS can be synthesized enzymatically using disaccharide solutions (e.g., sucrose) or other sucrose-containing substrates. Examples of underutilized or discarded materials that serve as substrates include Prosopis nigra (carob) flour, Daucus carota (carrots), and Vitis vinifera (grapes). These materials not only serve as sources of the required carbohydrates but also add valuable phytochemicals to the final product.

FOS derived from underutilized products can be incorporated into functional foods (e.g., breads, snack bars), enriching them with prebiotic compounds and phytochemicals. This not only enhances the nutritional and health benefits of these prebiotics but also aligns with Circular Economy principles.

Keywords: Underutilized Products, Prebiotics, Production

FACE TO FACE

ABSTRACT

ORAL PRESENTATIONS

The Role of Crop Rotation in Increasing the Productivity of Agricultural Crops

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ABSTRACT: The growth of production in agriculture has created a significant dependence on the application of highly efficient varieties, modern technology and technical tools, plant protection measures, as well as the use of existing agricultural and technical agro-technological resources.

The main goal of conducting the research is to define specialized crop rotation schemes for each region of our republic, taking into account climate changes occurring in the world, and most importantly, drought resistance, and apply cultivation technology with high adaptability. Considering the importance of using the land correctly and efficiently, growing different agricultural crops in the regions and achieving food security, a research study was conducted in order to study the effect of short rotation crop rotation on plant productivity, which provides biological diversity. The field experiment of the study was carried out according to the following schemes (with 3 replications): Crop rotation: 1. Forage peas 2. Winter wheat 3. Barley Continuous crops: 1. Forage peas 2. Winter wheat 3. Barley

From the results of the studies, it is clear that the green mass of fodder peas in the sowing cycle was 21.2 s/ha at the branching stage, 323.7 s/ha in the flowering phase, 597.6 s/ha during the formation of beans, 584.4 s/ha ha during grain formation, which corresponds to continuous cultivation of 0.6; 15.0; 17.8 and 11.8 s were high.

In winter wheat, the yield of green biomass at the end of the tillering phase was 81.5-74.1/ha, in the booting phase - 162.7-152.2/ha, in the waxy ripening phase - 290.8-278.0/ha. Dry biomass, respectively, 16.3-14.8; 40.7-38.1; 96.6-92.6 s. was noticed. It was also found that the total yield of above-ground dry biomass of barley plants was 6.4 s per hectare higher in the crop rotation option than in the continuous sowing option.

Keywords: Soil, Plant, Crop Rotation, Diversification, Continuous Crops

Anti-Diabetic Properties of Kombucha Made from Dried Coffee Peel: Flavonoid Content and Inhibitory Activity against α-glucosidase

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ABSTRACT: Indonesia is rank 4th as the world's largest coffee producers. A significant coffee production volume leads to a substantial amount of waste in the form of coffee cherry husks. These husks contain several bioactive components and can be processed into tea. The processing of dried coffee peel into kombucha increase its phenolic and flavonoid content, which in turn enhances its α-glucosidase inhibitory activity. This study aims to determine the effects of dried coffee peel concentration and fermentation time on total α-glucosidase inhibitory activity, total phenolic and total flavonoid content in dried coffee peel kombucha. The results showed that dried coffee peel concentration, fermentation time, and their interaction significantly affected α-glucosidase inhibitory activity, total phenolic and total flavonoid content ($p<0.05$). The highest total phenolic content 842.76 ± 10.84 µg GAE/mL and flavonoid content 0.087 mg QE/mL were obtained in kombucha fermented for four days with a dried coffee peel concentration of 3%. The highest α-glucosidase inhibitory activity 91.33 ± 0.41% was observed after eight days of fermentation with a dried coffee peel concentration of 3%. Overall, an 8-day kombucha fermentation with a 3% dried coffee peel concentration provided the best results regarding total phenolic content, total flavonoid content and α-glucosidase inhibitory activity.

Keywords: Coffee peel, Fermentation, Flavonoid, α-glucosidase

The Impact of Climate Change on Rain-Fed Agriculture of Field Crops in Ajloun Governorate

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ABSTRACT: The study aimed to study the impact of climate change on rain-fed agriculture of field crops in Ajloun Governorate, which numbered approximately (6554) farmers, and the study population included all farmers of different demographic characteristics, areas and crops, and the researcher followed the random sample method in distribution, where she distributed (362) questionnaire to the study sample. The researcher used the statistical analysis program, 25SPSS, to analyze the data collected from the study tool, and used descriptive statistics represented by arithmetic mean, standard deviation, percentages, frequency, relative importance, analysis of Cronbach alpha coefficients, and simple linear regression analysis.

The results showed that there is knowledge and awareness among the sample members of climate change and its phenomena. The vast majority had yes answers to a change in some weather phenomena. There has been a change at the beginning and end of winter over the past years. There is also a change in temperatures. The results showed from the point of view of the sample members. The level of climate change impact has a role on the productivity of rain-fed field crops is high, as it achieved an arithmetic average of (3.80), which is within the high relative importance, and in the year (2015) it achieved the highest rainfall rate, while the lowest rainfall rate was in the year 2000, and the highest temperature was recorded in the year (2016) where it reached (18.2) degrees Celsius, while the lowest temperature was in the year (2000), when it reached (12.7) degrees Celsius. The study recommended the creation of a flexible plan to manage the production of rain-fed field crops according to the emerging conditions of climate change

Keywords: Climate Change, Field Crops, Rain-Fed Agriculture, Ajloun

Awareness of Chicken Breeders about Effects of Climate Change

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ABSTRACT: This research was conducted to study awareness of chicken farmers about climate change in northern Jordan. Data were collected for some demographics, chicken farms, economic characteristics, and four axes on how chicken farmers get information, awareness of climate change, problems caused by climate change, and adaptation strategies. Source of information about effects of climate change had been more on personal experience, family, friends, and agricultural sites. Chicken farmers were aware of problems and effects of climate change and adopted strategies to meet challenges caused by impact of climate change. Significant differences were observed according to governorate, breeder's qualifications, and work experience on type of production activity, but there were no differences in volume of production. Statistically significant differences were found in responses of chicken breeders according to qualifications and practical experience. In general, associations between study indicators were low to very low. The research recommended providing services to chicken breeders to face effects of climate change due to importance of chicken production in Jordanian food security.

Keywords: Chicken Farmers, Climate Change, Jordan

Characteristics of Sambalingkung Made from Snakehead Bone Stock with the Addition of Kepok Banana Heart (*Musa paradisiaca* L.)

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ABSTRACT: Sambalingkung is a traditional dish primarily made from fish, originating in the province of South Sumatra, Indonesia. The dish resembles serundeng or abon in both form and texture. This study aimed to evaluate the effect of adding kepok banana (*Musa paradisiaca* L.) heart on the production of sambalingkung using snakehead fish bone stock. The research employed a non-factorial Completely Randomized Design (CRD) with one factor: the concentration of kepok banana heart (A1: 5%, A2: 10%, A3: 15%, A4: 20%, and A5: 25%). Each treatment was replicated three times. The parameters observed included physical characteristics (color L*, a*, b*), chemical characteristics (moisture content, ash content), and sensory attributes assessed via a hedonic test (appearance, aroma, taste, and texture). The optimal treatment was determined based on physical properties (angle of repose), chemical composition (fat content, protein content, and crude fiber), and sensory evaluations. The results indicated that the concentration of kepok banana heart significantly affected color (lightness (L*), yellowness (b*)), moisture content, ash content, and sensory characteristics, particularly appearance and aroma. The A2 treatment (10% kepok banana heart) yielded the best results, with the highest hedonic test scores for appearance (3.44) and aroma (3.36), as well as favorable physical and chemical characteristics: 55.75 for L*, 4.52 for a*, 17.95 for b*, 3.10% for moisture content, 9.22% for ash content, 33.17% for fat content, 18.95% for protein content, and 5.61% for crude fiber in the final sambalingkung product.

Keywords: Sambalingkung, Traditional Food, Kepok Banana Heart, Snakehead, Fish Bone Stock

Morphological Characteristics of *Lactococcus garvieae* Strains Isolated from Farmed Rainbow Trout*

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ABSTRACT: Aim: This study aimed to determine the similarities and differences in the morphological and microbial characteristics of *Lactococcus garvieae* strains isolated from rainbow trout farms in Van province.

Materials and Methods: Symptomatic fish were collected from five registered rainbow trout farms in Van province, with six fish sampled from each farm. Necropsy procedures were performed under aseptic conditions. Kidney tissues were inoculated onto TSA (Tryptic Soy Agar) medium using sterile loops and incubated at 21°C for 24 hours. Identification of bacteria colonies developed on the medium was conducted using Real-Time PCR with 16S rRNA gene-specific primers 27F-1492R. Positive colonies were then classified based on color, diameter, border characteristics, oxidase, catalase activity, motility, and Gram staining properties. Phenotypic classification was conducted by evaluating the number of positive samples from each farm and analyzing morphological features quantitatively.

Results: It was observed that none of the farms used water disinfection methods, and most relied on river water for fish farming. All bacteria strains isolated from the sampled farms tested positive for 16S rRNA genes, producing sigmoidal curves in PCR analysis. Bacterial growth was observed on TSA media from all PCR-positive samples. Morphologically, all *L. garvieae* strains were found to be catalase and oxidase negative, non-motile, and Gram-positive, forming 0.8–1.2 mm cream or light-colored colonies with smooth edges. Six *L. garvieae* strains were isolated from three farms, five strains from one farm, and four strains from another.

Conclusion: The isolation of *L. garvieae* strains from all five farms indicates the prevalence of Lactococcosis, an infection causing significant mortality in fish when water temperatures exceed 15°C. The findings highlight the need for dual approaches in disease management. Recommendations include collaborating with producers to implement preventive measures, developing vaccines with strains of diverse characteristics, encouraging the use of vaccines, and raising awareness among farm operators to prevent disease transmission between facilities.

Keywords: Fish Diseases, *L. garvieae*, Real-Time PCR, TSA, Phenotype

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*This study was supported by the Van Yüzüncü Yıl University Scientific Research Projects Coordination Unit, project number TYL-2024-11346, as part of a master's thesis project

Bioinformatics in Legume Genomics: Unlocking Genetic Potential for Agricultural Innovation

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ABSTRACT: Legumes are an important part of agriculture around the world since they are a significant source of protein, and they encourage environmentally responsible agricultural practices. Legume research has been revolutionized as a result of recent advancements in bioinformatics, which have made it possible to investigate vast genomic databases and have revealed crucial genetic variables that influence characteristics like yield, resistance to disease, and environmental adaptability. This review examines the incorporation of bioinformatics in legume genomics, emphasizing genome annotation, transcriptomics, molecular marker development, and comparative genomics. The utilization of RNA sequencing and computer platforms has expedited the understanding of legume biodiversity, genetic enhancement, and evolutionary biology. The paper emphasizes the difficulties in handling intricate datasets and using computational tools, highlighting bioinformatics' potential to improve legume productivity, sustainability, and resilience to climatic concerns. The integration of bioinformatics and precision breeding presents exciting opportunities for enhancing food security and fostering agricultural innovation.

Keywords: Bioinformatics, Annotation, Comparative Genomics, Legumes

The Effect of Using Insects in the Diet and Its Effect on the Growth and Performance of Aquatic Animals

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ABSTRACT: According to the Food and Agriculture Organization (FAO) of the United Nations, insects can be a sustainable source of proteins. Insect meal provides a good source of amino acids, lipids, minerals, vitamins, and energy. Currently, the aquaculture industry is looking for alternative protein sources for aquaculture - proteins that are good candidates for maintaining performance and growth as well as improving resistance to aquatic diseases. Therefore, the use of insects in the aquatic meal can play an important role in the economy and sustainability of breeding compared to plant-based fish food. After preparing meal worm larvae and keeping them for 24 hours to empty their intestines and then drying and powdering meal worm, they were added to the diet of rainbow trout with different percentages of 0% (control), 15 %, 30 % and 45% and after a full period Various analyzes were carried out on them. Of course, during the growth phase, biometrics was performed 3 times and was analyzed. The larval stage of the yellow meal worm, Tenebrio molitor, and larvae powder is a good candidate to be used as a high protein feed ingredient that could replace FM for carnivorous aquaculture species. In this research, the best rate of consumption of mealworm larvae powder was 30%, which showed the best rate of growth and performance.

Keywords: Aquatic Animals, Diet, Insects, Growth, Mealworm

Melanin Production by Locally Isolated Streptomyces Strains*

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ABSTRACT: Bacterial strains belonging to the genera such as *Streptomyces* and Bacillus can naturally produce melanins. The melanins obtained from bacteria exhibit some bioactive properties that make them essential for pharmaceutical and cosmetic industries. Streptomyces strains mainly produce eumelanin (dark brown-black color) or pheomelanin (yellow-red color). This work was performed (I) to isolate a new *Streptomyces* strain which can produce extracellularly melanin, and (II) to perform the molecular identification of this strain. The isolation experiments were performed on tyrosine agar medium. The melanin production abilities of the isolates were tested in tyrosine broth medium. The identification of hyper-melanin producer isolate was performed based on 16S rRNA sequence analysis. Wavelength scanning for melanin was performed at 200-700 nm using a UV-VIS spectrophotometer. Among a total of 18 bacterial isolate, the strain SY8 isolated from potato field soil was determined to produce the maximum amount (1.87 g/L) of melanin. This isolate was identified as S. bottropensis. The maximum absorbance for the melanin (dark drown/black color) purified from this bacterium was measured at 235 nm. The maximum production of the melanin was achieved in PYITB medium (peptone-yeast extract-iron-tyrosine broth). This is the first report on the melanin production potency of *S. bottropensis*.

Keywords: *Streptomyces*, Melanin, Soil, Isolation

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*This study is a part of the Sevval YILDIRIM’s master thesis accepted by Institute of Science and Technology, Ataturk University

Changes in Botanical Composition of Rangeland Sites at Different Altitudes*

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ABSTRACT: Rangelands are composed of many different plant species and knowing the characteristics of these species is very important for rangeland management. While different rangeland sections show a certain degree of similarity among themselves, the similarity of vegetation cover may change with grazing and sudden changes in climatic factors. The rate of vegetation cover varies according to altitude, orientation and ecological factors. In this study, botanical composition, soil cover ratio, rangeland condition score and rangeland condition and health classes were determined while considering three different rangeland sections according to altitude. The proportions of wheat, legumes and other families in the botanical composition determined according to different altitudes showed significant changes. On average, 30.74% of the botanical composition was wheatgrass, 22.03% legume and 48.55% other family species. It was concluded that it would be better to review the rangeland grazing principles in the section where the study was carried out, especially in the section subjected to heavy grazing, and to make a grazing planning that will positively affect the rangeland health.

Keywords: Rangeland, Botanical Composition, Soil Coverage Ratio

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*This study is a part of the Ahmet HANCI's master thesis accepted by Graduate School of Natural and Applied Sciences, Ataturk University

Effects of Different Salt Levels on Forage Pea Varieties*

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ABSTRACT: One of the most common problems in agricultural production is salinity. In arid and semi-arid regions, approximately 50 % of irrigated areas are faced with salinity problems at various levels. Salinity stress, which is an abiotic stress factor that severely limits yield, causes significant losses in plant yield and quality, especially by changing the soil structure. Forage pea, a legume forage crop, is of great importance in animal nutrition. In this study, it was tried to determine the salinity tolerance of 3 varieties of forage pea (Servet, Taskent and Töre). In the study, different doses of NaCl were applied and as a result, parameters such as plant height, root length, plant wet weight, root wet weight, plant and root dry weight were analysed. While it was determined that the plant was adversely affected with the increase in salt concentration, it was determined that all three varieties were resistant to doses below 200 mM.

Keywords: Stress Physiology, NaCl, Forage Crops

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*This study is a part of the Funda KAYA's master thesis accepted by Graduate School of Natural and Applied Sciences, Ataturk University

Evaluation of Antifungal Activity of Bacillus subtilis TV-17C Against Some Fungal Pathogens Causing Postharvest Diseases in Citrus

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ABSTRACT: Citrus fruits are popular fruits that are widely preferred around the world. The most well-known members are oranges, tangerines, lemons, grapefruits and citruses. In the world market, Turkey has an important place in the production and export of citrus fruits. However, spoilage caused by various pathogenic fungi such as Penicillium digitatum, Penicillium italicum, Geotrichum citri-aurantii at different stages of harvest causes significant losses in the quality and marketing of citrus fruits. Biopesticides containing antagonistic bacteria against the negative effects of chemical products used to reduce these negative effects are a promising alternative for sustainable agriculture to prevent post-harvest diseases.

In this study, some fungal pathogens causing postharvest diseases in citrus fruits were isolated and tested for pathogenicity and virulence. The antifungal activity of the bacterium against selected pathogenic fungi was determined using Bacillus subtilis TV-17C bacterial isolate, which has a broad spectrum against post-harvest pathogens in citrus. The aim of the study was to develop and utilize microbial products, which are becoming increasingly widespread worldwide but have limited use in our country, and to create a domestic product.

As a result of the study, the most virulent pathogenic fungi were selected as a result of pathogenicity and virulence tests. According to the antifungal activity results of TV-17C bacterial isolate, the percentage inhibition rate of the selected fungal pathogens was determined in the range of 66-87%. As a result of these results, it is aimed to create solid formulations using TV-17C bacterial isolate due to its low cost, ease of storage and longer shelf life.

Keywords: Fungus, Bacteria, Biopesticide, Antifungal Activity

Optimization of Chitinase Production by *Bacillus amyloliquefaciens* N33

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ABSTRACT: Environmental factors such as nutrient sources and growing conditions have a great influence on enzyme production by microorganisms. In this context, the present study aimed to determine the optimum colloidal chitin concentration, temperature, pH and incubation time for chitinase production by growing B. amyloliquefaciens N33 strain under different environmental conditions. *B. amyloliquefaciens* N33 was grown at different colloidal chitin concentrations and the highest enzyme activity was observed in the medium containing 5 g/L colloidal chitin. To determine the optimum incubation time for N33 to produce chitinase, its activity was measured every 24 hours for 7 days and 24 hours was determined to be the optimum incubation time. In order to determine the pH and temperature values at which the N33 strain showed maximum chitinase activity, the strain was grown at different temperature values in culture media adjusted to different pHs. The temperature and pH values at which the strain showed the highest chitinase activity were 35 °C and pH 6, respectively. The results show that strain N33 produces optimum chitinase under mesophilic and slightly acidic conditions. Furthermore, the strain's ability to reach maximum chitinase production in a short time will provide advantages in shortening the process and reducing resource utilization in industrial production.

Keywords: *Bacillus amyloliquefaciens,* Chitinase, Optimization

Rapid Detection of E. coli O157:H7 in Foods Using Immunomagnetic Separation Combined with Real-Time PCR

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ABSTRACT: An approach integrating immunomagnetic separation and real-time PCR was employed to identify Escherichia coli O157:H7 from foods. Commercially prepared monoclonal antibodies targeting the E. coli O157 antigen were employed to coat magnetic particles. These particles were used to selectively capture and concentrate E. coli O157:H7 cells from food samples prior to real-time PCR analysis. The bacterial cells were recovered from the magnetic beads, and their DNA was extracted using a heat-assisted alkaline lysis procedure. The bacterial DNA was then analysed by real-time PCR, employing primers and a probe specifically designed to target the Z3276 gene within the genome of E. coli O157:H7 strain EDL933. This rapid and sensitive detection method was able to detect as few as 102 CFU/25g of E. coli O157:H7 in spinach, raw milk, and chicken meats. This integrated approach of immunomagnetic separation and real-time PCR enables the rapid, specific determination of E. coli O157:H7 without the enrichment culture step.

Keywords: *E. coli O157*, Immunomagnetic Separation, Food, Polimerase Chain Reaction

Mulberry Production Cost and Marketing in Uzundere District

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ABSTRACT: The study was conducted in 2022 in Uzundere district of Erzurum province to analyze the cost and profitability of mulberry production. Every stage of the production process, including maintenance, harvest, processing, and marketing, was examined in detail. The study evaluates factors affecting the costs of mulberry producers in Uzundere district as well as the challenges and opportunities they encounter. The main objective of the research is to develop recommendations that encourage producers to use their existing resources more efficiently. The study aims to analyze the cost structure of mulberry production in Uzundere and to reveal its marketing structure. In this context, various analyses were conducted, and suggestions were made to help shape farmers' decisions and improve their success in this field. A total of 100 individuals, 57 men and 43 women, residing in Uzundere participated in the study. Simple random sampling was used to select the sample enterprises. The demographic, economic, socioeconomic characteristics, and land structures of the mulberry producers who participated in the study were examined, along with their marketing structures. The cost of establishing a mulberry orchard was calculated as 12,001.85₺, with an annual depreciation of 200.03₺. Additionally, the total production cost of mulberries was found to be 4,268.54₺. The cost of 1 kg of fresh mulberry was calculated as 5.02₺, while its profit was determined to be 5.85₺. Mulberry production is a significant agricultural activity that can contribute to rural development with proper planning and cost management. This study provides producers with guidance and recommendations to help them achieve more efficient and profitable production. As a result, rational information was provided to mulberry producers, offering them insights on how to use their resources more effectively and turn challenges into opportunities in mulberry cultivation.

Keywords: Mulberry, Cost Analysis, Profitability, Marketing Strategies, Facility Cost, Production Cost

Genes Involved in Elongation and Desaturation of Fatty Acids in Chicken Liver

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ABSTRACT: Liver fat synthesis plays a crucial role in determining overall metabolic health, growth performance, and product quality in chickens. The liver, as the primary site of lipogenesis in poultry, is responsible for synthesizing and storing fats essential for energy homeostasis. However, excessive fat accumulation in the liver can lead to metabolic disorders that negatively affect poultry production. Several genes are involved in regulating liver fat synthesis, among which fatty acid desaturase (*FADS*) and very long-chain fatty acid elongase (*ELOVL*) genes stand out. *FADS* genes regulate fat metabolism by converting saturated fatty acids to unsaturated fatty acids through fatty acid desaturation. *FADS1* and *FADS2* genes play a significant role in the synthesis of omega-3 and omega-6 fatty acids. *ELOVL* genes play a critical role in the production of long chain fatty acids by providing fatty acid elongation. *ELOVL1* and *ELOVL6* genes influence liver fat storage by regulating cellular fatty acid balance. Additionally, transcription factors such as SREBP, PPAR, and ChREBP, which control liver fat synthesis, are also involved in regulating this process by managing the expression of enzymes responsible for fatty acid synthesis and storage. Moreover, insulin and glucose metabolism affect lipogenesis, further regulating liver fat accumulation. In conclusion, understanding the genetic mechanisms that influence liver fat synthesis in chickens is critical not only for healthy growth and development but also for nutritional efficiency and product quality.

Keywords: Fatty Acid Metabolism, Chicken Liver, *FADS*, *ELOVL*, Desaturation, Elongation

The *Bruchidius* Schilsky, 1905 (Coleoptera: Chrysomelidae: Bruchinae) Species and Their Host Plants detected in the Northeastern Anatolia Regio

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ABSTRACT: The Bruchinae (Coleoptera: Chrysomelidae) subfamily includes about 1700 species and known as seed beetles. The *Bruchidius* Schilsky, 1905 is one of the largest genera of the subfamily Bruchinae. So far 72 species of *Bruchidius* have been detected in Turkey. There is a good interaction between host plant and seed beetles. Most of them specialized to the Fabaceae family (%85). The Northeastern Anatolia Region is a rich region in terms of both cultivated plants and wild herb forms of the Fabaceae. In this study, thirteen species were detected in Northeastern Anatolia Region. The eight species were detected on flowers or seeds of Fabaceae plants which are as follows; *Bruchidius astragali* (Boheman, 1829), *Bruchidius lucifigus* (Boheman, 1833) on *Astragalus* L., *Bruchidius lutescens* (Blanchard, 1844) on *Onobrychis* L., *Bruchidius glycyrhizae* (Gyllenhal, 1839) on *Glycyrrhiza* L. *Bruchidius dilutus* (Motschulsky, 1874) on *Alhagi* Adans., *Bruchidius pusillus* (Germar, 1824) on *Securigera* DC., *Bruchidius quinqueguttatus* (Olivier, 1795) on *Vicia* L. and *Bruchidius villosus* (Fabricius, 1792) on *Genista* L.. *Bruchidius cinarescens* (Gyllenhal, 1833) collected from flowers of *Eryngium* L. (Apiaceae). Other species detected are *Bruchidius holosericeus* (Schoenherr, 1832), *Bruchidius monstrosicornis* (Pic, 1904), *Bruchidius mordelloides* (Baudi di Selve, 1886) and *Bruchidius talyshensis* Ter-Minassian, 1969.

Keywords: Bruchinae, *Bruchidius*, Northeastern Anatolia Region, Species diversity, Host plants

POSTER PRESENTATIONS

In Vitro and In Vivo Evaluation of Anti-Inflammatory Activity of *Eriobotrya Japonica* Leaves Aqueous Extract

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ABSTRACT: The objective of our study is to evaluate the anti-inflammatory effects of aqueous extract of *Eriobotrya japonica* leaves in vivo and in vitro, in Wistar rats and on RAW 264.7 macrophage cells, respectively. Diclofenac was used as a conventional anti-inflammatory treatment in vivo. The plant mixture was prepared with 1g of plant (50/50)/100 mL water. Oedema was induced with 1% carrageenan in Wistar rats after one hour of oral treatment. The thickness of the legs was measured every hour (for 6 hours). The anti-inflammatory potential was studied on lipopolysaccharide (LPS)-stimulated macrophages (RAW 264.7) by evaluating the effect of the extract on cellular viability and nitric oxide (NO) production. The concentration that inhibited NO production by 50% (IC50) was 345.25 ± 3.12 µg/ml. This result was confirmed in vivo where we observed a significantly reduction of the paw inflammation (Oedema thickness) after three hours of carrageenan induction. This reduction in oedema indicates that the EJ extract contains active compounds capable of modulating inflammatory processes by inhibiting prostaglandin synthesis. Furthermore, hematological results revealed that pretreatment with EJ extract helped normalize C-reactive protein (CRP) levels. In addition, the EJ extract contributed to maintaining oxidative homeostasis by preserving catalase levels, despite the induced inflammation.

Keywords: *Eriobotrya japonica*, Anti-inflammatory, Extract, Macrophages, Nitric Oxide, Carrageenan

Enhancing Potato Resistance to Late-Blight through Serendipita indica Colonization

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ABSTRACT: Potato (*Solanum tuberosum*) is one of the most important staple crops. Late-blight, caused by Phytophthora infestans (Pi), poses a significant threat to potato production, leading to substantial yield losses. In this research the impact of *Serendipita indica* colonization investigated on potato resistance to late-blight. The objective of this study was to investigate the effect of P. indica on Pi. Potato cultivars “Agria and Jelly” selected for the greenhouse studies. The use of S. indica was conducted concurrently with the planting of the tubers in the soil, while zoospore inoculation was performed on the aerial parts. The results showed that Pi infection was significantly reduced in both cultivars when potato roots were colonised with S. indica. This enhanced resistance is a consequence of the modulation of antioxidant and defense enzymes/genes in the host by S. indica. Notably, the activities of enzymes such as Ascorbate-Peroxidase, Peroxidase, PolyPhenol-Oxidase, Phenylalanine-Ammonia-Lyase and H_2O_2 content were markedly elevated in the Pi infection in the S. indica colonised plants in comparison to controls. Additionally, the inoculation of S. indica into the roots of the potato plants resulted in a modification of gene expression associated with defense mechanisms, including PAL, PPO, MAPK and WRKY. This leads to the rapid and efficient activation of potato defense mechanisms, which is comparable to the response observed in potato plants infected with Phytophthora. Overall, the findings suggest that the application of S. indica during potato cultivation represents a novel and effective strategy to enhance plant resistance and mitigate the impacts of Late-blight disease.

Keywords: Antioxidant Enzymes, Gene Expression, Potato, Phytophthora Infestans, *Serendipita Indica*, Sustainable Agriculture

FULLTEXT

ORAL PRESENTATIONS

Effects of Carboxymethyl Cellulose Applications on Soil Physical Properties and Plant Growth

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ABSTRACT: In this study, the effects of different doses (0 – 0,5 – 2 – 8gr) of carboxymethyl cellulose (CMC), a soil amendment hydrogel, on soil and plant properties were investigated. It was determined that CMC applications supported plant growth at the lowest application dose, but had a negative effect on the physical properties of the soil depending on the applied dose. In the applications where urea was added with CMC, the deterioration in soil physical properties was at a lower level. The findings show that low and medium doses of CMC + urea applications incr eased plant biomass, but high dose applications inhibited plant emergence. Especially in 8 g CMC and 8 g CMC + 0.10 g urea treatments, there was no plant growth in the pots. In terms of soil properties, CMC applications caused significant changes in water permeability, porosity, bulk density and soil aggregate stability. It was determined that CMC applications increased the water holding capacity of soils but decreased water permeability values because they reduced infiltration. Porosity measurement values decreased partially depending on CMC applications, but increased in CMC + urea applications. It was determined that soil aggregate stability values decreased continuously depending on the dose increase of CMC, but increased in CMC + urea applications at every dose compared to CMC only applications. Corn plant (Zea mays L.) was included in the experiment. In terms of plant characteristics; stem length, root collar width, stem/root wet and dry weights were evaluated. Compared to the control group, a (2 g) CMC applications, while a significant positive increase was detected in CMC + urea applications. In the 3rd dose (8 g) and 3rd dose + urea (8 g CMC and 0.1 g urea) treatments, since the soil permeability and soil aggregate stability values decreased significantly, the water added to the pots remained on the soil surface and evaporated after a while and the plant seeds could not survive in this non-leaking water and no plant emergence was observed.

Keywords: Carboxymethyl cellulose (CMC), Soil, Plant production, Soil physical properties, Urea

INTRODUCTION

The unique element required to meet the nutritional needs of societies is soil. Soil is indispensable for the nutrition of living beings and the continuation of human life. Soil fertility is of great importance in this context. The way to increase agricultural production is possible by increasing the amount of product to be obtained from a unit area in existing agricultural lands (Hacımüftüoğlu and Öztaş, 2017). Improving soil physical properties is very important in terms of plant cultivation and soil protection. In order for plants to develop well in the soil environment, the physical and chemical properties of the soil must also be in a good condition. This is also possible with additional inputs applied in today's conditions. In addition to soil conditioners in improving the physical properties of soils, fertilization techniques that increase the amount of organic matter in the soil traditionally come to the fore. These practices provide many benefits in terms of plant growth by positively affecting the soil coming to the pan and aggregate formation in the soil (Bender et al., 1998).

The use of hydrogels in agriculture has recently increased considerably. One of these hydrogels is sodium carboxymethyl cellulose. Sodium carboxymethyl cellulose (CMC) is a water soluble cellulose ether. It is produced by reacting sodium monochloro acetate with alkaline cellulose. CMC hydrogels cause high swelling potential (Elbarbary et al., 2017; Mali et al., 2018). CMC applications have a positive effect on the water holding capacity of soils (Nie et al., 2004; Akalin and Pulat, 2020). It allows the negative charges in the carboxymethyl group to interact with the cations of the soil solution, which improves plant water use and reduces plant stress conditions (Wang et al., 2023). CMC is a water soluble anionic polymer. Thanks to its densifier, binder, stabilizer, film-forming and gelling functions, CMC is used in various industries such as Food, Drilling, Mining, Construction, Paper, Detergent, Paint, Textile, Pharmaceuticals and Personal Care. In the food industry, Sodium Carboxymethyl Cellulose is often used as a thickener in ice cream, yogurt, beverages, desserts and baked goods. CMC is also found in cosmetics, some medicines, eye drops and toothpaste. CMC is an environmentally friendly and non-polluting hydrogel used in agricultural activities (Chen et al., 2017; Isobe et al., 2018). In terms of increasing the water holding capacity of soils in agricultural activities, it is seen that CMC applications at the ideal dose can have a beneficial effect. CMC, which is known to increase the water holding capacity of soils, has a very new usage area in agriculture. In this study, it was aimed to determine and record the positive or negative situations that may occur in soil and plant development with the use of CMC.

Materials and Methods

The experimental soil was obtained from Atatürk University Plant Production Center, prepared under appropriate conditions and transferred to the pots.

Carboxymethyl Cellulose

In the study, Carboxymethyl Cellulose (CMC) and CMC+urea were applied to the experimental soil. The structural content of CMC is given in Table 1 and the chemical scheme is given in Figure 1.

Table 1. Content of Carboxymethyl Cellulose (O. Kimya A.Ş., 2018)

Specification	Analysis
CMC content (Dry basis)	%60±2
pH (%1 solüsyon)	8-11
Viscosity (%2 Sol. Hoeppler 20C)	70-100
Moisture (packaged)	%10 max.
Appearance white color and cream, powder or granule form	

Methods

Soil physical, chemical and plant analyses and statistical evaluations were determined by the following methods.

Soil Analysis Methods

Soil Texture was determined by Bouyoucos hydrometer method (Gee and Bauder, 1986), Aggregate Stability was determined by Kemper method using Yoder type wet sieving device, Electrical Conductivity was determined by electrical conductivity device (Demiralay, 2013), Organic Matter content was determined by Smith-Weldon method, Soil Reaction (pH) was measured by pH meter with glass electrode at 1: 2.5% soil-water ratio was measured with a glass electrode pH meter (McLean, 1982), Lime content was determined volumetrically by Scheibler calcimeter (Nelson, 1982), Bulk Weight was determined by cylinder method (Demiralay, 2013), Porosity value was determined by using the volume weight and grain density values of the soils (Demiralay, 2013).

Plant Analyses

Plant height and stem diameter, plant wet and dry weight were determined according to the standard method (Kacar, 2014).

Statistical Evaluation

Duncan's multiple comparison test was performed between the data obtained in the studied soils (SPSS, 2011).

Setting up the Trial

Carboxymethyl Cellulose hydrogel to be used in the experiment was left to melt at 60 °C for 24 hours. The amount of soil to be used in the experiment was determined as 1000 g (<4 mm) per pot on weight basis. CMC was applied to the soil at 4 different doses (0 g-control; 0.5 g; 2 g; 8 g) in 3 replicates. In the second part of the experiment, 0.1 g urea was added to the CMC applications with 4 different doses to the soils with the same properties in 3 replicates.

Urea was not added to the control group, so the experiment was established with $4^{x}3 + 3^{x}3=21$ pots in total.

The experiment was conducted under laboratory conditions. Khan F1 variety sweet corn (*Zea mays* L.) was planted in the soil prepared for the experiment and then the soil was irrigated with pure water. The pots were watered with pure water at 2-4 day intervals during the experiment. The ambient temperature varied between 24 ± 2 °C during the experiment. The experiment was terminated after 50 days and the plants were loosened with water and separated from the soil with their roots. The plants were dried at 68 °C for 48 hours and then weighed to determine the dry matter content (Kacar, 2014). The appropriate amounts of soil separated from the pots were sieved through a 2 mm sieve and used for certain physical analyses.

Figure 1. Photograph of the establishment of the experiment

Figure 2. Photograph of the first irrigation process of the experiment

Findings and Discussıon

Standard soil was used during the research. Some physical and chemical properties of this soil are given in Table 2. The soil used in the research is classified as sandy loam texture class. The soil reaction is slightly alkaline and the amount of organic matter is 0.58%.

Table 2. Some physical and chemical properties of the soil and Carboxymethyl Cellulose used in the study

Property	**Soil**	**CMC**
Clay	53	-
Silt	35	-
Sand	12	-
Texture class	Sandy Loam	-
pH	7.71	9.5
Lime, %	4.77	-
Organic Matter, %	0.58	-
Moisture	2.67	10

Carboxymethyl Cellulose at different doses applied to the soil in the experiment was found to change the physical properties of the soil (Table 3).

Table 3. Effects of carboxymethyl cellulose application on soil physical properties

Soil	Volume Weight g/cm^3	Porosity	Water Permeability	Aggregate Stability
Control	1,63^a	37,67^d	5,35^a	37,67^a
Dose 1	1,62^{ab}	38,33^{cd}	2,89^{bc}	30,33^c
Dose 1 + Urea	1,58^{bcd}	40,0^{ab}	5,75^a	35,67^b
Dose 2	1,58^{bcd}	39,67^{abc}	2,54^c	22,67^e
Dose 2 + Urea	1,57^{cd}	40,00^{ab}	3,58^b	28,00^d
Dose 3	1,61^{abc}	38,6^{bcd}	1,16^d	15,33^g
Dose 3 + Urea	1,54^d	41,00^a	1,82^d	19,67^f

Water permeability and aggregate stability values were evaluated as follows;

Water Permeability

The effects of different doses of CMC and CMC + Urea combinations on soil water permeability were studied in the cultivation of sweet corn. Water permeability data helped us to understand how CMC and Urea treatments affect soil water permeability. Control Group (Water Permeability: 5.35 cm/s); 0.5 g CMC Treatment (Water Permeability: 2.89 cm/s); 0.5 g CMC + 0.10 g Urea Treatment (Water Permeability: 5.75 cm/s); 2 g CMC Treatment (Water Permeability: 2.54 cm/s); 2 g CMC + 0. 10 g Urea Application (Water Permeability: 3.58 cm/s); 8 g CMC Application (Water Permeability: 1.82 cm/s); 8 g CMC + 0.10 g Urea Application

(Water Permeability: 1.16 cm/s). Based on the investigations, the use of CMC in the cultivation of sweet corn significantly affected soil water permeability. In general, CMC applications reduced water permeability, which means that CMC increases soil water holding capacity. This makes plants more resistant to water stress. 0.5 g CMC + 0.10 g Urea treatment showed 7.48% higher water permeability compared to the control group. This indicates that while CMC increases the water holding capacity, the addition of urea balances this effect by partially increasing the water permeability. On the other hand, the 8 g CMC + 0.10 g Urea treatment had the lowest water permeability, indicating that high CMC doses significantly reduced soil water permeability. These findings are consistent with other studies in the literature. For example, CMC has been reported to increase soil water holding capacity in many studies. Similarly, the effects of nitrogen fertilizers such as urea on soil water holding capacity have been widely discussed in the literature. This study contributes to the literature by evaluating the effects of CMC and urea combinations together. Statistical calculations were made for a more detailed evaluation of the findings. The water permeability rates of the other groups compared to the control group are as follows (Table 4; Figure 3):

Table 4. Proportional changes of the experimental groups in terms of water permeability compared to the control group

0.5 gr CMC Application	%54.02
0.5 gr CMC + 0.10 gr Urea Application	%107.48
2 gr CMC Application	%47.48
2 gr CMC + 0.10 gr Urea Application	%66.92
8 gr CMC Application	%34.02
8 gr CMC + 0.10 gr Urea Application	%21.68

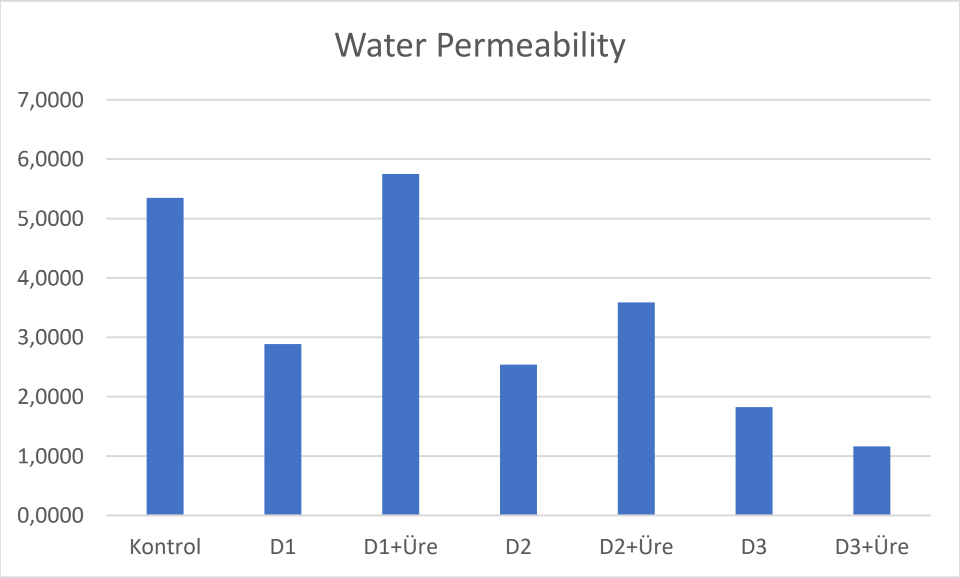

Figure 3. Water permeability values of soils depending on carboxymethyl cellulose application

These ratios clearly show the effect of applying CMC at different doses to reduce water permeability. Furthermore, the addition of urea increases water permeability and partially balances the effect of CMC. This emphasizes the importance of determining the optimal doses of CMC and urea combinations for water management and plant nutrition. CMC increases water holding capacity by reducing soil water permeability in sweet corn cultivation. The addition of urea partially offset this effect, but high doses of CMC significantly reduced water permeability.

Aggregate Stability

The effects of different doses of CMC and CMC + Urea combinations on soil aggregate stability were investigated in sweet corn cultivation. Aggregate stability data helped us to understand how CMC and Urea treatments affect soil structure. The findings were evaluated on the basis of the following groups. Groups; Control Group (Aggregate Stability: 37, 38, 38%), 0.5 g CMC Treatment (Aggregate Stability: 30, 31, 30%), 0.5 g CMC + 0.10 g Urea Treatment (Aggregate Stability: 37, 35, 35%), 2 g CMC Treatment (Aggregate Stability: 23, 22, 23%), 2 g CMC + 0. 10 g Urea Application (Aggregate Stability: 28, 30, 26%), 8 g CMC Application (Aggregate Stability: 20, 20, 19%), 8 g CMC + 0.10 g Urea Application (Aggregate Stability: 15, 16, 15%), as a result of the study. Aggregate stability is an important soil property that determines soil resistance to water and wind erosion. Compared to the control group, CMC treatments and CMC + Urea combinations affected soil aggregate stability at different rates. CMC and CMC + Urea treatments significantly affected soil aggregate stability. Compared to the control group, low doses (0.5 g) of CMC and CMC + Urea treatments decreased aggregate stability relatively less, while high doses (8 g) significantly decreased stability. This indicates that CMC may negatively affect soil structure depending on the dosage. These findings are partially consistent with other studies in the literature. Although the potential of CMC to improve soil structure is known, it has been reported in some studies that high doses of CMC applications may negatively affect soil aggregate stability. The potential of urea to improve soil structure and increase aggregate stability is supported in the literature. This study contributes to the literature by evaluating the effects of CMC and urea combinations on aggregate stability together.

The aggregate stability ratios of the other groups compared to the control group are as follows (Table 5; Figure 4):

Table 5. Proportional changes of the experimental groups in terms of aggregate stability compared to the control group

0.5 g CMC Application	%19.48 reduction
0.5 g CMC + 0.10 g Urea Application	%5.31 reduction
2 g CMC Application	%39.82 reduction
2 g CMC + 0.10 g Urea Application	%25.67 reduction
8 g CMC Application	%47.79 reduction
8 g CMC + 0.10 g Urea Application	%59.29 reduction

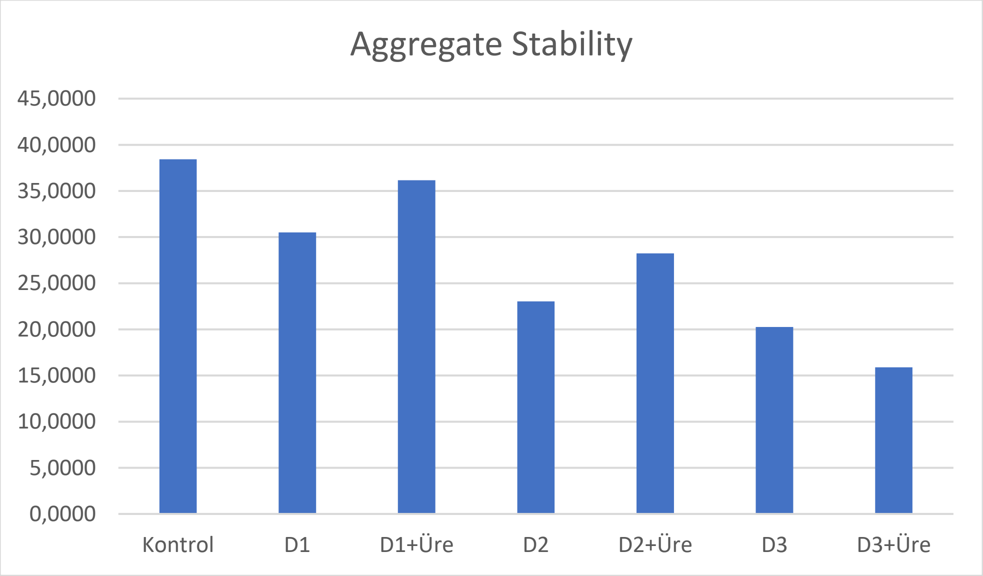

Figure 4. Aggregate stability values of soils depending on carboxymethyl cellulose application

These ratios clearly show how the application of CMC at different doses affects soil aggregate stability. The addition of urea partially reduces the negative effects of CMC, which is important for maintaining soil structure. Careful dosing of combinations of CMC and urea is critical to support soil stability and thus plant growth. CMC is an important factor affecting soil aggregate stability in sweet corn cultivation. At low doses, combinations of CMC and urea have the potential to maintain soil structure and promote plant growth, while at high doses, applications can negatively affect soil stability. These findings provide important information to understand the potential benefits and risks of CMC and urea combinations in agricultural production.

Effects of Carboxymethyl Cellulose on Plant Properties of Soil

As a result of the experiment, dry and wet weights of the plants, plant height and root collar width were investigated. The data obtained as a result of the research are given in Table 8.

Table 6. Effects of Carboxymethyl Cellulose on plant characteristics

Dose Amount	Stem Length	Root Collar Width	Stem Wet Weight	Root Wet Weight	Stem Dry Weight	Root Dry Weight
Control	47	0,44	1,80	0,25	0,18	0,09
0,5 gr CMC	38	0,28	1,32	0,1	0,12	0,03
0,5 gr CMC + Urea	60	0,55	3,76	0,65	0,32	0,13
2 gr CMC	43	0,26	1,23	0,19	0,10	0,03
2 gr CMC + Urea	52	0,40	2,67	0,54	0,24	0,16
8 gr CMC	0	0	0	0	0	0
8 gr CMC + Urea	0	0	0	0	0	0

Among the parameters, stem length, root collar width and root wet weights were evaluated as follows;

Stem Length

Stem length is an indicator of plant growth and health. Compared to the control group, CMC treatments and CMC + Urea combinations affected plant stem length at different rates. CMC and CMC + Urea treatments significantly affected plant stem length. Compared to the control group, CMC application at low dose (0.5 g) decreased stem length, but CMC + Urea application at the same dose increased stem length. Medium dose (2 g) CMC application slightly decreased stem length, while CMC + Urea application at the same dose increased stem length. High dose (8 g) CMC application completely prevented plant emergence (Table 6; Figure 5).

These findings are consistent with other studies in the literature. Although the potential of CMC to improve plant growth is known, some studies have reported that high doses of CMC may negatively affect plant growth and even prevent plant emergence. The potential of urea to promote plant growth is supported in the literature. This study contributes to the literature by evaluating the effects of CMC and urea combinations on plant stem length.

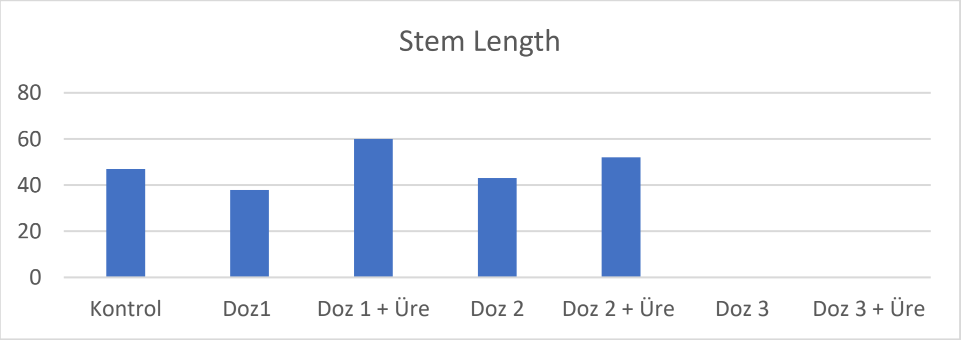

Figure 5. Stem length values of plants depending on carboxymethyl cellulose treatment

These ratios clearly show how the application of CMC at different doses affects plant stem length. The addition of urea partially reduces the negative effects of CMC, which is important for plant growth. Careful dosing of combinations of CMC and urea is critical to promote plant growth. CMC is an important factor affecting plant stem length in sweet corn cultivation. Combinations of CMC and urea at low doses have the potential to promote plant growth, while applications at high doses can completely inhibit plant emergence. These findings provide important information to understand the potential benefits and risks of CMC and urea combinations in agricultural production.

Root collar width

Root collar width is a critical parameter to assess the development and health of the plant root system. Compared to the control group, CMC and CMC + Urea treatments affected plant root collar width at different rates. CMC and CMC + Urea treatments caused significant differences on root collar width. Compared to the control group, CMC application at low dose (0.5 g) decreased the root collar width, but CMC + Urea application at the same dose increased the root collar width. Medium dose (2 g) of CMC further decreased the root collar width, while CMC + Urea at the same dose kept the root collar width close to the control group. High dose (8 g) CMC application completely prevented plant emergence (Table 6; Figure 6). These findings are consistent with other studies in the literature. Although the potential of CMC to improve plant root growth and general health is known, some studies have reported that high doses of CMC may negatively affect plant growth and even prevent plant emergence. The potential of urea to promote plant growth is supported in the literature. This study contributes to the literature by evaluating the effects of CMC and urea combinations on plant root collar width.

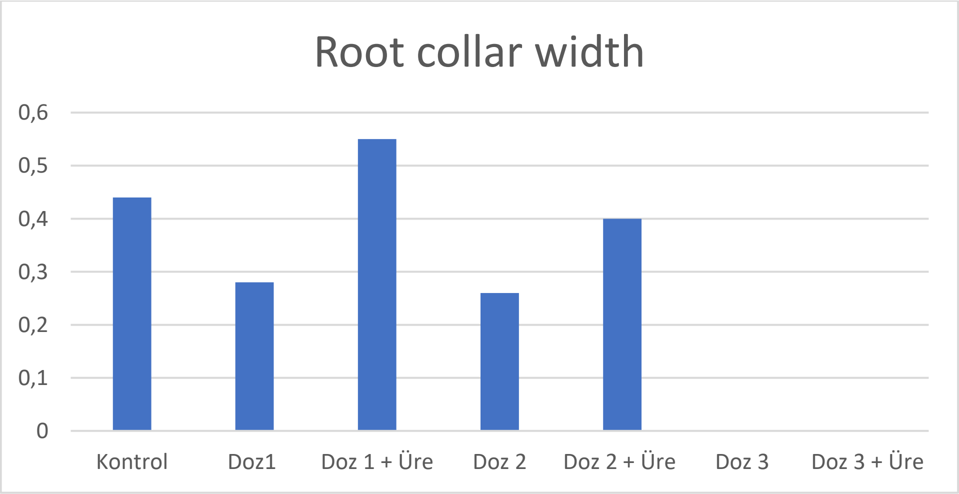

Figure 6. Root collar width values of plants depending on carboxymethyl cellulose treatment

These ratios clearly show how the application of CMC at different doses affects plant root collar width. The addition of urea partially reduces the negative effects of CMC, which is important for plant development. Careful dosing of combinations of CMC and urea is critical to promote plant root development. CMC is an important factor affecting root collar width in sweet corn cultivation. At low doses, combinations of CMC and urea have the potential to promote plant root development, while at high doses, applications can completely inhibit plant emergence. These findings provide important information to understand the potential benefits and risks of CMC and urea combinations in agricultural production.

Root Dry Weight

Root dry weight provides critical information on plant biomass and growth performance. Compared to the control group, CMC and CMC + Urea treatments affected root dry weight at different rates.

CMC and CMC + Urea treatments caused significant differences on root dry weight. Compared to the control group, low dose (0.5 g) CMC treatment decreased root dry weight, but CMC + Urea treatment at the same dose significantly increased root dry weight. Medium dose (2 g) CMC application further decreased root dry weight, while CMC + Urea application at the same dose increased root dry weight. High dose (8 g) CMC application completely prevented plant emergence (Table 6; Figure 7).

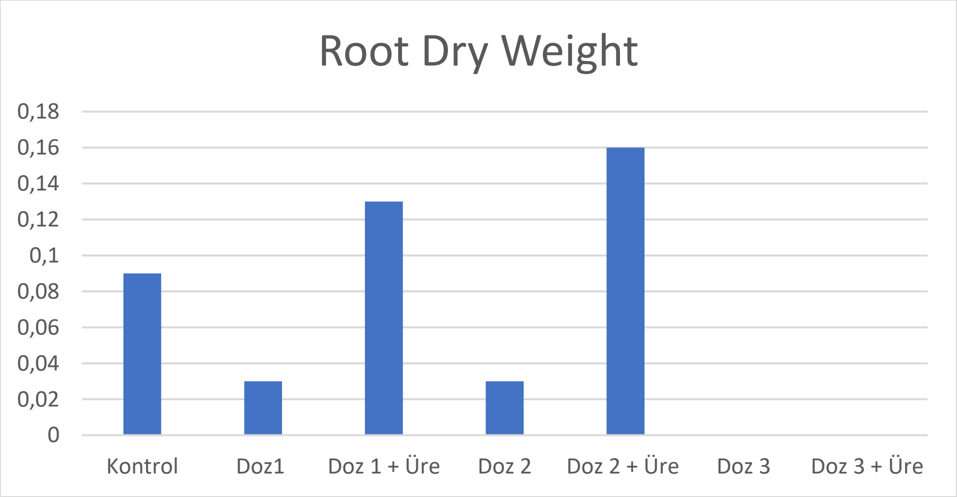

Figure 7. Root dry weight values of plants depending on carboxymethyl cellulose treatment

These ratios clearly show how different doses of CMC affect plant root dry weight. The addition of urea partially mitigates the negative effects of CMC, which is important for plant development. Applying combinations of CMC and urea at careful dosages is critical to support plant biomass. These findings are in agreement with other studies in the literature. Although the potential of CMC to increase plant biomass is known, some studies have reported that high doses of CMC can negatively affect plant growth and even prevent plant emergence. The potential of urea to promote plant growth is supported in the literature. This study contributes to the literature by evaluating the effects of CMC and urea combinations on plant root dry weight. In conclusion, CMC is an important factor affecting root dry weight in sweet corn cultivation. At low doses, combinations of CMC and urea have the potential to increase plant biomass, while at high doses, treatments can completely inhibit plant emergence. These findings provide important information to understand the potential benefits and risks of CMC and urea combinations in agricultural production.

Conclusion

As a result, although the use of CMC in agricultural production is thought to be an important advantage and is commercially available in the market, the findings and results of this study show that while CMC has a positive effect on plant growth at very low doses, the use of CMC at medium and high doses adversely affects plant growth by deteriorating the physical properties of soils.

Although the highest dose used in the study, 8 g, was less than 1%, it was determined that it could cause rotting of plant roots by forming a completely impermeable layer on the soil surface. This decline in soil physical properties could be partially improved with the optimum dose of urea added to the soil. The results of the study showed that the use of CMC should be controlled and high doses should be avoided for sustainable agricultural activities.

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Exposure to Acute Changes in Temperature Results in Transient Oxidative Stress and Changes in Antioxidant Enzyme Genes Expression in Fish

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ABSTRACT: Fish are an integral part of aquatic ecosystems and play important ecological, economic, and cultural roles worldwide. Climate change is known to impact aquatic environments, including changes in water temperature that can adversely affect fish populations. It is well established that fish are ectothermic organisms that are sensitive to temperature changes, and it is critical to understand how they respond to these changes at the molecular level. In this article, we explore the impact of acute increases in temperature on oxidative stress and changes in antioxidant enzyme gene expression in fish. This research sheds light on how fish respond to temperature changes, providing insight into the potential consequences of climate change on fish populations.

Keywords: Antioxidant Enzyme, Gene Expression, Fish, Water Temperature

INTRODUCTION

Oxidative stress is a state in which the production of reactive oxygen species (ROS) exceeds the antioxidant capacity of an organism. ROS can cause damage to DNA, lipids, and proteins, leading to cellular dysfunction and tissue damage (Castro et al., 2020). Fish are particularly susceptible to oxidative stress because they have a high metabolic rate and are exposed to a variety of environmental stressors (Wiens et al., 2017).

Antioxidant enzymes are enzymes that help protect cells from oxidative damage by neutralizing ROS. Fish have a variety of antioxidant enzymes, including superoxide dismutase (SOD), catalase (CAT), and glutathione peroxidase (GPx). These enzymes are key components of the fish oxidative defense system (Lisser et al., 2017).

To identify antioxidant enzyme genes in fish, researchers can use a variety of molecular biology techniques, including polymerase chain reaction and gene sequencing. These methods can help researchers identify and analyze the expression of specific genes involved in fish oxidative stress responses.

Fish are ectothermic, meaning their body temperature is largely determined by their surrounding environment (Anlauf-Dunn et al., 2022). Therefore, temperature changes can have a significant impact on their physiology and over all health. With global temperature trends on the rise, it is imperative to understand how fish respond to these changes. This can help us predict and mitigate potential negative impacts on fish populations and the ecosystems they inhabit. There is a growing body of research on the effects of temperature changes on fish (Clark et al., 2013). However, much of this research has focused on chronic temperature changes rather than acute changes, which occur rapidly over a short period of time (Pörtner and Farrell, 2008; Clark et al., 2013; Biro and Stamps, 2015; Farrell, 2016). Additionally, there are much studie sof the specific molecular mechanisms underlying fish responses to acute temperature changes (Biro and Stamps, 2015; Fernandes et al., 2013; Santos et al., 2015).

Metabolic and Moleculer Responses of Fish to Extreme Temperature of Water

Aquaculture fish are sensitive to changes in environmental temperature caused by climate change. Climate change-induced extreme temperature events can have a variety of negative impacts on aquaculture fish, including changes in physiological processes, reduced reproductive success, and increased mortalities. Adaptation strategies are needed to mitigate these impacts and ensure the sustainability of aquaculture production. Ectothermic organisms experience an increase in metabolic rate of two to three times for every 10°C rise in water temperature. However, it is important to note that the magnitude of these changes is not consistent across every 10°C change, as there is typically a decrease in metabolic rate at higher temperatures. As a result, enzymatic reactions, cellular respiration, and metabolic rates exhibit variations with temperature (Islam et al., 2021).

There are much studies which have investigated the effects of temperatures on the molecular and metabolic stress responses in fish species. This review aims to provide a summary of the impact of extreme ambient temperatures on these stress responses and how they influence antioxidant enzyme genes epreesion in fish.

Analyzing the antioxidant system biochemically and molecularly in fish organs like gills and liver provides valuable insights into the alterations occurring in the aquatic environment. This approach serves as a reliable indicator of environmental changes. In a study by Ozdemir and Bayır (2022), the expression levels of sod1 gene were examined in various tissues of brown trout (*Salmo trutta*), with a specific emphasis on the liver and gills, under stress conditions. The results indicate that the mRNA levels of sod1 in the tissues of brown trout exposed to stressors can serve as a valuable biomarker for oxidative stress. When fish are exposed to different stress factors, the production of ROS is triggered, leading to the creation of a harmful environment for aquatic species.

Studies have shown that acute temperature changes can result in oxidative stress in fish. One possible mechanism is through the activation of heat shock proteins, which can lead to the production of ROS. Increased metabolism and respiration rates at higher temperatures can also contribute to oxidative stress. However, the specific pathways involved in this process are not well understood.

In some studies, researchers exposed fish to acute temperature increases and analyzed the resulting changes in oxidative stress and antioxidant enzyme gene expression. The fish were exposed to a range of temperatures for a short period of time and then sampled for analysis. The molecular response of fish to acute temperature changes in water can involve a variety of physiological and behavioral changes. Here are some findings from the provided search results: Acute thermal stress induces a significant antioxidant response in fish, as demonstrated by several studies. In a study conducted by Madeira et al. (2016), it was found that gilthead seabream (*Sparus aurata*) exposed to temperatures exceeding 24°C for a duration of 48 hours exhibited increased activities of superoxide dismutase (SOD), glutathione-S-transferase (GST), catalase (CAT), lipid peroxidation (LPO), and cytochrome (CYP1A). Similarly, Kyprianou et al. (2010) found increased antioxidant enzymatic activities, including SOD, GST, CAT, and lipid peroxidation, in the same fish species when exposed to temperatures below 14°C for 10 days, indicating a stressful condition. The objective of the study which conducted by Kang et al., 2018 was to assess the health status of Atlantic salmon (Salmo salar) fry under elevated water temperatures (20°C) compared to optimal water temperature (15°C). The researchers employed NGS RNAseq analysis to detect biomarker genes and evaluate their expression patterns using RT-qPCR analysis. The biomarker genes included interferon alpha-inducible protein 27-like protein 2A transcript variant X3, protein L-Myc-1b-like, placenta growth factor-like transcript variant X1, fibroblast growth factor receptor-like 1 transcript variant X1, transferrin, intelectin, thioredoxin-like, c-type lectin lectoxin-Thr1-like, ladderlectin-like, and calponin-1. The results from NGS RNAseq analysis indicated that these selected biomarker genes were sensitive to changes in water temperature. In another study, Clotfelter et al. (2013) observed a significant increase in glutathione (GSH), glutathione reductase (GR), CAT, and GST in snakehead (*Channa punctata*) exposed to 32°C for 3 hours, further highlighting the antioxidant response to thermal stress.

The antioxidant response is not limited to acute stress but also occurs during chronic exposure to temperature stress. Madeira et al. (2013) and Vinagre et al. (2012) studied European seabass (*Dicentrarchus labrax*) and white seabream (*Diplodus sargus*) exposed to both high temperatures (28, 32, and 33.3°C) and low (12–18°C) for a long trial time (14 days). The study revealed increased levels of GST, CAT, LPO, and malondialdehyde (MDA) activities in fish exposed to elevated temperatures compared to those maintained at 24°C. Similarly, Islam et al. (2021, 2021b) and Islam, Kunzmann, Bögner, et al. (2020) reported significantly increased antioxidant responses in the same fish species at temperatures below 8°C and above 32°C compared to 16°C. In medaka (*Oryzias melastigma*), Almeida et al. (2015) observed elevated activities of glutathione peroxidase (GPx), CAT, SOD, GR, and LPO in fish exposed to 25°C for 3 weeks compared to those at 18°C. Carney Almroth et al. (2019) investigated Atlantic halibut (*Hippoglossus hippoglossus*) and found increased antioxidant activities and protein carbonyl (PC) activities in fish exposed to 5°C compared to those at 18°C during a 96-day.

To summarize, various fish species demonstrate an increased antioxidant response when subjected to acute or chronic thermal stress, as evidenced by changes in enzymatic activities and oxidative stress markers such as lipid peroxidation and protein carbonylation.thermal exposure study.

Results and Discussion

While selective breeding for disease resistance in fish is a valuable approach to prevent diseases, the biological mechanisms underlying stress response and disease resistance are not yet well-defined. Extensive research is still needed to fully comprehend the genetic basis and control of these pathways. This particular study contributes to our current understanding of stress response pathways in fish. The findings not only reveal the structure and conservation of antioxidant enzyme genes in fish but also demonstrate how specific aquaculture stressors can impact the expression of these genes in multiple tissues. These effects are likely associated with oxidative stress.

The studies mentioned above have highlighted the molecular and metabolic stress responses in fish when exposed to thermal stress. These responses have implications for crucial aspects of fish biology, such as growth, immunity, and disease resistance. With future climate scenarios predicting more frequent and intense temperature events, these metabolic and molecular impairments become a significant concern for the aquaculture industry.

However, it is important to note that there are numerous variables that can influence the extent of these responses in fish. Additionally, there can be significant intra- and interspecific variations in how different fish species respond to thermal stress. These factors make it challenging to establish a definitive limit for metabolic and molecular responses that would optimize growth and disease resistance in fish.

In summary, the complexity of fish responses to thermal stress, combined with the variability among species, poses a significant challenge in generalizing the findings. Determining the precise threshold for metabolic and molecular responses that would ensure optimal growth and disease resistance capabilities in fish remains a difficult task.

Conclusion

In conclusion, while selective breeding for disease resistance in fish is a valuable approach to prevent diseases, the biological mechanisms underlying stress response and disease resistance are not yet well-defined. Extensive research is still needed to fully comprehend the genetic basis and control of these pathways. The studies mentioned above have highlighted the molecular and metabolic stress responses in fish when exposed to thermal stress. These responses have implications for crucial aspects of fish biology, such as growth, immunity, and disease resistance. With future climate scenarios predicting more frequent and intense temperature events, these metabolic and molecular impairments become a significant concern for the aquaculture industry. However, it is important to note that there are numerous variables that can influence the extent of these responses in fish. Additionally, there can be significant intra- and interspecific variations in how different fish species respond to thermal stress. These factors make it challenging to establish a definitive limit for metabolic and molecular responses that would optimize growth and disease resistance in fish. The complexity of fish responses to thermal stress, combined with the variability among species, poses a significant challenge in generalizing the findings. Determining the precise threshold for metabolic and molecular responses that would ensure optimal growth and disease resistance capabilities in fish remains a difficult task.

Funding

The research did not receive any funding or financial support.

Statement of Conflict of Interest

The authors declare that they are no conflict of interest

Authors' Contributions

MB, ST, BNU, and GA designed the research, and worked on the preparation of this article. All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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Organic Forage Farming

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ABSTRACT: In conditions of deepening ecological crisis, the need for environmentally friendly food products of animal origin is increasing. The production of such food can be provided by organic feed production, which is a strong unifying bond between plant growers and animal husbandry. Organic feed production is not only the production of safe feed as raw material, but also the production of ecologically safe feed. The lands where feed is grown play an enormous nature conservation balancing role in agricultural areas, protecting soils from erosion and water resources from pollution. In the lands where feed is grown, especially in meadows, a network of flora and fauna care, wildlife conservation areas, hunting and animal husbandry is generated.

Keywords: Organic farming, Forage, Feed

INTRODUCTION

The aim of organic production is to conserve the natural resources of the soil, to ensure organic food production, to raise the living standards of producers, to establish constructive relationships between production and the natural ecosystem as well as quality food production; to reduce and/or prevent and control soil erosion and increase its fertility; to reduce all types of pollution occurring in the production process; to maintain genetic diversity within the production system through the protection of crops and natural habitats and to influence the social and ecological impact of farmers (Golijan et al., 2017). The basic principles of organic production are focussed on the production of high quality food that contributes to the protection of the health and welfare of animals and humans as a preventive measure. Furthermore, there is an emphasis on the importance of providing animals with opportunities to exhibit their natural behaviour, receive feed appropriate to their physiology and live in a natural environment (Lund, 2006). It is important that the animals are fed organic crops produced on the farm itself or on neighbouring organic farms and that the animals have access to open air or grazing areas as much as possible. Forage crop production has a very important role in organic farms, is essential for livestock production based on organic system methods and is functional for the ecological and economic sustainability of farms (Golijan et al., 2017).

Organic farming is based on principles aimed at maintaining or improving the biological activity of soils. More diverse crop rotations are used and synthetic fertilisers and pesticides are prohibited. In this way, plant availability of nutrients in organically managed soils is more dependent on natural ecosystem processes (Lynch, 2014). In recent years, organic farming has become widespread, developed and now represents an important part of agriculture. Initially, organic farming was an ideological concept of alternative culture, in contrast to existing models of economic development and social organisation. Today, organic farming has become an established production system that attracts both human and financial resources, is profitable and meets the demands of a rapidly growing market (Doyle and Topp, 2004).

The organic food market is growing. Recently, increasing problems with animal product safety are, at least temporarily, pushing consumers in developed countries to buy more organic food. Organic milk and processed organic milk have higher market shares compared to organic meat. Organic milk production has gained importance in Europe, for example. The European Union has introduced regulations to standardise organic production in all member states. The market for organic products is constantly increasing, but has not yet reached market stability. The high prices of organic products keep farms marginalised. In many cases, the market is still encouraging because the limiting factor is still the availability of organic products (Rosati and Aumaitre, 2004).

In high latitudes the grazing season is short and dairy farmers have to feed their cows indoors for up to 8-9 months, resulting in a high dependence on preserved forage crops and concentrates. These limitations lead to higher input costs compared to pasture-based systems and the need for a trend towards high input-output dairy production systems, also for organic farmers. Such strategies require high digestibility feeds and a fairly high proportion of concentrates in the diet. In organic dairy farming, feed efficiency is lower, purchased feeds are more expensive and organic standards restrict the level of concentrate in the diet compared to non-organic systems (Flaten et al., 2019).

Effects of Organic Farming on Soil Fertility and Quality

Soil is recognised as a living system that converts nutrients into plant-available forms, rather than as a medium for nutrient uptake by the plant. Soil fertility in organic farming systems is largely managed through efficient on-farm cycling of nutrients and cropping systems that include legumes in rotation (Woodley et al., 2014).

In organic cropping systems, green manures should be grown as part of the crop rotation to enrich the soil with nitrogen (N). In integrated crop-livestock systems, plant, animal and soil productivity depends on a number of factors such as plant nutrient composition, developmental stage, morphology, biomass production, herbivore species, age and physiological condition and most importantly grazing intensity (de Faccio Carvalho et al., 2010). Therefore, when designing integrated crop-livestock systems, the selection of compatible ruminant and plant species that can adapt to local soil and climatic conditions should take precedence over other considerations. Most of the nutrients digested by ruminants (i.e. N, P, K) are returned to the soil in faeces, but the amount of nutrients retained and returned is directly influenced by plant nutrient composition. Therefore, the subsequent crop response to grazing is mainly a function of the productivity and nutrient composition of the green manure species. In general, the N present in plant material can be divided in faecal output into ruminant-metabolisable N (3-15%) and plant-available N (85-95%), but there are significant differences in N, P and K cycles depending on the system and region. Phosphorus deficiency in organic systems is well documented. Animal integration in organic systems has been proposed as a way to recycle P from plant material to the rumen and back to the soil in plant-available forms. Studies on faecal matter decomposition have shown that grazing increases plant-available soil inorganic P. Animal ingested plant material contains less inorganic P than faecal material and plant uptake of P from faeces can be as effective as synthetic P fertilisers. Potassium in organic systems is also a limiting nutrient and plant demand for K increases with the increasing availability of N. Most K is excreted in the urine and little is known about the transformation of K in urine particles. In grazed grasslands, productivity and uptake of K by plants are increased around urinary sites with high K concentrations (Cicek et al., 2014).

With the ban on soluble synthetic P fertilisers, the management of soil P fertility poses a challenge in organic crop production systems. Soil N inputs can be replenished by the natural process of biological N2 fixation by legumes, while P removed from the farm by crops must eventually be added by soil amendments. Phosphorus in organic systems is usually recycled through the application of organic matter such as compost, green manure and animal manure. Inorganic P-rich sources such as ground and chemically untreated phosphate rock can also be applied; however, P in these sources tends to remain largely insoluble, especially in the neutral to slightly alkaline soil pH range common in many calcareous agricultural soils (Schneider et al., 2016).

Improving soil quality is one of the key objectives of sustainable crop production given the agricultural benefits such as increased soil moisture retention, improved soil fertility, improved crop yields and yield stability, as well as potential global climate benefits from increased soil carbon (C) sequestration (Powlson et al., 2011). In organic farming systems, integrating perennial forage crops into the crop rotation has the potential not only to improve soil quality but also to increase soil fertility, reduce weed pressure and reduce pests for subsequent crops compared to crop rotations with annual crops (Inwood et al., 2015).

To promote conservation tillage in organic farming systems, weed control and field weeding should be optimised in field-to-field rotation (Krauss et al., 2010).

For many producers in the most developed countries of the world, obtaining the most environmentally friendly agricultural products is becoming an urgent task. One of the most effective solutions is the widespread use of occupied fallows, planting green manure crops and sowing green manures after the main crop, burying the plant mass mainly in the soil, improving its agrochemical indicators (the content of nitrogen, humus, microelements, structure). This use of plants in this way has the following effects: 1) simultaneously with the germination of the sown crop, weed seeds also germinate, which are destroyed together with green manure and subsequently cannot harm the main crop; 2) sowing green manure crops immediately after harvesting one of the main crops prevents the soil from drying out and protects the soil from erosion; 3) many green manure crops cause activation of insect pests and pathogens that die when green manures are buried in the soil, and the soil improves; 4) when cereals are sown, the top layer of the soil is loosened and its structure improves, the water-holding capacity of the soil increases; 5) when legumes are sown, deeper soil layers are loosened, and most importantly, nitrogen is bound and stored for the next year; 6) the use of cruciferous plants provides suppression of seedlings of many weeds, and the roots also perfectly loosen the soil (Kostenko et al., 2021).

When growing most crops, the focus is on: 1) Productivity of the variety, its resistance to the main diseases and pests. 2) Its resistance to abiotic factors (lack of moisture, low temperature, high temperature, soil acidity, etc.) 3) Content of useful substances (protein, fats, certain amino acids). 4) Absence of harmful substances (hydrocyanic acid, glucosinolates, alkaloids, etc.) 5) Varieties intended for green manure do not have hard-shelled impermeable seeds. The germination of such seeds in the second and subsequent years will have highly undesirable consequences for crops grown in organic farming, because it is not possible to use the pesticides that would be required in this case. This is particularly important for legumes, because their seeds can remain in the soil for up to 10-15 years without germination. For example, this phenomenon occurs in clover and sweet clover. 6) For green manure varieties, the rapid formation of the root system in the surface layer of the soil is more important than the penetration of individual roots to a greater depth. Compared to conventional organic fertiliser application, green manure requires much lower costs; sowing 10-50 kg of seeds per hectare is much cheaper than transporting and spreading tens of tonnes of manure or peat (Kostenko et al., 2021).

Animal Welfare in Organic Farming, Animal Nutrition and Its Effects on Animal Health

There is a growing interest in animal health and welfare worldwide (Rosati and Aumaitre, 2004). Increased consumer awareness of food safety issues and environmental concerns over the last few years has contributed to the growth of organic livestock farming. Feeding strategies to meet organic standard requirements (EU Rule no. 1804/1999) is one of the solution efforts in organic livestock production (Marino et al., 2006). The organic livestock production guidelines (EU Regulations 2092/91 and 1804/99) recommend that the daily feed intake (pasture, hay and silage) for cattle should be at least 60% and concentrates should not constitute more than 40% of the diet. While hay production with organic farming practices does not pose a particular problem when forage legumes are used, concentrate and silage production with grain cereals is much more difficult because the absence of chemical fertilisers and herbicides significantly reduces their yield. In particular, the feed yield of winter cereals is less affected than maize, because winter cereals require less nutrient inputs, are more competitive against weeds and can often be grown without irrigation (Mariotti et al., 2006).

Annual forage crops also have the potential to be economically valuable intermediate or intermediate crops in organic rotations, can play a role in weed management, and can provide increased flexibility in management decisions in an organic crop rotation using cover crops. The USDA-National Organic Programme rule is that 30% of ruminant dry matter intake should come from grazing during the grazing season (a period of at least 120 days, determined by site conditions and regional climate) (USDA-AMS, 2014).

Organic farming management does not automatically reduce the health risk for farmed animals. It is difficult to make precise comparisons between conventional and organic farming, because in both cases there are difficulties in defining the type of prevention and treatment to be used and the complexity of classifying the level of disease. Organic farming does not protect dairy cows from mastitis. One of the biggest problems in animal nutrition in organic dairy farming is protein, mineral and trace element deficiencies, especially for animals reaching high production. Limits on the use of concentrates in the feed ration reduce milk production levels. The quality of dairy products has not changed in European dairy farming with the implementation of organic regulations. More ‘natural’ milk management on organic farms is considered to improve animal welfare and animal health. The use of more pasture compared to the more intensive dairy system for conventional herds certainly improves animal welfare, but animal health is not always improved due to the limited use of pesticides in organic systems. Organic farming systems are more ‘environmentally friendly’ than conventional management, especially due to the lower eutrophication potential of organic herds. However, in organic production, the same amount of milk is obtained by utilising a larger area of pasture than in conventional (Rosati and Aumaitre, 2004).

Forage Crops in Organic Farming

Ecological parallels between forage crops and natural vegetation make it easier to utilise natural processes to perform agricultural services (Ann Clark, 2009). The production of organic beef is considered problematic in marginal areas where cereal production is difficult and organic cereals are expensive. Moreover, maximising grazing as recommended in the organic system can be difficult in areas with low summer rainfall and poor pasture quality (Marino et al., 2006).

Organic farming should be self-sufficient in nitrogen, as the use of mineral nitrogen fertilisers is excluded. The cornerstone of soil fertility in organic farming is the use of legumes to fix atmospheric N2. In organic farming, the entire crop rotation process is highly dependent on the performance of forage legume crops (Pietsch et al., 2007). Alfalfa (Medicago sativa L.) can play an important role in organic crop-livestock systems due to its low input, suitability for rainfall-dependent conditions, positive effects on soil fertility and nitrogen balance, and the high protein content and quality of its forage. Moreover, alfalfa cultivation can improve the energy balance and thus the sustainability of organic systems. However, there is a lack of information on different variety recommendations for organic and conventional systems and their actual performance in organic farming is unknown (Annicchiarico and Pecetti, 2010).

Similarly, specific breeding programmes for organic systems are very rare for alfalfa or other forage crops. Adaptation specific to organic farming may result from differences between varieties in traits such as competitiveness against weeds, tolerance to major biotic stresses or nutrient utilisation efficiency. Research on cereal crops provides inconsistent evidence of adaptation specific to organic systems. Although older varieties show greater competitive ability, they may not outperform modern varieties in organic farming due to their lower yield potential. A study on forage crops revealed that the variety × production system interaction in Lolium spp. is mainly related to the ploidy level. This is due to the tendency of tetraploid varieties to respond relatively better under organic management (Boller et al., 2008). It is not known whether the unconventional semi-erect or semi-recumbent alfalfa germplasm recently developed for improved grazing tolerance has better competitive ability against weeds than modern conventional germplasm. Furthermore, seed production may be an issue for organic alfalfa growers in the perspective of higher seed price compared to conventionally produced seeds and mandatory adoption of organically produced seeds in organic systems (Annicchiarico and Pecetti, 2010).

Livestock and legume species are essential elements of organic farming systems because agronomic use of manure and biological nitrogen fixation are essential for providing nutrients to crops (Doyle and Topp, 2004).

Among perennial species that are widely used in forage systems in the southeastern USA and can be integrated into organic production systems for grazing or mechanical harvesting, alfalfa is associated with high forage quality, long production season and drought tolerance, and high protein production per land area. For organic producers, its high biological N fixation rate makes alfalfa a useful rotation crop for systems (Inwood et al., 2015).

Changing from a conventional livestock production system based on fertilised herbaceous crops to an organic management system requires the establishment of legume-based crops to replace purchased fertiliser nitrogen. Experimental results from trials conducted at a wide range of locations in Europe indicate that potentially red clover (Trifolium pratense) and to a lesser extent white clover (Trifolium repens) and alfalfa (Medicago sativa) can produce higher profits per hectare than grass-based systems using high levels of nitrogen fertiliser. Galega (Galega orientalis) and lotus (Lotus corniculatus) can, under certain conditions, compete economically with fertilised grass lawns, but they are generally not the first choice forage legumes. From an economic point of view, forage legumes are probably best grown in mixtures with grass (Doyle and Topp, 2004).

Intercropping

Increasing crop diversity and growing legumes is increasingly recognised as an important lever for sustainable agro-ecological development. This is the basis of organic farms. On a farm without livestock, the choice of crop species is small and the use of forage legumes is limited. In many subsistence or low input/resource limited farming systems intercropping is important

(Brooker et al., 2015). Intercropping, the simultaneous cultivation of multiple crop species or genotypes in the same field, is a practical application of basic ecological principles. Intercropping effects consist of competition (niche differentiation, resource sharing and weed control), diversity (insect and disease control), facilitation (physical support, nitrogen fixation and removal of allelochemicals and modification of the rhizosphere) and associated diversity (habitats for natural predators, waste diversity and improved soil microbial diversity) (Hauggaard-Nielsen et al., 2008).

Strip, mixed and relay intercropping can be used to increase crop yields through resource sharing and facilitation. Relay intercropping involves staggered planting of two or more crops such that only part of their life cycles overlap. Farmers often sow forage legumes to winter or spring cereals as a way of increasing crop diversity and augmenting the variable nitrogen reserve. This cropping system works particularly well due to the different phenologies of the two crops, which minimises light competition and differences in nutrient acquisition (Wanic et al., 2016).

Mixed cropping can enable better utilisation of subsoil resources and thus reduce the need for inputs and help prevent nutrient losses. Moreover, one crop can provide resources to another, with a favourable interspecific interaction underlying facilitation processes. Cropping systems improve soil temperature and moisture regulation; erosion, nutrient runoff and leaching are reduced; weeds are controlled, insect and disease development cycles are interrupted, and soil organic matter content is improved by making recycled nutrients available to subsequent crops (Arlauskiene et al., 2019).

In this cropping system, there is competition between plants. It is one of the many ecological processes that shape the composition, dynamics and productivity of the plant community. Mainly, plants compete for soil resources and light. These interactions influence plant density and plant growth rhythm, productivity and reproduction. Plant competition in cereal-legume intercropping systems in spring can be regulated by appropriate selection of plant species, optimum plant seed rate and sowing time and methods. Relay intercropping systems are an important cropping strategy for sustainable agriculture in many countries as they provide benefits in terms of better utilisation of soil resources, weed control and yield diversity (Gecaite et al., 2021).

Weed Control in Organic Forage Crops Cultivation

The transition to organic practices often results in higher weed populations in crop fields, which are often perceived by other growers as a sign of poor farm management. Surveys of conventional growers have identified that increased weed pressure and inadequate control methods in organic systems are perceived as the greatest barriers to adopting organic production practices, and weed control remains a major concern for organic farmers (Rodriguez et al., 2009). Similar to integrated pest management (IPM), integrated weed management (IWM) applies multiple physical and ecological tactics to control weeds, combining cultural (e.g. variety selection, seed sowing rate and date, etc.), physical (e.g. mowing, pre-sowing tillage, mulching, etc.), preventive (stubble and residue management, clean machinery, field edge management, etc.) and biological control practices. Integrated weed management is highly suitable for adoption by organic farmers who do not have the option of using conventional herbicides to reduce weed outbreaks and integrates a variety of weed management methods. However, generalisations about the weed management approaches of growers of particular species should be made with caution. Many IWM practices are crop-specific, meaning that a tactic found to be effective in one crop may have neutral or even negative effects in another crop. Therefore, the usefulness of IWM practices in the context of crops grown on the farm should be assessed for each individual case and not all crop rotations should be treated as equal candidates for the effective use of IWM practices (Tautges et al., 2016). The degree to which physical and cultural approaches are integrated on organic farms has been found to vary, with some studies placing more emphasis on physical controls and others placing more emphasis on cultural controls, while preventive and biological controls are rarely mentioned. Turner et al. (2007) surveyed 52 organic farmers in the UK on weed control measures and found that physical controls were mentioned more frequently than cultural controls as weed management techniques. In contrast, a national survey of US organic farmers found that producers most frequently used cultural controls such as crop rotation and late sowing for weed control, and a limited number of physical measures. A survey of organic growers in the Midwestern region of the United States found different emphases on cultural and physical controls among growers (DeDecker et al., 2014). Researchers found that the number of weed management practices used by growers was influenced by a number of factors, including the amount of formal training, farming experience and growers' information-seeking behaviour. In addition, farmer age, background, education level and farm size are important factors. Weed management behaviours and practices may also differ between regions (Tautges et al., 2016).

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Isot Pepper Spice (Capsicum annum L.), Antıoxidant and Antibacterial Activities

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ABSTRACT: Various antioxidant and antimicrobial substances are used to protect foods from spoilage and increase their shelf life. Due to increasing concerns about the reliability of synthetic antioxidant and antimicrobial substances, research on natural antioxidant and antibacterial sources has intensified and research on medicinal and aromatic plants has accelerated due to the high levels of antioxidant and antibacterial activity compounds they contain. Isot spice is produced domestically and industrially from isot pepper (*Capsicum annum* L.) especially in Şanlıurfa region in our country. In our study, the antioxidant and antibacterial properties of isot pepper were investigated. It was determined that many isot extracts contained high levels of phenolic substances and showed antibacterial activity against foodborne pathogens. Their antimicrobial effects were examined in vitro against *Escherichia coli*, *Bacillus cereus*, *Staphylococcus aureus* and *Salmonella typhimurium* according to the agar well diffusion method; and their antioxidant effects were, Total phenolic substance and DPPH Radical Scavenging Method were tested in isot extracts. As a result; considering the values, it was determined that isot spices used in the study have high antimicrobial and antioxidant effects.

Keywords: Isot Pepper, Antioxidant, Antimicrobial

INTRODUCTION

In addition, it has been determined that it facilitates digestion, reduces rheumatism, joint and tooth pain, relieves cramps, has a positive effect on many diseases, especially cholera and gout, reduces the possibility of cancer, increases sweating, eliminates cough and sore throats, and is a natural sedative for nervous problems (Akıncı and Akıncı 1999). Red pepper (*Capsicum annuum* L.) is bought fresh as a salad variety in most parts of the world. It is the most important ingredient of Indian, Thai, Mexican and Bangladeshi dishes. It contains a large amount of fiber, vitamins and minerals with a small amount of fat and cholesterol. It has been determined that the hot and spicy taste of red pepper is mainly due to capsaicin. The heat produced by red pepper has an effect such as reducing pain. In addition, it has been determined that red pepper is rich in Vitamin C, Iron, Beta carotene and antioxidants that protect the body against free radicals due to its natural antioxidant structure. With its zero-calorie value, it acts by accelerating the body's metabolism within three hours after consumption. (Arokia rajan et al. 2020). Isot is a local spice widely used in the Southeastern Anatolia region, especially in Şanlıurfa and its surroundings. Red pepper produced in Şanlıurfa and its surroundings is first dried under the sun and then obtained by heating in bags. Depending on the amount of drying and heat treatment

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*Bu çalışma Atatürk Üniversitesi Bilimsel Araştırma Projeleri Birimi tarafından “13955” numaralı proje ile desteklenmektedir.

applied, the initial red color changes from purple to black. In this process, not only the color but also the taste and smell of the product change. Traditionally produced for home consumption, isot has also started to be produced by industrial methods as a result of increasing demand due to changing living conditions (Tarla, 2011).

Red pepper has been consumed for medicinal purposes for centuries. It is known that pepper acts on the nerves, stomach and glands and is a diuretic (Topak et al. 2008).

This study on the antibacterial and antioxidant effects of isot shows that isot spice, which is widely used in Turkish cuisine, has a very important potential in terms of production and export. In Turkey, which has a very important potential in terms of production and export of isot spice, production has become more important and should be done consciously with the increase in the areas of spice usage. and obtaining better quality and hygienic products by developing new technologies in this field, the data we obtained as a result of our findings, the development of medicine and pharmacy, food science, etc. It is intended to contribute to many areas.

Material and Method

In this study, isot spice will be used as material and its antimicrobial properties will be determined against Escheria Coli, Bacillus cereus, Staphylococcus aureus and Salmonella Typhimurium bacteria by Agar Well Diffusion method. Antioxidant activities will be determined by DPPH Radical Scavenging Method, Total Phenolic Substance Amount and Vitamin C Determinations.

Results and Discussion

Studies on antioxidant and antimicrobial properties of spices are gaining more and more importance especially in their medical evaluation. In this study, which was carried out to contribute to this field, antioxidant and antimicrobial activities of isot spice obtained by industrial method from red peppers grown in Şanlıurfa were investigated. Three different methods were used to determine the antioxidant properties of isot spice: Folin-Ciocaltaeu method, DPPH free radical scavenging and spectrophotometric method for determination of ascorbic acid amount. Antimicrobial activity was evaluated by agar well diffusion method for *Staphylococcus aureus* (Gram-positive bacteria), *Escherichia coli*, *Bacillus cereus* and *Salmonella Typhimurium* (Gram-negative bacteria). The sample used in the study (İsot) was obtained as a result of industrial processing of red peppers harvested in Şanlıurfa province and was supplied fresh (harvest time) from 5 different herbalists selling in Erzurum province and was stored at +4 °C from the time of supply until the analysis was completed.

The antimicrobial activities of isot were investigated using the agar well diffusion method. Antibacterial activity was determined against Staphylococcus aureus, Escherichia coli, Bacillus cereus and Salmonella Typhimurium microorganisms in 50 and 75 µL extract concentrations. According to the results, it was seen that isot had different effects against each microorganism and the highest inhibition zones were formed against Staphylococcus aureus and the lowest inhibition zone formation belonged to Bacillus cereus. According to these results, all samples showed the highest antimicrobial effect against Staphylococcus aureus and the lowest antimicrobial effect was against Bacillus cereus. It was observed that isot had significant inhibitory effects against Staphylococcus aureus, Escherichia coli, Bacillus cereus and Salmonella Typhimurium microorganisms.

Table 1. Variance analysis results of the inhibition zone values of 50 and 75 µL isot extracts against the bacteria used in the study.

Featеres	*Salmonella tyhimurium* 50	*Salmonella typhimurim* 75	*Escheria Coli* 50	*Escheria Coli* 75	*Bacillus cereus* 50	*Bacillus cereus* 75	*Staphylococcus aureus* 50	*Staphylococcus aureus* 75
1	14,50±0,71	16,00±1,41	15,50±0,71	16,50±0,71	17,00±0,00	18,00±0,00	16,50±0,71	18,50±0,71
2	15,00±0,00	16,50±0,71	15,50±0,71	18,00±0,00	17,50±0,71	16,00±1,41	17,50±0,71	18,00±0,00
3	15,50±0,71	16,50±0,71	17,00±1,41	16,00±0,00	12,00±1,41	12,50±0,71	17,50±0,71	18,00±1,41
4	15,00±0,00	16,00±0,00	14,50±0,71	18,00±1,41	10,50±2,12	12,00±1,41	16,00±0,00	17,50±0,71
5	14,50±0,71	15,50±0,71	16,50±2,12	18,50±0,71	10,00±1,41	11,00±2,83	13,00±1,41	15,00±1,41

It was observed that the samples formed the highest inhibition zones against Staphylococcus aureus in both concentrations. The lowest inhibition zones of the samples were measured against Bacillus cereus. According to these results, all samples showed the highest antimicrobial effect against Staphylococcus aureus and the lowest antimicrobial effect against Bacillus cereus. While the zone diameters were small in the 50 µL concentration, they were larger in the 75 µL concentration. This study (Altemimi et al. 2017) is parallel to the research result of ‘it is possible to observe an increase in the inhibition zone as the concentration increases. According to all the results obtained, the antibacterial activities of spice extracts against standard bacterial strains were found to be lower compared to the control antibiotic.

Dorantes et al. (2002) examined the effect of Capsicum annuum extracts on some pathogenic bacteria in their study and stated that pepper extracts prevented the growth of S. aureus, L. monocytogenes, S. typhimurium and B. cereus. The inhibitory effect varies in direct proportion to the extract concentration. It is possible to observe an increase in the inhibition zone as the concentration increases (Altemimi et al. 2017).

The studies of Dorantes et al. (2002) and Altemimi et al. (2017) are similar to this study. Sharma and Golhani (2017), C. annum They found that methanol and acetone extracts of fruits showed maximum inhibitory effect against S. aureus (23 mm) and B. subtilis (19 mm). Unlike the results of this study, the zone formation of Staphylococcus aureus was measured as 16.50±0.71 mm at the highest and 13.00±1.41 mm at the lowest in this study. It is thought that these differences may be due to the use of different strains of the same bacteria (Bagamboula et al. 2003). Three different methods were used to determine the antioxidant properties of isot spice: Folin-Ciocaltaeu method, DPPH free radical scavenging and spectrophotometric method for the determination of ascorbic acid amount.

Table 2. Duncan Multiple Comparison Test Results of Means of DPPH Free Radical Scavenging Activity (IC_{50} Value) of Isot Extracts

Features	DPPH· IC_{50} (mg/mL)
1	$1{,}83 \pm 0{,}15^e$
2	$2{,}18 \pm 0{,}18^d$
3	$3{,}23 \pm 0{,}18^b$
4	$3{,}78 \pm 0{,}22^a$
5	$2{,}90 \pm 0{,}21^c$

* Means indicated with the same letter are statistically no different from each other ($p<0.05$).

The IC_{50} value, which is the effective antioxidant concentration required to destroy 1/2 of the DPPH• radical during the reaction, is inversely proportional to the radical scavenging activity (İşbilir 2008). In order to determine the radical scavenging activities of the examined samples according to the DPPH method, the IC_{50} values were determined and the samples were compared with each other. Accordingly, it was seen that Sample 1 with the lowest IC_{50} value showed the highest radical scavenging activity. It was seen that Sample 4 with the highest IC_{50} value showed the lowest radical scavenging activity.

Table 3. Duncan Multiple Comparison Test Results of Average TPC (Total Phenolic Substance) Amount Values of Isot Extracts

Features	Total Phenolic Substance (mg GAE/kg)
1	$13605{,}99 \pm 1048{,}58^a$
2	$12230{,}57 \pm 974{,}35^b$
3	$7384{,}19 \pm 979{,}92^d$
4	$7488{,}65 \pm 399{,}12^d$
5	$9470{,}37 \pm 698{,}40^c$

* Means indicated with the same letter are statistically no different from each other ($p<0.05$).

As can be seen in the table above, the total phenolic content of the samples is quite different from each other. It was determined that the highest total phenolic content was Sample 1, and the lowest was Sample 3. It was determined that the samples containing high phenolic compounds had high antioxidant effects, respectively 1>2>5>4>3. In the reviewed studies conducted by Ciz et al. (2010), the total phenolic content of many vegetables was determined and the amount of phenolic substance in red pepper was stated as 115.7 mg gallic acid/100 g fresh sample. Again, in the study reviewed by Erdoğan (2013), the total phenolic substance content of red pepper was determined as 15929.63 mg/kg km. These values are parallel to our study (13605.99±1048.58mg GAE/kg and 12230.57±974.35 mg GAE/kg km).

Table 4. Duncan Multiple Comparison Test Results of Average Vitamin C Values of Isot Extracts

Features	Vitamin C (mg/100g)
1	$24{,}27 \pm 3{,}57^{a}$
2	$24{,}59 \pm 0{,}82^{a}$
3	$9{,}18 \pm 2{,}09^{c}$
4	$12{,}99 \pm 2{,}38^{b}$
5	$10{,}32 \pm 3{,}08^{bc}$

* Means indicated with the same letter are statistically no different from each other (p<0.05)

As seen in Table 4, it is possible to say that the vitamin C values of samples 1 and 2 are statistically equal to each other (p<0.05).

As a result of the research, it was determined that the highest vitamin C activity was 24.27±3.57 mg/100g and 24.59±0.82 in Sample 1 and Sample 2, and the lowest ascorbic acid activity was 9.18±2.09 mg/100g in Sample 3.

It can be said that isot has high antioxidant activity in all spectrophotometric methods used to determine Folin-Ciocaltaeu, DPPH and ascorbic acid values.

Based on these results, it was determined that isot can prevent cellular damage caused by free radicals and therefore can be used as an option instead of synthetic antioxidants with carcinogenic effects in protecting human health.

The values obtained at the end of the study were subjected to variance analysis using the SPSS (version 20.0) package program. Significant variation values were compared with Duncan's Multiple Comparison Test. The study was conducted in 2 repetitions and 3 parallels.

Conclusion

According to the results obtained, the antioxidant and antimicrobial effects of the samples are quite strong. The study results show that this spice has a high antioxidant capacity and has a strong antimicrobial effect especially against Staphylococcus aureus. It can be suggested that this spice grown in Şanlıurfa should be evaluated as an important herbal resource in terms of both health and economy by supporting its potential medical and industrial applications.

Acknowledgement

I would like to express my endless gratitude and thanks to Prof. Dr. Ahmet ERDOĞAN, who was my advisor and supported me throughout my graduate education from the selection of the research topic to its completion; to İsa Arslan KARAKÜTÜK, one of my doctoral students, who shared his professional and scientific knowledge, views and experiences with me until the completion of the thesis study and whose opinions and suggestions on statistics I benefited from; and to my family, colleagues and friends, who supported me throughout my thesis study with their morale and support, as they did at every stage of my life.

The author İsa Aslan KARAKÜTÜK, is supported by the TUBITAK BİDEB 2211/A National Ph.D. Scholarship Program.

Funding

This study is supported by Atatürk University Scientific Research Projects Unit with ID number 13955.

Statement of Conflict of Interest

There is no conflict of interest among the authors

Authors' Contributions

Fatma GÖLELİ designed the research and analyzed it together with Ahmet ERDOĞAN. İsa ASLAN KARAKÜTÜK helped with the analysis work and the creation of statistics. Fatma GÖLELİ worked on the preparation of the pictures and tables. All authors contributed to the writing of the article, participated in the publication process of the article, and read and approved the article.

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Agricultural Importance of Sainfoin (*Onobrychis viciifolia* Scop)

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ABSTRACT: Sainfoin (*Onobrychis viciifolia*) is a perennial plant belonging to the legume family, known for its resilience to dry climate conditions and its value as a nutritious forage crop. It is primarily grown in regions such as Central Asia, the Mediterranean, and the Middle East. Sainfoin is used in the livestock industry as high-quality feed for animals like cattle, sheep, and goats, and it is particularly notable for its high protein content. Sainfoin plays an important role in improving soil fertility due to its nitrogen fixation ability. By forming a symbiotic relationship with Rhizobium bacteria, it helps transfer atmospheric nitrogen into the soil, providing a significant advantage for sustainable farming practices. Additionally, Sainfoin offers environmental benefits through its erosion control capabilities, as its strong root system helps prevent soil erosion. Sainfoin also has some traditional medicinal uses, particularly for its digestive and diuretic effects, and is commonly used in folk medicine. Furthermore, it is an important plant for beekeeping, as it provides a rich nectar source for bees.

Keywords: Forage, *Onobrychis viciifolia*, Feed, Animal

INTRODUCTION

Sainfoin (*Onobrychis viciifolia*) is a perennial herbaceous plant from the legume family, primarily cultivated as a forage crop. It is widely grown in various regions of Anatolia and is typically used by farmers engaged in livestock farming, especially to meet the protein needs of animals and for roughage. *O. viciifolia* has a broad root system and the ability to fix nitrogen, which improves soil health and enhances fertility. Additionally, its resistance to drought and semi-arid climatic conditions makes it particularly suitable for agriculture in regions with low rainfall (Chen et al., 2023). Sainfoin provides a high-protein feed source for ruminants, such as cattle, sheep, and goats, promoting faster growth rates and supporting milk production. It is also an important nectar source for honeybees, contributing to pollination. Sainfoin offers ecological benefits, such as preventing soil erosion and increasing the organic matter content of the soil. Moreover, Sainfoin seeds are used as food by some local communities due to their rich fatty acid profile. The areas where Sainfoin is grown also contribute to increasing biodiversity and preventing soil erosion (Ren et al., 2025).

The cultivation of *O. viciifolia* presents a broad research area in terms of genetic diversity and adaptability. Topics such as the plant's productivity under different ecological conditions, how it copes with soil characteristics and climate change, could provide important strategic information for agricultural production efficiency. Additionally, the resistance of Sainfoin species to diseases and pests further enhances the potential of this plant for sustainable agricultural practices (Kumar et al., 2020; Häfner et al., 2024).

In conclusion, *O. viciifolia* stands out as an ideal plant for environmentally friendly agricultural practices due to its contributions to soil health, biodiversity, and ecosystem services. Its nitrogen fixation capacity, ability to improve soil health, and potential for integrated use in livestock farming make it a crucial option for sustainability in agriculture (Kumar et al., 2020). Sainfoin offers a productive and cost-effective alternative, especially in organic farming and forage production, and could play a larger role in future agricultural systems. Therefore, increasing the efficiency of Sainfoin production and its environmental contributions has great potential for both agricultural output and environmental sustainability.

Taxonomy and Morphological Features

Sainfoin (*Onobrychis viciifolia*) is a perennial plant belonging to the legume (*Fabaceae*) family and is one of the prominent species in this family used as forage. O. viciifolia was first described by Linnaeus in the 18th century and is widely found in regions with a Mediterranean climate, especially in Central Asia, Anatolia, and other areas with similar climates. The plant typically grows between 60-90 cm in height, but this length may vary depending on local climatic conditions. Sainfoin is known for its fine and deep root structure, which increases its drought resistance. This root system allows the plant to endure dry conditions and plays an important role in preventing soil erosion. Its stem is upright, and its leaves are compound and hairy. Each leaf contains between 6 and 14 leaflets and is lance-shaped (Tan & Sancak, 2009; Özaslan Parlak et al., 2014). The flowers are purple, pink, or white, which not only provide a pollen source for bees but also play a crucial role in ecosystem health (Liu et al., 2019).

Sainfoin's seeds are small and kidney-shaped, with its fruit being a single-seeded pod encased in a hard shell. Since the germination rate is low, various pre-treatment methods (e.g., mechanical scarification or acid treatment) are recommended to improve seed germination capacity. These botanical characteristics directly affect the plant's agricultural production potential and support its widespread use. As a legume, Sainfoin has the ability to fix atmospheric nitrogen. In a symbiotic relationship with Rhizobium bacteria, the plant contributes to the nitrogen cycle, enhancing soil fertility. This feature is particularly important in organic and sustainable agricultural practices. Additionally, Sainfoin can adapt to various soil types, including calcareous soils (Hoste et al., 2015; Hayot Carbonero et al., 2011).

Agricultural, Economic and Ecological Importance

Sainfoin is a forage crop that is resilient to climate change and different soil conditions, and it holds strategic importance both economically and environmentally. It can be efficiently grown, especially in dry climates. Economically, Sainfoin is of great importance in agricultural production due to its capacity to provide high-quality feed. This plant, offering high protein content for animals, is a highly nutritious feed source, especially for ruminants (cattle, sheep, goats). Its high protein content and digestibility make *O. viciifolia* a preferred plant for roughage (Germida et al., 2020). With its protein content ranging from 15-22% and its palatability, it is a common feed source in the livestock sector. It is especially highly digestible for ruminant animals and stands out from other legumes due to its non-bloating properties. Animals fed with Sainfoin have shown increases in milk and meat production (Luciano et al., 2019; Hoste et al., 2015). Additionally, the high fat content of Sainfoin seeds is another valuable feature for animal feeding.

Sainfoin is widely preferred in sustainable agricultural practices due to its ability to improve soil structure, assist with erosion control, and increase organic matter content. Growing Sainfoin also helps prevent soil erosion. The plant's strong root system, especially on slopes, helps prevent soil displacement, thus reducing erosion (Varela et al., 2022). This is another indication that Sainfoin farming contributes to ecosystem services. Ecologically, Sainfoin offers benefits such as protecting soil from erosion, fixing nitrogen, and reducing carbon emissions. Its deep root system improves soil structure and helps retain water in the soil. Additionally, it promotes high biodiversity, aiding in the preservation of environmental balance. Sainfoin has a significant biological impact on soil, particularly by increasing soil nitrogen levels. This occurs as the plant’s nodules absorb nitrogen from the atmosphere, which not only enhances soil fertility but also supports environmental sustainability by reducing the use of chemical fertilizers (Gül & Özdemir, 2018).

Moreover, Sainfoin is a valuable nectar source for the beekeeping industry. This supports pollination, promotes biodiversity, and enhances ecosystem health. Sainfoin’s richness in secondary metabolites not only makes it useful as a forage crop but also gives it antimicrobial and antioxidant properties (Hayot Carbonero et al., 2011; Luciano et al., 2019).

Sainfoin also provides high yields even on marginal agricultural lands, making it valuable in economically disadvantaged regions. This contributes to rural development and strengthens local economies.

Nutritional Facts of Sainfoin

Sainfoin contains high-quality protein and carbohydrates in animal feed. It is particularly suitable as a feed source for ruminant animals (cattle, sheep, goats). Additionally, Sainfoin may positively affect digestive health due to its low-fat content and high fiber levels. One of its most valuable characteristics is that the quality of the feed improves with age. It is also a good source of fiber, which can help regulate the digestive system. Moreover, it is an important source of vitamins (especially vitamins A and C) and minerals (such as iron, magnesium, phosphorus, and potassium). In terms of nutritional value, as a legume, it contains high-quality protein, which is essential for muscle structure and repair. Numerous studies have highlighted the high protein content of Sainfoin, making it a highly nutritious source (Mitsopoulos et al., 2020).

In terms of fiber, Sainfoin is particularly rich in insoluble fiber. Fiber helps regulate digestion, supports gut health, and promotes a feeling of fullness (Sadeghi et al., 2019). It may also contribute to lowering cholesterol levels. In terms of vitamins and minerals, Sainfoin is a good source of vitamins A and C. Vitamin A supports eye health, while vitamin C strengthens the immune system. Additionally, Sainfoin is rich in minerals such as iron, magnesium, potassium, and phosphorus, which improve overall health (Ramos et al., 2021).

Sainfoin also stands out for its high antioxidant content. Compounds such as flavonoids and saponins can neutralize free radicals in the body, reducing cellular damage and lowering the risk of chronic diseases (Li et al., 2018).

Sainfoin contains nutrients that provide various health benefits to the body. Research shows that it strengthens the immune system, improves the digestive system, and supports cardiovascular health (Khayat et al., 2019). Additionally, due to its high protein and fiber content, it helps provide a prolonged feeling of fullness, which can facilitate weight management.

Sainfoin and Climate Change

In recent years, the effects of climate change have led to significant changes in agriculture and ecosystems, particularly manifested through reduced water resources, temperature fluctuations, and abnormal weather conditions. Sainfoin (*Onobrychis viciifolia*) is a plant that stands out for its adaptation capacity and resilience to these changes. Given its role in both agricultural production and ecosystems, scientific research to understand the impacts of climate change and how to cope with them is becoming increasingly important. Sainfoin, as a plant resistant to drought and semi-arid climate conditions, could play a significant role in combating climate change. *O. viciifolia* can grow efficiently even under water stress conditions, making it a preferred choice in regions with limited water resources for agriculture (Marty et al., 2021). Additionally, Sainfoin can withstand not only heat and drought but also some degree of soil acidity and salinity, making it a sustainable crop in diverse ecological conditions (Marty et al., 2021).

One of the most significant effects of climate change is the increase in temperatures and the reduction of water resources. Sainfoin, being resistant to drought and high temperatures, stands out for its ability to withstand such climatic stresses. Some Sainfoin species grown in the desert climate of Central Asia can survive even in water-limited environments (Yuan et al., 2019). This feature suggests that Sainfoin could be an important agricultural solution in combating the increasing water stress and drought associated with climate change.

Sainfoin is also known for its nitrogen fixation ability, contributing to the nitrogen cycle in the soil. This trait can play a vital role in combating the decline in agricultural productivity due to climate change. Nitrogen fixation enhances soil fertility, reduces the need for chemical fertilizers, and thus minimizes the environmental impact of agriculture (Rao et al., 2020). Sustainable solutions like this are crucial in mitigating the effects of climate change on agriculture.

Additionally, Sainfoin can compete with invasive species that hinder the growth of other plants. With the effects of climate change, plant communities in ecosystems may change, and some invasive species may become more prevalent. Sainfoin can contribute to controlling these invasive species, thereby helping maintain ecosystem balance (Barton et al., 2019).

The adaptation of Sainfoin to climate change is important for the future of agricultural production and ecosystem services. To cope with the negative effects of climate change, the widespread use of resilient and sustainable plants like Sainfoin can increase diversity in agriculture and support environmental sustainability. Sainfoin can also improve soil structure, reduce erosion risk, and help protect soil against extreme rainfall and flooding events, which are becoming more frequent due to climate change (Liu et al., 2018).

Sainfoin's Genetic Diversity and Recovery Efforts

Sainfoin (*Onobrychis viciifolia*) is commonly found in regions with Mediterranean and Central Asian climates, and within this broad geographical area, there are many different species and varieties that have adapted to various climatic conditions and soil characteristics. Genetic diversity is a key factor enabling these species to withstand various environmental stresses. The adaptation abilities of Sainfoin species to adverse conditions such as drought, high temperatures, and low soil nutrient levels are a result of their genetic diversity (Zhang et al., 2020). Additionally, some Sainfoin species improve ecosystem services by enhancing soil fertility through nitrogen fixation (Xie et al., 2019).

The conservation of genetic diversity has become increasingly important, especially given the impacts of climate change on agriculture. Sainfoin represents a crucial genetic resource that can help the plant adapt to future environmental changes by preserving this diversity. Furthermore, the genetic differences between Sainfoin species offer the potential for selecting more efficient species and variants in breeding programs (Molek et al., 2018).

Genetic studies on Sainfoin have revealed the potential to enhance its adaptation abilities and productivity. As a plant with high genetic diversity, Sainfoin is suitable for improvement programs aimed at increasing the adaptation capacity of local varieties. These efforts could lead to the development of varieties resistant to diseases and pests, as well as traits that enhance its productivity (Seddigh et al., 2018). Additionally, through genetic engineering and molecular biology techniques, the development of more efficient and resilient varieties of Sainfoin is a goal.

Despite its potential as an important crop for agricultural production, Sainfoin requires genetic improvement to enhance traits such as productivity and resilience to environmental stresses. Genetic improvement of Sainfoin species can facilitate the development of more efficient and resistant varieties, particularly in the face of challenges like drought, high temperatures, and low soil nutrient levels. Genetic improvement could also enhance the plant's nitrogen fixation capacity, providing sustainable solutions for agricultural production (Chai et al., 2020).

Molecular biotechnology techniques are used in genetic improvement programs. Specifically, genetic mapping, genetic variation analysis, and biotechnological methods aim to develop desired traits in Sainfoin species, such as drought resistance and disease resistance. Sainfoin’s genetic diversity serves as an important resource in these improvement efforts. Moreover, by using molecular markers, it is possible to develop new varieties that are both more productive and resilient to environmental stresses (Jia et al., 2021).

Uses of Sainfoin

Onobrychis viciifolia, commonly known as sainfoin, is widely used as a forage crop in the livestock sector. Due to its high-quality protein content and good nutritional value, this plant serves as an important feed source for animals such as cattle, sheep, goats, and horses (Yılmaz et al., 2020). In addition to its use as animal feed, sainfoin is also utilized in soil improvement and bioenergy production. Furthermore, some studies focus on the potential health benefits of this plant for humans. Due to the presence of bioactive compounds such as phytoecdysteroids, flavonoids, and saponins, research is being conducted not only for its traditional uses but also for its applications in the pharmaceutical industry. *O. viciifolia* increases soil fertility through its nitrogen fixation ability, which is crucial for soil enhancement and sustainable agriculture (Öztürk et al., 2018).

In addition to its soil improvement properties, this plant is also used for erosion control. Thanks to its strong root system, *O. viciifolia* can prevent soil erosion and reduce erosion, especially on sloped lands (Bahar and Erdem, 2019). This characteristic makes it a valuable plant in areas subjected to environmental stress.

O. viciifolia also has some traditional medicinal uses. The plant is used in folk medicine for digestive issues and as a diuretic (Aydın et al., 2021). Additionally, since the plant’s flowers are an important nectar source for bees, it is beneficial for honey production (Kara and Demir, 2020).

Current Research and Resources on Sainfoin

Agricultural Aspects: Recent research on the agricultural productivity of *Onobrychis viciifolia* focuses on its cultivation in different climatic conditions and soil management. Studies in recent years provide in-depth investigations into the plant's adaptation to arid climates and its contribution to soil health (Sakhraoui et al., 2024).

Animal Feeding: Studies on the effects of *O. viciifolia* fodder on the growth performance of livestock and the enhancement of its nutritional value demonstrate recent developments in the more efficient use of this plant (Getu et al., 2024).

Bioactive Compounds and Health: Recent research on *O. viciifolia* explores the potential health benefits of compounds found in the plant, such as antioxidants and anti-inflammatory properties (Yeniçeri et al., 2024).

Onobrychis viciifolia and Bioenergy: Studies on the biomass production and bioenergy potential of *O. viciifolia* highlight the growing interest in its use as a renewable energy source (Häfner et al., 2024).

Conclusion and Future Perspective

Onobrychis viciifolia is not only an economically valuable forage crop but also plays a crucial role in environmental sustainability. Its ecological contributions, such as nitrogen fixation, prevention of soil erosion, and enhancement of biodiversity, make it an indispensable species in agricultural production and environmental conservation practices. The efficient production of Sainfoin stands out as an important strategy for addressing global environmental issues such as climate change. Therefore, the cultivation of Sainfoin should be expanded, and its potential should be increased.

Sainfoin, as a plant with high genetic diversity and resistance to environmental stresses, holds significant potential in agriculture. Genetic improvement efforts are crucial to enhance its productivity and enable it to cope more effectively with environmental challenges. In the fight against global threats like climate change, preserving and improving the genetic diversity of resilient plants such as Sainfoin is emerging as a critical strategy for sustainable agricultural practices.

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Use of Agriculture 4.0 Early Warning and Forecast Systems in Viticulture; Example of Üzümlü

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ABSTRACT: The shrinking of agricultural lands and the increase in the human population are increasing the demand for food day by day. Increasing demand makes it necessary to use the existing lands in the most efficient way. For this reason, adopting Agriculture 4.0 methods is important in terms of sustainability in order to solve the problems encountered in production in the fastest and most rational way. One of the sustainable agriculture examples of Turkey is the Karaerik grape cultivation in Üzümlü District of Erzincan which dates back thousands of years. The Karaerik grape variety is in high demand in the domestic market due to its unique appearance and taste and is one of the grape varieties with the highest commercial value in Turkey. However, climate change, increasing disease and pest populations in recent years significantly affect sustainability and cause disruptions in production. In order to prevent these disruptions, the necessity of using technology and artificial intelligence is becoming more and more necessary. In this context, the use of the agriculture 4.0 Early Warning and Forecast System in Üzümlü vineyards brings a different management approach to the vineyards with the adoption of precision viticulture. The system constitutes an important decision support mechanism for farmers in operations such as pruning, fertilization, irrigation, harvesting, and especially in combating diseases and pests. The use of the agriculture 4.0 early warning and forecasting system in Üzümlü vineyards is of vital importance in terms of preserving the commercial value of the Karaerik (Cimin) grape variety, which has a geographical indication and is the only standard grape of the region, and ensuring the sustainability of a natural heritage.

Keywords: Agriculture 4.0, Erzincan, Forecasting, Karaerik, Viticulture, Warningsystem

INTRODUCTION

Agriculture is a vital activity for the continuation of human life and provides food, feed, fuel and industrial raw materials. The world population is expected to reach 8 billion in 2025 and 10 billion in 2050 (Anonymous, 2017). This will lead to a significant increase in the quality and quantity of numerous human needs, especially food. In order to meet these needs, world food production must increase by approximately 60-70% (Powell et al., 2012; Anonymous, 2016). However, traditional agricultural methods are insufficient to meet the needs of humanity in the face of a growing population. Reasons such as climate change, depletion of natural resources, increased environmental pollution, ensuring sustainable production and food security have necessitated new approaches in agricultural production (Stocker, 2013). These approaches have gone through various stages throughout history from the most primitive level to the present level. These development phases in agricultural production are divided into 4 long periods and are called Agriculture 1.0, Agriculture 2.0, Agriculture 3.0 and Agriculture 4.0 (Ercan et al., 2019).

The period from ancient times, when farmers used hand tools based on water, steam, human and animal power, to the beginning of the 20th century, when traditional agricultural methods were used, is considered Agriculture 1.0. The most basic feature of this period is that the production method, which is low in yield and labor-intensive, is dominant. Agriculture 2.0 covers the period until the mid-20th century, when agricultural machinery was used in cultural processes such as tillage, irrigation, sowing, planting and harvesting, and tractors were put into mass production, called the ‘‘Green Revolution’’ (Y.Liu et al., 2021). The Agriculture 3.0 period is called “Precision Agriculture” and refers to the period that started with the use of automation systems in greenhouses and irrigation systems. (Ahmad et al., 2021). Agriculture 4.0, which was first mentioned in Germany in 2011 with Industry 4.0, refers to the latest period in which information systems and industry will work together, production techniques will be applied with maximum efficiency with integrated computers, artificial intelligence will come to the fore and production will be digitalized. (Figure 1, Anonymous 2021), (Saygılı, et al. 2018).

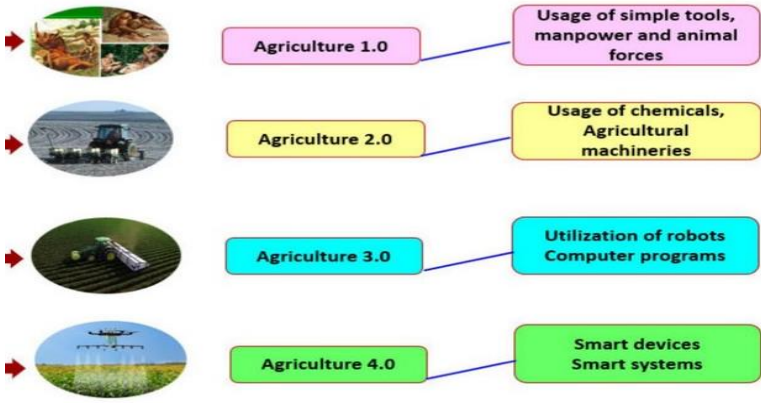


Figure 1. Periods in agricultural production

This period, also called Smart Agriculture, is a management concept that uses modern technology to increase efficiency and quality in agriculture. Especially information and capital are important for smart agricultural technologies (Trendov et al., 2019). Agriculture 4.0 is the period of information-based agricultural production that produces by managing the components of nature. In other words, Agriculture 4.0 can be defined as the use of technological tools and equipment in the agricultural sector that offer solutions to problems that arise in all stages of agricultural production and all post-consumption services by utilizing data platforms such as digital devices (tablets, computers, information technologies, etc.), business computers, IoT, GPS, sensors, chips, sensors, clouds, satellites and forecasts, and that increase efficiency and profitability (Kovács et al., 2018; Tekin, 2018; Zambon et al., 2019).

In Agriculture 4.0, agricultural vehicles and agricultural fields are equipped with sensors and sensors, and agricultural vehicles are allowed to communicate with each other. Thanks to the sensors used, climate components such as humidity, vegetation, temperature, steam and weather conditions can be measured in detail, plant species can be distinguished with remote sensing, stress conditions, drought, soil and plant conditions are monitored, data are collected and analyzed. (Figure 2). In this way, it will be possible to obtain a multi-faceted perspective in agricultural production and more products with less input (water, fertilizer, fuel, etc.) (Saygılı et al., 2018; Kaya, 2019; Kılavuz and Erdem 2019).

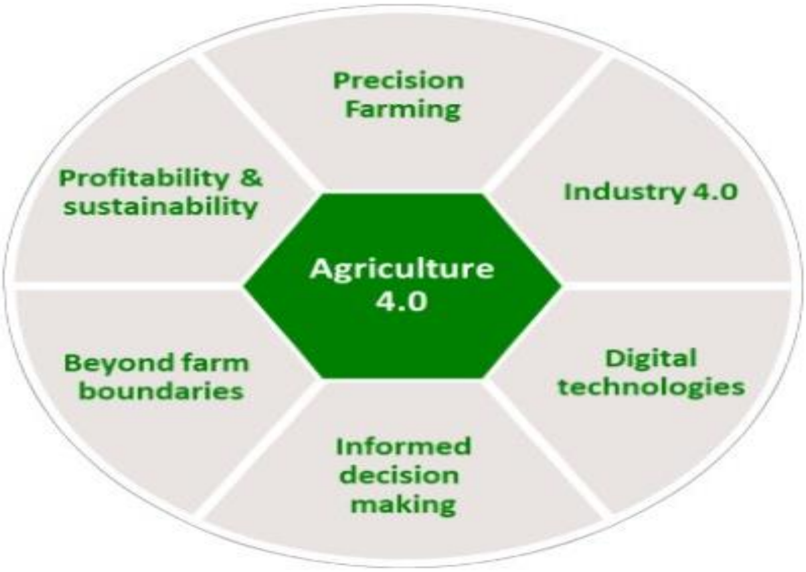


Figure 2. Multiple perspectives of agriculture

Agriculture 4.0 Application Tools

Cloud Computing

Cloud computing is a technology that enables data, documents, information, software, and applications to be stored in a virtual repository on the Internet and accessed over the Internet (Çark, 2019). In this technology, issues such as collecting data collected with the help of devices and sensors in an imaginary pool, analyzing it, processing raw data, storing it, and making it easily accessible when necessary are solved with the cloud computing method. (Çetin et al., 2013; Araújo et al., 2021). In the past decade, cloud computing has attracted great attention because it plays an important role in the cheap storage of agricultural data for farmers, the conversion of stored raw data into information, and decision-making mechanisms based on quantitative analysis (Shi et al., 2016).,

Internet of Things (IoT)

The Internet of Things (IoT) is a term used to describe the connection between physical and digital "things" through standard and interoperable communication protocols (Shi et al., 2019). IoT technology offers farmers the ability to remotely control their lands via phone or tablet. This technology consists of systems that help track many issues, from which seeds to plant on agricultural land and when, to the amount of fertilizer required, from spraying and harvesting times to tracking changing climate conditions (Ercan et al., 2019).

Big Data (Analytics)

Big data is defined as data that is too large to be analyzed with traditional analysis methods and cannot be managed (Ohlhorst, 2013). Big data is generally defined in the literature as five dimensions (5V), namely volume, speed, accuracy and value (Demchenko et al., 2013). Big data analytics plays an important role in transforming data into added value for producers, thanks to its capacity to meaningfully bring together, process and visualize large data sets. Examples of opportunities for big data in agriculture include comparison, predictive modeling, sensor use, calculation and systems used to manage the risk of product spoilage. Big data applications provide farmers with clues from data collected in real time from different sources (Uzun et al., 2018; Ercan et al., 2019). Sustainable food supply estimates can be given as an example for big data by analyzing data from websites containing land use and production information of 13,000 farmers in 17 countries in Africa (Frelat et al., 2016). In addition, more widely applied applications that aim to maximize efficiency by analyzing optimum climate parameters (temperature, precipitation) based on historical and multi-site datasets are also examples of big data (Majumdar et al., 2017).

Satellite and Air Vehicles

In recent years, satellites and aircraft have been used frequently in agricultural work. Especially thanks to the optical sensors placed on aircraft, yield estimation and efficient use of land can be achieved. In the analysis made with image processing techniques on satellite images, areas of the land where fertilizer and irrigation are needed can be determined, thus making it easier for producers to focus on problematic areas (Tamura et al., 2018).

Autonomous Vehicles and Robotic Systems

Although these systems are used in many areas in agricultural activities, they require large land sizes in order to be cost-effective. For example, distinguishing straw and hay in the field with autonomous combine harvesters and planting seeds at the most suitable point in the field with precision tractors can be given as examples of these systems (Uzun et al., 2018).

Artificial Intelligence and Machine Learning

Artificial intelligence; It is one of the main driving forces behind the applicability of Agriculture 4.0 combined with Cloud Computing and the Internet of Things. Machine learning systems are the general name of computer algorithms that model a problem according to the data belonging to that problem and are systems established to give the highest performance with the existing data set and the algorithm used (Atalay and Çelik 2017). These systems include applications such as image collection, processing, and analysis and are low-cost and reliable systems. In machine vision systems, data is collected and processed quickly (Uzun et al., 2018; Ercan et al., 2019).

Erzincan Viticulture Specific to Üzümlü

Türkiye ranks 6th in the world in terms of grape production. Its climate advantage and being at the intersection of two important gene centers have led to the emergence of many local and commercial varieties in terms of viticulture. Erzincan has made a name for itself in grape production due to its microclimate, climate characteristics and topographic structure. Indeed, Erzincan's only standard table variety, Karaerik grape is one of the grape varieties with the highest commercial value in Turkey with its unique taste and attractive appearance. Another aspect that distinguishes the Karaerik grape variety, which has a geographical indication from other varieties is its training system. This system, called "baran" in the Erzincan region, can be described as a system in which the grape trunk is taken underground, the arms and rods are left above the soil and the soil is raised from the ground in the form of a herringbone (Figure 3) (Özoğul, 2024)

Figure 3. Traditional baran training system

It is known that the most important feature of this training system is to protect the plant against frost damage in the region. As a matter of fact the plant trunk remaining underground and the arms and branches remaining under the snow cover are minimally affected by low temperature damage and the baran training system comes to the fore as a sustainable production method. It is reported that the grape production method in the region has remained unchanged since 800 BC (Küpe, 2019; Taşkesenlioğlu et al., 2022). It is known that this system has some disadvantages as well as important advantages. The fact that the vegetative part is intertwined with the soil increases the humidity rate in the vineyard especially during the period when the shoots are elongated and makes it difficult for the moisture to escape. The insufficient air circulation in the baran system causes humid and hot air to be trapped between the soil layer and the leaves. This situation both triggers fungal diseases and makes the spraying difficult. With the elongation of the shoots during the vegetation period, only the leaves are visible in the vineyard and it becomes impossible to see the fruit and other parts. The agricultural chemicals used in spraying against diseases and pests remain only on the outer surface of the plant and cannot penetrate into the system. For this reason, the desired efficiency cannot be obtained in spraying against diseases and pests and yield losses are experienced. In addition to the disadvantages of the baran system in disease and pest control another issue is not being able to start spraying at the right time. Spraying periods against fungal diseases such as vineyard powdery mildew (Erysiphe necator), vineyard downy mildew (Plasmopara viticola) and lead mold (Botrytis cinerea) and against grapevine moth pest (Lobesia botrana) which frequently cause damage in the vineyards in the region are generally determined according to phenological periods. However wrong decisions can be made for starting spraying in this visual monitoring.

At this point, benefiting from early warning and forecasting systems in viticulture activities in the region is important both in terms of starting spraying at the right time. Early warning and forecasting systems are important decision support mechanisms for farmers since they monitor climatic parameters as well as phenological development, soil moisture, soil salinity, effective heat summetion (EHS), global radiation, plant water stress, etc. (Figure 4).

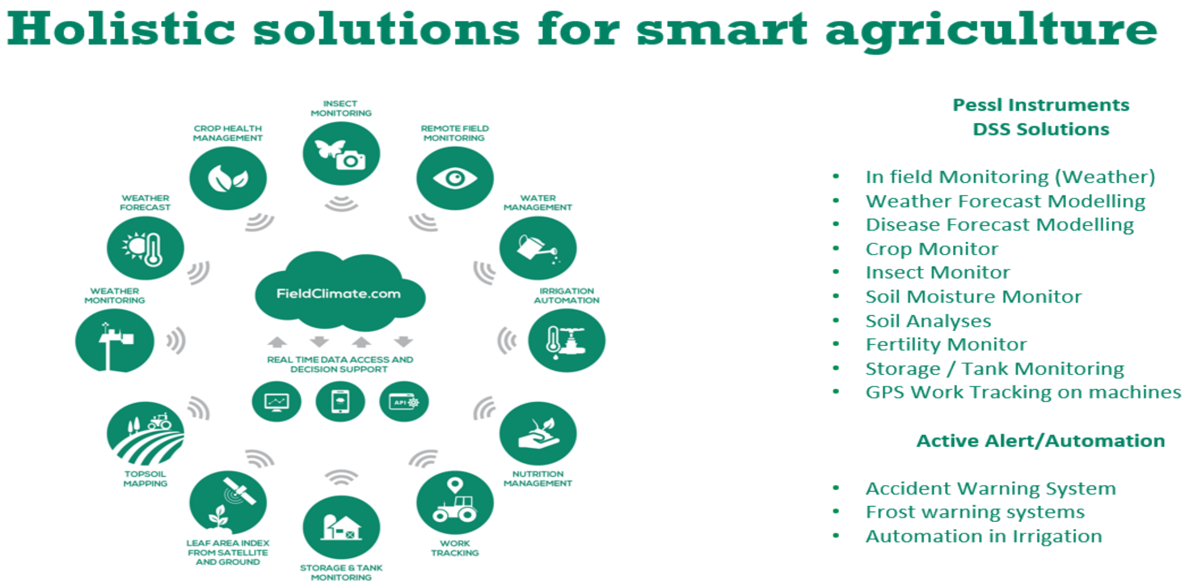


Figure 4. Some advantages of early warning and forecast system

Functions of the Early Warning and Forecast System Established in Üzümlü

Climate Station

The climate station records and analyzes temperature, precipitation, humidity, dew point, solar radiation, open vapor pressure, sunshine duration, Delta T, soil temperature, ET0, soil EC, wind direction, wind speed and storm speed data (Figure 5). There is a battery and a solar energy panel on the station and the collected data is collected on the website and mobile application and sent to farmers as SMS. The time of cultural processes to be carried out in the vineyards can be determined correctly by analyzing the data obtained from the climate station by artificial intelligence and big data. For example, days when wind speed is suitable for agricultural spraying can be determined and producers can be informed (Figure 6). Again thanks to rain and temperature sensors, the most ideal days for cultural processes such as harvesting, tillage, pruning, fertilization, etc. can be determined and growers can make a plan according to meteorological conditions. Since the data obtained by the climate station is collected on the system the climate data of the region for many years is also recorded. In this way, changes in the climate can be determined on a monthly and annual basis.

Figure 5. Climate station and some data collected

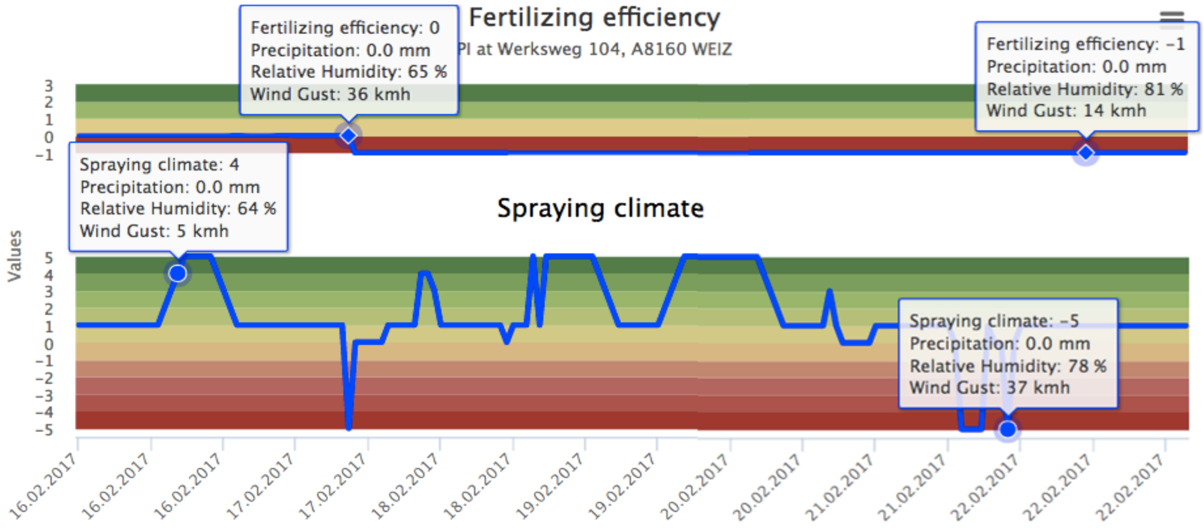


Figure 6. Determination of suitable days by the system

Phenology Camera

Phenological observations have been used to program agricultural work since the beginning of agricultural activities until today. Depending on the developmental stage of grapevines their resistance to frost or pests varies. Phenological observations provide important recommendations for frost warnings and pest control as well as providing important clues about the actual state of the plants. Phenological stages vary greatly from year to year and are affected by environmental factors (micro and macro scale weather and climate conditions, soil conditions, water supply, diseases, competition, etc.) (Koch et al., 2007). In addition, long-term phenological records are needed to clearly demonstrate the changes caused by climate change in phenological periods. Thanks to the phenological cameras (10mp) in the early warning and forecast system established in Üzümlü (Figure 7), 2 daily photographs are taken from the vineyard established with the Karaerik grape variety and stored on the cloud system. Thanks to these stored photographs the differences in the periods of awakening, flowering, veraison and harvest in the vineyards can be compared with climatic parameters and the effects of climate change on the vines can be revealed. In this way it will be possible to make a periodic plan by taking into account the restrictive effect of the climate in the cultural processes to be carried out in the vineyards.

Figure 7. Phenology camera and some of its photographs

Trap with Pheromone Camera

The pheromone camera (Figure 8) which is included in the early warning and prediction system offers solutions based on automatic identification against pests in the vineyard. The pheromone camera can recognize and diagnose 65 pests defined in the system and supports the decision on when to start the fight by monitoring the number of pests and the size of the population on a daily basis. In this way by detecting pests that are difficult to follow with the eye at an early stage and starting to spray at the right time according to the population size unnecessary use of pesticides will be prevented and economic gain will be provided and the amount of residue in the grapes will be reduced and healthy products will be consumed. Since manual traps used instead of pheromone cameras require on-site counting and diagnosis, they require frequent checks. This method causes losses in both time and economic terms.

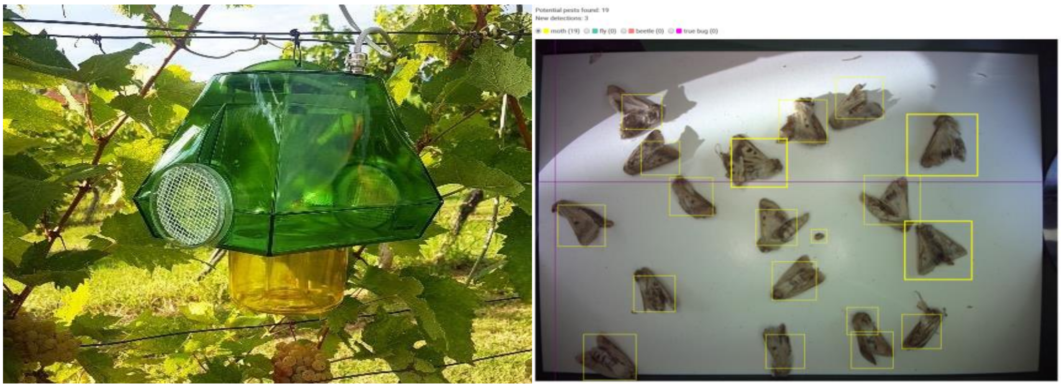


Figure 8. Trap with pheromone camera

Soil Moisture Sensor

It has been reported that the seasonal water requirement of the vineyard is between 500 and 1200 mm, depending on the climate and the length of the growth period, and the maximum daily water consumption of the plant is 5-6 rum. Although the vines adapt to limited irrigation conditions due to their root structure, the yield increases only in the case of supplementary irrigation (Kasimatis 1950; Doorenbos and Kassam 1979). In the early warning and forecasting system, the soil water balance, evapotranspiration level, and daily rainfall (mm) amount can be measured by 3 different sensors placed in the soil at 10 cm, 20 cm and 30 cm depth, and the irrigation water requirement of the vineyard can be determined. In this way, it is evaluated that both yield increase and water saving can be achieved by ensuring that the vineyard is irrigated at the right time and amount (Figure 9).

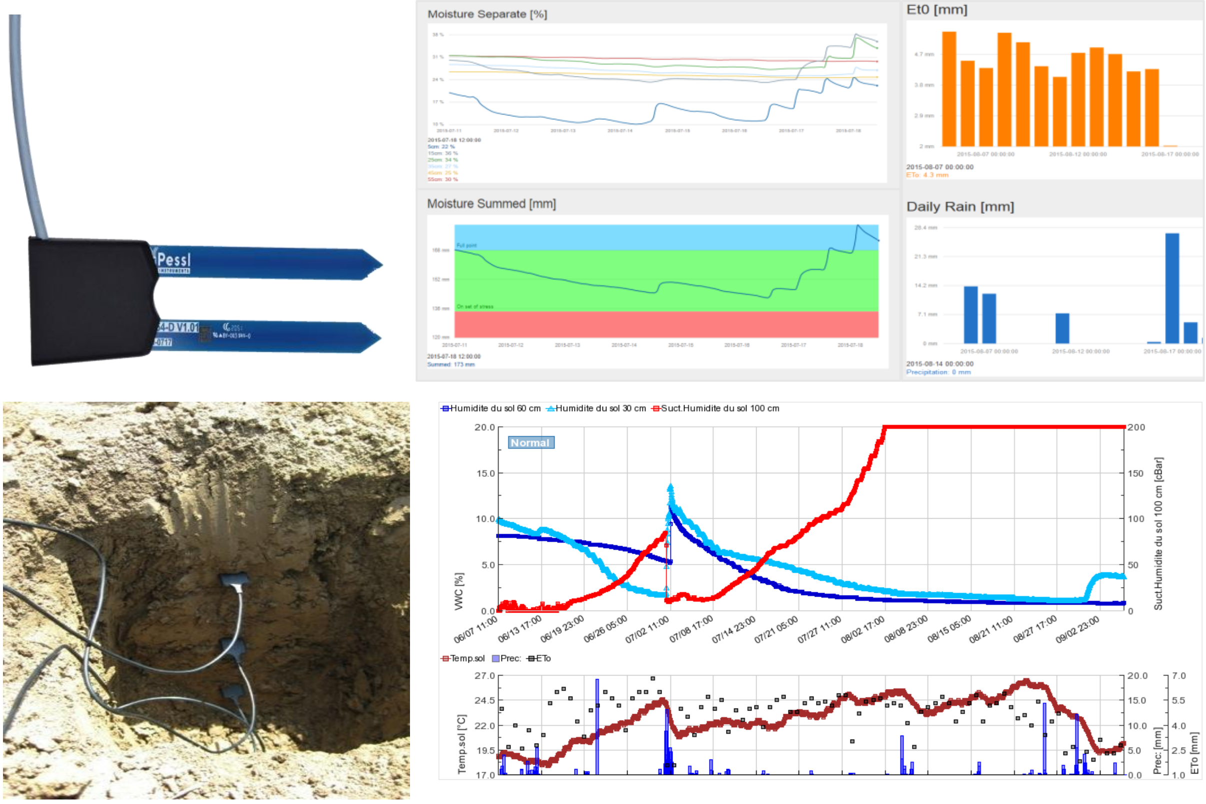
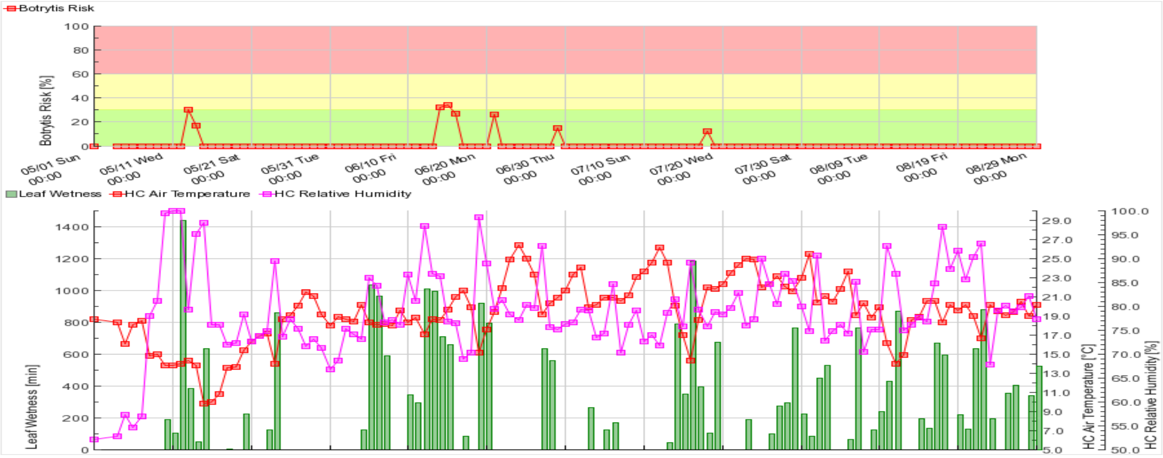


Figure 9. Soil moisture sensor and some collected data

Leaf Wetness Sensor

The sensor on the system acts as a vine leaf and collects data such as the moisture accumulated on the leaf, the duration of sunlight on the leaf and the exposure of the leaf to wind. After the data obtained from this sensor and the data obtained from the climate unit are collected in the cloud system and analyzed with big data (Figure 5), a warning is made against fungal diseases in the primary period. While farmers or technical personnel decide to start spraying according to phenological periods or observations made on the leaf under normal conditions thanks to this system, spraying against diseases is started at the most appropriate time thanks to the analyzed data without the need for any observation or comment (Figure 10).



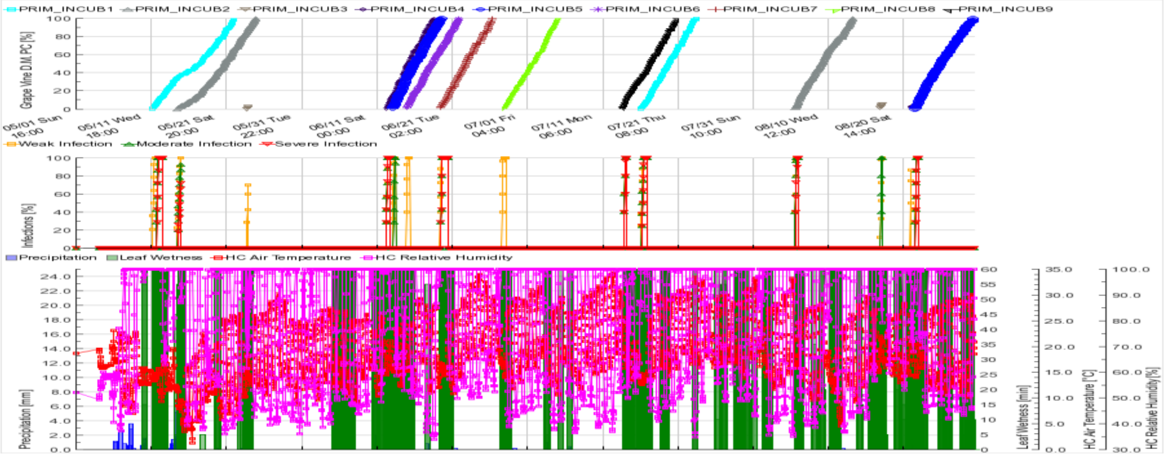


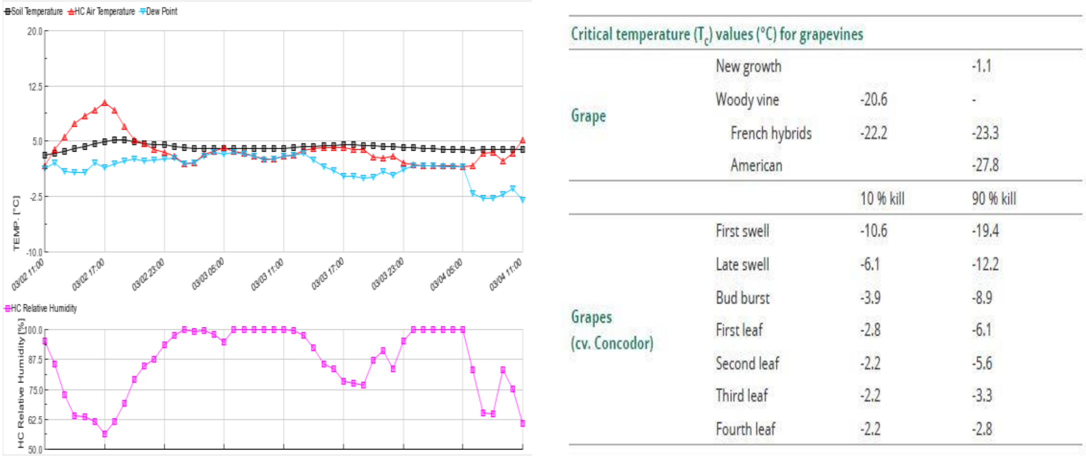
Figure 10. Disease warning by the system

Frost Warning System

Low temperatures and frost events reduce yield in grapevines causing significant product loss and sometimes even causing complete death of the grapevine (Sağlam and Sağlam 2023). Although our country has an important advantage in terms of viticulture in terms of climate conditions, low temperatures and frost events cause yield loss and economic losses in vineyards. Viticulture activities in the Eastern Anatolia Region are faced with many negative effects of the continental climate. For *V. vinifera* L. varieties, low temperatures in winter cause damage at -120 °C in winter buds, -160 °C in branches and -200 °C in branches (Köse and Güleryüz 2009). In fact, according to research it is estimated that approximately 5-15% of world grape production is lost each year due to cold damage (Rende 2017).

In Üzümlü District of Erzincan, where black grapes are grown, the vegetation period is limited and frost events occur frequently. The frost events that occur cause economic losses in the black grape variety which is the only standard variety in the region and finds buyers at high prices in neighboring provinces with its unique taste and appearance (Özoğul 2024).

The early warning system has the ability to send direct SMS warnings in the event of a frost event, giving the producer the opportunity to take measures to protect their productivity. The system monitors the wet and dry air temperatures to determine if there is a risk of frost in the vineyard (Figure 11).



Critical temperature (T_c) values (°C) for grapevines			
Grape	New growth		-1.1
	Woody vine	-20.6	-
	French hybrids	-22.2	-23.3
	American		-27.8
		10 % kill	90 % kill
Grapes (cv. Concodor)	First swell	-10.6	-19.4
	Late swell	-6.1	-12.2
	Bud burst	-3.9	-8.9
	First leaf	-2.8	-6.1
	Second leaf	-2.2	-5.6
	Third leaf	-2.2	-3.3
	Fourth leaf	-2.2	-2.8

Figure 11. Monitor the wet and dry air temperatures

Forecasting systems in viticulture are an important technological product that plays a role in the agricultural optimization and decision-making processes that Agriculture 4.0 offers to farmers (Villa-Henriksen et al., 2020). Real-time use of forecasting systems facilitates decision-making in all processes from product development to recording every stage of production and from pruning to harvest thus providing concrete contributions in terms of efficient use of resources, productivity, cost-benefit and sustainability in vineyards. In this context, Agriculture 4.0 will play a central role in shaping the food sector in the future by creating economic, social and environmental benefits, which are the three main dimensions of sustainability. In Erzincan vineyards, where the history of viticulture dates back thousands of years and has attracted the attention of travelers and historians throughout history, Agriculture 4.0 technology will undertake an important role in protecting the Karaerik grape variety as well as other local varieties that have no commercial value but are a genetic heritage and passing them on to future generations.

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A Study on Super Fruit Goji Berry (*Lycium* spp)

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ABSTRACT: Goji berry has long been used in Asia in areas such as food, medicine, pharmacology, textiles and cosmetics due to its rich nutritional value and bioactive content. Especially in the last twenty years goji berry fruits have been called super fruit and have become popular worldwide due to their natural antioxidant source and rich bioactive components (antiallergic, anticarcinogenic, antioxidant, anti-aging, antiviral, immune-improving, antidiabetic, hepatoprotective, cardioprotective, neuroprotective, cholesterol-lowering, anti-inflammatory, antiosteoporosis). Super fruit goji berry is a bush-like plant that can easily adapt to extreme hot and cold conditions, drought and different soil types and can grow even at an altitude of 3500 m. Thanks to these features goji berry which can be grown in almost every part of Turkey is especially important in terms of opening up agricultural lands that remain idle due to reasons such as unfavorable soil structure, water restrictions, fragmented and small land. It is estimated that this plant which has no market problems due to its different areas of use and attracts attention worldwide will attract attention from farmers as its awareness in Turkey increases and a high income will be obtained from a product with high added value.

Keywords: Goji berry, *Lycium*, *L. barbarum*, Superfruit, Wolfberry

INTRODUCTION

Fruits are frequently consumed worldwide because its rich in bioactive compounds that positively affect human health (Mikulic-Petkovsek et al., 2012; De Souza et al., 2014). In addition to vitamins, dietary fibers and minerals, fruits contain a large number of phenolic compounds and phytochemicals such as carotenoids which are antioxidants, anti-inflammatory and other human health enhancers (Golovinskaia and Wang, 2021). Fruits are consumed fresh, frozen or dried and used as ingredients in different food products and dietary supplements (Salo et al., 2014). Advertisements such as super fruits and functional foods are made as a marketing technique to promote the great benefits of fruits for human health. One of the fruits defined as super fruit is goji berry (Lasekan et al., 2014; Chang et al., 2016). Goji berry is a common name given to the fruits of the species *Lycium barbarum* L., *Lycium chinense* M. and *Lycium ruthenicum* M. which belong to the *Lycium* genus of the *Solanacea* family which includes tomatoes, potatoes and eggplants. *L. barbarum* was described by Carl Linnaeus in 1753 while *L. chinense* was named by Philip Miller in 1768 (Potterat, 2010; Donno et al., 2015; Yao et al., 2018). The *Lycium barbarum* species is best known worldwide as "goji berry" and "wolfberry"

(Sun et al., 2019). The term ‘‘Goji’’ means ‘‘wolf’’ expressed by the word ‘‘gou’’ and its fruits are generally called ‘‘wolf berries’’. It is thought that it was named wolf berries by Chinese farmers because wolves eat these berries. The different species of Goji berry grown in Turkey are also known by different names such as ‘‘atlangaç, şeytan ipliği, teke, teriye çalısı, sincan dikeni, gelecek and boz diken’’ (Güner and Aslan, 2012).

Goji berry an ellipsoid orange-red fruit with a sweet and sour taste about 2 cm deep and in the group of berry fruits is a perennial plant in the form of a bush. This fruit is called the "Super Fruit" of the 21st century (A magase and Nance, 2008). Although its homeland is considered to be China it is mostly grown in Tibet and Mongolia and even in the Himalayas which contain the highest mountains in the world. It is known that the goji berry has a history of 4000 years in China. Goji berry is commercially grown in the Gansu, Xinjiang, Shensi, Hebei and Inner Mongolia regions of China as well as in Japan, Korea, Taiwan and many European countries. Goji berry is also used as a hedge plant in North America and Australia (Hänsel et al., 1993). *L. chinense* is mainly cultivated in East Asia, Southern China, Korea and Japan while *L. barbarum* is cultivated in the Ningxia Hui region in Northern China and the Xinjigang Uygur region in the west (Figure 1) (Qian et al., 2004).

Figure 1. Distribution of *Lycium* in the world (Anonymous, 2019)

Although the genus *Lycium* has more than 80 species (Figure 2) there are 3 species traded in the world (Figure 3). These are *Lycium barbarum* L., *Lycium chinense* Miller, *Lycium ruthenicum* Murray (Wang et al., 2015).

· *L. acutifolium*	· *L. eenii*	· *L. parishii*
· *L. afrum* L.	· *L. europaeum* L.	· *L. pilifolium*
· *L. ameghinoi*	· *L. exsertum* A. Gray	· *L. puberulum*
· *L. amoenum*	· *L. ferocissimum*	· *L. pumilum*
· *L. andersonii*	· *L. flexicaule* Pojark.	· *L. potaninii* Pojark.
· *L. arabicum* Schweinf. ex Boiss.	· *L. fremontii*	· *L. ruthenicum* Murray
· *L. arenicola*	· *L. foetidum*	· *L. sandwicense* A.Gray
· *L. australe* F. Muell.	· *L. fremontii* A. Gray	· *L. schizocalyx*
· *L. austrinum* Miers	· *L. gariepense*	· *L. schweinfurthii*
· *L. barbarum* L.	· *L. halimifolium* Mill.	· *L. shawii* Roem. & Schult.
· *L. berlandieri* Dunal	· *L. grandicalyx*	· *L. shockleyi*
· *L. bosciifolium*	· *L. hassei*	· *L. sokotranum*
· *L. brevipes*	· *L. hirsutum*	· *L. strandveldense*
· *L. californicum*	· *L. horridum* Thunb.	· *L. tenue* L.
· *L. carolinianum* Walter	· *L. intricatum* Boiss.	· *L. tenuispinosum*
· *L. cestroides* Schltdl.	· *L. japonicum* Thunb.	· *L. tetrandrum*
· *L. chilense* Bertero	· *L. macrodon*	· *L. texanum*
· *L. chinense* Miller	· *L. mascarenense*	· *L. torreyi*
· *L. cinereum*	· *L. nodosum*	· *L. turcomannicum*

Figure 2. Species of the *Lycium*

Figure 3. (a) *L. barbarum*, (b) *L. chinense*, (c) *L. ruthenicum*

1) ***Lycium barbarum* L.;** The leaves of this species are lanceolate or long elliptical the flower stalk is 1-2 cm long and the calyx lobes generally contain 2 or 3 teeth at the tip. The corolla tube is 8-10 mm and is distinctly longer than the lobes (5-6 mm). The fruits of *Lycium barbarum* L. are red or orange-yellow, rectangular or oval in shape and the seeds are brown-yellow in color and usually 4-20 in number. Commercial gardens are usually established with varieties of this species and the most commonly used varieties are ‘‘NQ1, NQ3, NQ7, NQ9 and Damaye’’ (Mi et al., 2015).

✓ **NQ1:** The NQ1 variety is one of the varieties frequently preferred by those considering commercial goji berry cultivation. The variety has medium-sized fruits is quite resistant to diseases and pests and begins to bear fruit early. Its leaves are dark green and its thorns are significantly reduced. The average yield per plant in the full yield period is 8 kg. The variety also has the characteristic of rapid growth and development (Oğuz and Erdoğan, 2016).

- ✓ **NQ3:** The trees of this variety are short and start to bear fruit in a very short time. Thanks to the fast and easy growth feature of the variety, the fruits ripen in a short time but the fruits are small in size (Anonymous, 2023).
- ✓ **NQ7:** Most of the modern goji berry gardens established in recent years are established with this variety. Although it has similar characteristics to the NQ1 variety its fruits are larger and have a higher yield of approximately 34% (Oğuz and Erdoğan, 2016).
- ✓ **NQ9:** The variety has similar characteristics to NQ1 and NQ7 varieties its fruits are red, oval or rectangular in shape and its leaves are sharply oval and rectangular. Its seeds are numerous and brown-yellow in color (Oğuz and Erdoğan, 2016).
- ✓ **Damaye:** The Damaye variety is sweet, large and meaty and is a very popular variety. Its aroma is quite appreciated in this variety since the amount of water is low the volume loss is at a minimum level when dried. It has many thorns and is difficult to harvest (Oğuz and Erdoğan, 2016).

2) ***Lycium chinense* M.**: The leaves of plants belonging to this species can be rectangular, sharply oval, lancet or linear. The flower stalk is usually 1-2 cm and half of the calyx is in the form of 3-5 pieces. The corolla tube or lower lobes are shorter the lobes at the base are hairy. The stamen filaments are slightly fluffy hairy. The fruits of this species are red and the seeds are yellow and numerous (Mi et al., 2015).

3) ***Lycium ruthenicum* M.**: In plants of this species, the branches are numerous, the leaves are fleshy, semi-sessile, linear or slightly cylindrical and the flower stalk is usually 5-10 mm long. The calyx is sparsely lobed and irregularly shaped. The filaments are sparsely hairy and the fruit calyx is slightly swollen. In the species *Lycium ruthenicum* M., the fruits are usually spherical, purple-black in color, and sometimes notched on the edges or top. The seed color is brown (Mi et al., 2015).

Ecological Requirements and Cultivation Techniques of Goji Berry

Goji berry is quite resistant to adverse climatic conditions such as low temperature and drought. It can easily grow in dry conditions after the root system adapts to the soil. Although it can be grown in humid regions goji berry cultivation is generally not preferred in coastal areas due to the risk of fungal diseases and late ripening of the fruits. Goji berry plants love sunlight and can withstand temperatures of +39 °C in summer and -26 °C in winter. Goji berry can be produced in almost every region of Turkey and can be grown economically especially at an altitude of 800–2000 m above sea level (Oğuz et al., 2019a; Oğuz et al., 2019b). Goji berry plant is not very selective in terms of soil requirements and can easily grow in well-drained, permeable, slightly sandy, medium-strong, heavy clay loam, alkaline soils with a pH of 7-8 but it does not like acidic soils and soils with high groundwater levels (Maughan and Black, 2015). Regular irrigation is required for 1-2 years after planting in order for the seedlings to adapt to the environment and not dry out (Yılmaz and Kınay, 2016). Goji berry plants shed their leaves in winter and their cooling requirement is 1640 hours (Jing et al., 2004).

Productıon of Goji Berry in World and Turkey

China is the main producer and exporter of goji berry in the world (Amagase and Farnsworth, 2011). In 2014 China's goji berry production was mainly carried out in Ningxia, Qinghai, Qansu, Xinjiang, Inner Mongolia, Hebei, Shanxi, Shaanxi and Henan, covering an area of more than 153.300 ha. Zhongning city of Ningxia plays an important role in the region as an industrial area and the area of goji berry cultivation has reached 56.660 ha. The main areas where goji berry cultivation is in Qinghai are 29.330 ha, Gansu 23.333 ha, Xinjiang 21.333 ha, Inner Mongolia 13.333 ha, Hebei 5.333 ha and 4.038 ha in other regions. China's dried goji berry production is about 250.000 tons of which 10.000 tons are exported generating $120 million in revenue. The total value of Chinese wolfberries exceeds ¥30 billion (Wei, 2020). However, there is no definitive data on goji berry production in the world. In the research conducted in FAO no data on goji berry production could be reached. Goji berry production is carried out in large and small areas in leading countries such as the United Kingdom (UK), the United States (USA), Canada and Australia as well as in China and it is estimated that the total Goji Berry production in the world is of a considerable size today.

In Turkey in recent years, it has been produced in many provinces especially in Sivas, Kayseri, Aksaray, Isparta, Yozgat and Erzincan. It is known that high humidity in coastal areas reduces fruit yield shortens shelf life and that the plant can adapt to altitudes up to 3500 m (Oğuz et al., 2022). There is no official record of the amount of wolfberry produced in Turkey. However according to information obtained from interviews with goji berry producers it is seen that the amount of goji berry production for 2018 did not exceed 25 tons in dried form (Ministry of Agriculture and Forestry, 2021).

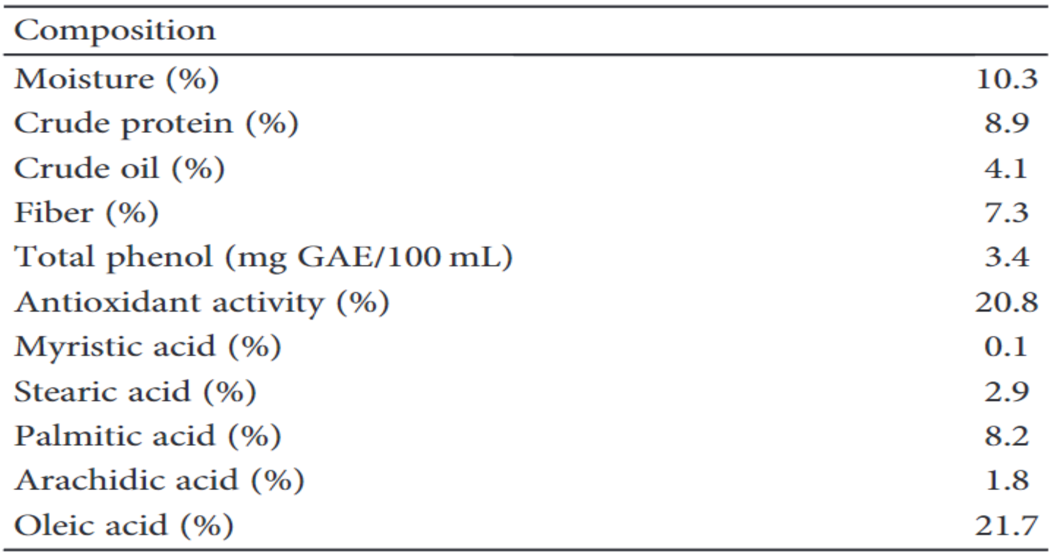
Yield

Goji berry plants start to bear fruit when they are one year old but they reach full yield in the fifth year. While 40 grams of fresh fruit is obtained per tree in the first year approximately 1.5 kg of fruit can be obtained per tree in the fifth year and 10 kg of fruit can be obtained in the tenth year. Similarly dry fruit yield starts from 10 grams in the first year and reaches 2.5 kg in the tenth year (Ministry of Agriculture and Forestry, 2018). According to data from China it is reported that red goji berry (*L. Barbarum* and *L. chinense*) plants reach full yield at the age of 5 and a maximum of approximately 780 kg of fresh fruit can be obtained per decare (Anonymous, 2021).

Nutritional Value and Bioactive Components of Goji Berry

Goji berries are increasingly accepted as a functional food worldwide (J. Cheng et al., 2015) and are marketed as a health food especially in western countries (Xin et al., 2013). Indeed, goji berries have recently gained significant popularity as a "super fruit" in North America and European countries due to their potential health-enhancing properties. Goji berries have been used since ancient times to extend life and for liver, kidney and eye health. Due to its rich medicinal properties and chemical composition goji berries have been consumed as an important food in healthy nutrition for hundreds of years (Potretat, 2010). Goji berries have many bioactive compounds with high antioxidant potential. Goji berries contain 46% carbohydrates, 16% dietary fiber, 13% protein and 1.5% fat. Therefore, goji berries are an excellent source of macronutrients. Goji berries also have micronutrients including vitamins and minerals (Luo et al., 2004). The main bioactive compounds found in goji berries are polysaccharides, carotenoids and phenolics. These functional compounds are closely related to the health-promoting properties of goji berries (Wang et al., 2010). The most important group of these compounds is polysaccharides. Polysaccharides constitute 5-8% of dried goji berries. These are arabinose, galactose, glucose, rhamnose, mannose, xylose and galacturonic acid (Kulczyński and Michałowska, 2016; Amagase and Farnsworth, 2016). Carotenoids are the color components of goji berries and are the second important group of active compounds. The carotenoid content varies from 0.03% to 0.5% in different dried goji berries. Carotenoids are responsible for the bright and vibrant orange to red color of goji berries and the most common carotenoid is zeaxanthin in the dipalmitin zeaxanthin form. In ripe goji berries, zeaxanthin content can account for approximately 77.5% of the total carotenoids (Wang et al., 2010). Phenolic acids and flavonoids can be given as examples of phenolic compounds found in goji berries. Phenolics such as caffeoylquinic acid (0.34 µg/g), caffeic acid (3.73 µg/g), p-coumaric acid (6.06 µg/g), chlorogenic acid (12.4 µg/g), quercetin-diglucoside (66.0 µg/g), rutin (42.0 µg/g) and kaempferol-3-O-rutinoside (11.3 µg/g) (Wang et al., 2010) found in goji berries have very high antioxidant capacity. Table 1 summarizes some of the chemical compounds found in goji berries (Endes et al., 2015).

TABLE 1: Some chemical compounds of goji berries.



Composition	
Moisture (%)	10.3
Crude protein (%)	8.9
Crude oil (%)	4.1
Fiber (%)	7.3
Total phenol (mg GAE/100 mL)	3.4
Antioxidant activity (%)	20.8
Myristic acid (%)	0.1
Stearic acid (%)	2.9
Palmitic acid (%)	8.2
Arachidic acid (%)	1.8
Oleic acid (%)	21.7

(Source: Ma et al., 2019)

Uses of Goji Berry

Goji berry is an important fruit in terms of nutrition with its rich antioxidants, flavonoids, phenolic acids, polysaccharides, carotenoids and vitamin C nutrients (Donno et al., 2016). In addition, it acts at the cellular level with its antioxidant properties and has very beneficial effects on health. (Amagase et al., 2009). The harvest of goji berries begins in late May and continues until mid-October (Çatav, 2019). The harvested berries are dried in the sun and traditionally dried goji berries are cooked before consumption. They are widely consumed in soups and herbal teas in China. Goji berries are also used in the production of tinctures, wine and fruit juice (Ma et al., 2019). Goji berries are added to bakery, confectionery, meat and dairy products, probiotic yogurt and cheese (Figure 4) due to their high antioxidant content and these foods gain antioxidant properties. Goji berries have been used as food and medicine in China for thousands of years and are increasingly consumed as a healthy food around the world (Taneva and Zlatev, 2020; Shori et al., 2021; Vidović et al., 2022).

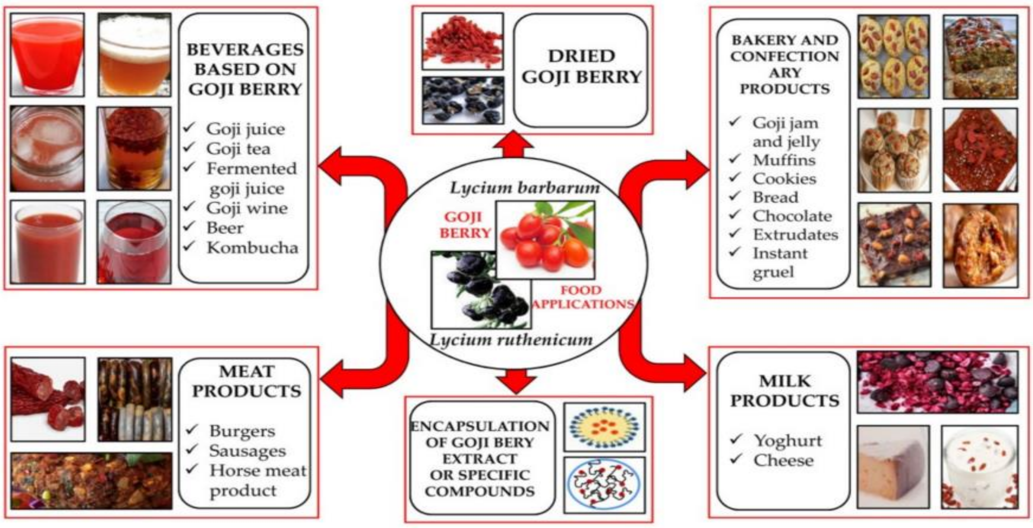


Figure 4. Goji berry-based functional food products

Antioxidant Properties of Goji Berries

Compared to other common berries, goji berries have less antioxidant capacity than black currants and blueberries but they contain more antioxidants than kiwi, raspberries and oranges. Black goji berries (*Lycium ruthenicum*) have stronger antioxidant properties than red goji berries. The antioxidant activity of goji berries is closely related to the presence of polysaccharides, carotenoids, flavonoids and AA-2βG (Xin et al., 2017; Ilic et al., 2020; Liu et al., 2020). In a study it was stated that *L. barbarum* fruit aqueous extract has lipid peroxidation inhibitory, superoxide radical scavenging and superoxide blocking properties depending on the concentration (Xin et al., 2007). In a clinical study investigating the general effects of goji berry juice an increase in energy levels, intelligence, ability to focus, sleep quality, happiness and comfort levels was observed in the juice group (n=16) and a decrease in stress and fatigue rates was observed. Improvement in digestive functions was also detected (Amagase and Nance, 2008). In another study after 50 g/day of goji berry fruit was given orally to 25 healthy individuals between the ages of 64-80 for 10 days an increase in superoxide dismutase (SOD) and hemoglobin levels was observed while a decrease in lipid peroxide levels was observed (Khan and Abourashed, 2010). The antioxidant capacity of goji berry is reported in Table 2.

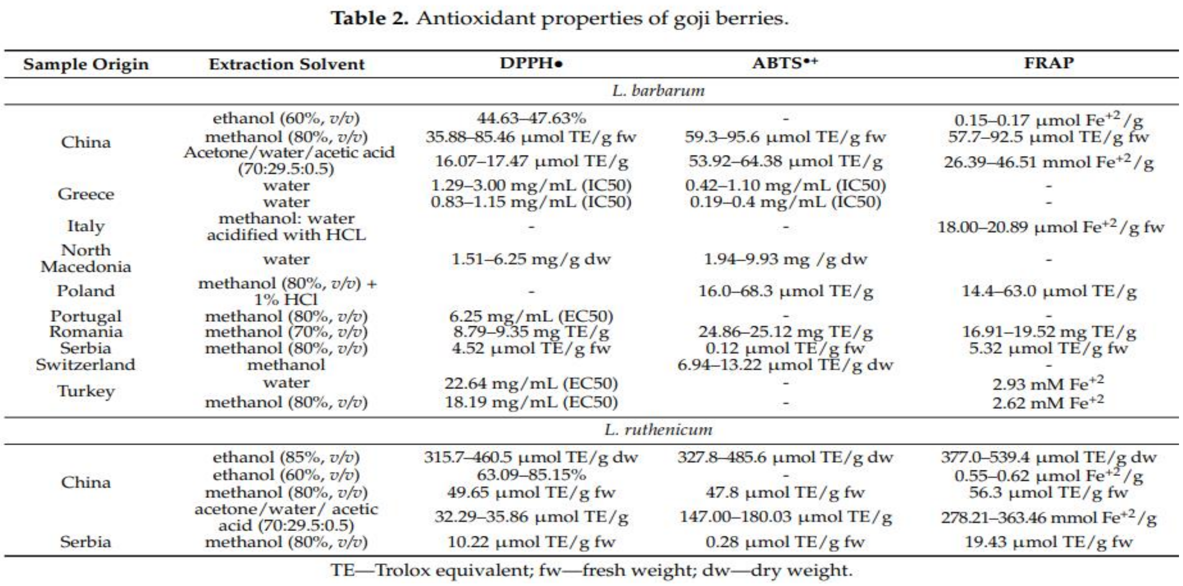


Table 2. Antioxidant properties of goji berries.

Sample Origin	Extraction Solvent	DPPH•	ABTS$^{\bullet+}$	FRAP
		L. barbarum		
China	ethanol (60%, *v/v*)	44.63–47.63%	-	0.15–0.17 μmol Fe^{+2}/g
	methanol (80%, *v/v*)	35.88–85.46 μmol TE/g fw	59.3–95.6 μmol TE/g fw	57.7–92.5 μmol TE/g fw
	Acetone/water/acetic acid (70:29.5:0.5)	16.07–17.47 μmol TE/g	53.92–64.38 μmol TE/g	26.39–46.51 mmol Fe^{+2}/g
Greece	water	1.29–3.00 mg/mL (IC50)	0.42–1.10 mg/mL (IC50)	-
	water	0.83–1.15 mg/mL (IC50)	0.19–0.4 mg/mL (IC50)	-
Italy	methanol: water acidified with HCL	-	-	18.00–20.89 μmol Fe^{+2}/g fw
North Macedonia	water	1.51–6.25 mg/g dw	1.94–9.93 mg /g dw	-
Poland	methanol (80%, *v/v*) + 1% HCl	-	16.0–68.3 μmol TE/g	14.4–63.0 μmol TE/g
Portugal	methanol (80%, *v/v*)	6.25 mg/mL (EC50)	-	-
Romania	methanol (70%, *v/v*)	8.79–9.35 mg TE/g	24.86–25.12 mg TE/g	16.91–19.52 mg TE/g
Serbia	methanol (80%, *v/v*)	4.52 μmol TE/g fw	0.12 μmol TE/g fw	5.32 μmol TE/g fw
Switzerland	methanol		6.94–13.22 μmol TE/g dw	-
Turkey	water	22.64 mg/mL (EC50)	-	2.93 mM Fe^{+2}
	methanol (80%, *v/v*)	18.19 mg/mL (EC50)	-	2.62 mM Fe^{+2}
		L. ruthenicum		
China	ethanol (85%, *v/v*)	315.7–460.5 μmol TE/g dw	327.8–485.6 μmol TE/g dw	377.0–539.4 μmol TE/g dw
	ethanol (60%, *v/v*)	63.09–85.15%	-	0.55–0.62 μmol Fe^{+2}/g
	methanol (80%, *v/v*)	49.65 μmol TE/g fw	47.8 μmol TE/g fw	56.3 μmol TE/g fw
	acetone/water/ acetic acid (70:29.5:0.5)	32.29–35.86 μmol TE/g	147.00–180.03 μmol TE/g	278.21–363.46 mmol Fe^{+2}/g
Serbia	methanol (80%, *v/v*)	10.22 μmol TE/g fw	0.28 μmol TE/g fw	19.43 μmol TE/g fw

TE—Trolox equivalent; fw—fresh weight; dw—dry weight.

(Source: Vidovi´c et al., 2022)

Goji berry fruits have many beneficial effects including anti-aging, cancer protection, immune response enhancement, increased antioxidant activity, blood sugar regulation, anti-viral, cardioprotective, neuroprotective, hypolipidemic properties. Goji berry is also thought to have positive effects on reproductive health (Cheng et al., 2014; Ma et al., 2019; Alp 2023).

Conclusion

Goji berry has the characteristics to grow easily all over Turkey. There are thousands of hectares of agricultural land in Turkey that are not used due to social and economic reasons. One of the main reasons for this situation is that it is not possible to make economic profit in fragmented and small agricultural lands. In addition, agricultural lands that are not cultivated due to water restrictions also have an important share. Even if goji berry cultivation is done in small areas the use and processing of the fruit obtained in many areas allows export and provides profit. It is evaluated that by making this fruit more known and grown in Turkey the country's lands can be used efficiently and it can have a strong economic share especially in the European and US markets in terms of exports.

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Electrochemical Detection of 5-hydroxymethylfurfural with Bismuth Oxide Nanoflower Electrode

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ABSTRACT: Hydroxymethylfurfural (HMF) is formed when sugary foods are stored at inappropriate temperatures or subjected to high temperature heat treatment during production. The present study reported the electrochemical determination of 5-hydroxymethylfurfural (HMF) obtained with Bi_2O_3 nanoflower (the chemical selectivity) electrodes synthesis by electrodeposition method. The aim of this study is to determine the amount of HMF in honey by using the electrochemical cyclic voltammetry (CV) method, which is a direct and rapid technique, by synthesizing Bi_2O_3 nanoflower-shaped electrodes with high selectivity and large surface area by the electrodeposition method. Electrochemically produced bismuth oxide nanoflower films with high crystallinity were characterized by deposition on indium tin oxide. The influence of coating period on the shape, structure, and characteristics of electrochemically formed metal oxides was also examined. Bi_2O_3 modified metal oxide electrode was successfully manufactured using an electrochemical method and characterized using potential controlled electrochemical deposition, scanning electron microscopy, X-ray diffraction techniques, and UV-VIS measurements.

Keywords: Bismuth Oxide Nanoflower Electrode, Hydroxymethylfurfural, Electrochemical Sensor, Electrodeposition Method

INTRODUCTION

Nanomaterials including titanium oxide (TiO_2), silicon oxide (SiO_2), silver, iridium oxide, graphene, bismuth (III) oxide (Bi_2O_3), and fullerenes, among others, are commonly employed in electrochemical sensors and biosensors. These biosensors have been effectively employed for sensor preparation, and they are stable and simple to make. Because of its distinctive features such as energy bandgap, wide surface area, electrochemical stability, and excellent catalytic activity applications, Bi_2O_3 is regarded one of the most encouraging electrode substances for electrochemical sensing devices among all nanomaterials. Its sensitivity, electrical conductivity, chemical stability and a favourable electrochemical sensor for voltammetric measurement have all been demonstrated (McAllister et al., 2007, Anandan et al, 2010, Kim et al, 2012, Mathkar et. al, 2012). Bismuth (III) oxide is also non-toxic and chemically inert, as well as biocompatible. Nanoscale bismuth (III) oxide offers more benefits than macroscale bismuth (III) oxide, and its higher surface free energy makes it suited for biomolecule adsorption. It has also turn up as one of the strongest competitors among the most common UV-active TiO_2 photocatalyst, especially Bi2O3 (Kamat, 2011). Bismuth is non-poisonous in its oxide shapes and can be used in active apps such as piezoelectric material (Kuma&Devi, 2011), biosensors functional glasses, etc. (Panda, 2009). Current research on the photocatalytic activities of the distinct phases of Bi_2O_3 indicates that they are non-toxic and resistant to photo corrosion (Ünlü et al, 2021, Molinari et al, 2020).

Hydroxymethylfurfural (HMF) is a cyclic aldehyde, formed by the degradation of hexose, caramelization, and Maillard reaction during food processing and shelf-life (Özyurt et al, 2023). The formation of HMF in food depends on temperature, type of sugar, pH, water activity, and concentration of divalent cations in the media (Capuano and Fogliano, 2011). It can present in overly processed foods such as baked, toasted, fried, roasted food and sterilized products. Also, it is one of the most important quality indicators, since it can be used as a denoter for food freshness. Therefore, sensors that enable the detection of low amounts of HMF are being developed (Barzegar and Kamankesh, 2021). Among sensor technologies, electrochemical methods have many advantages over others in terms of accuracy, precision and cost. It is very important that the electrodes used for the electrochemical detection of HMF are non-toxic, low-cost, and have good detection properties (Reyes-Salas et al. 2016).

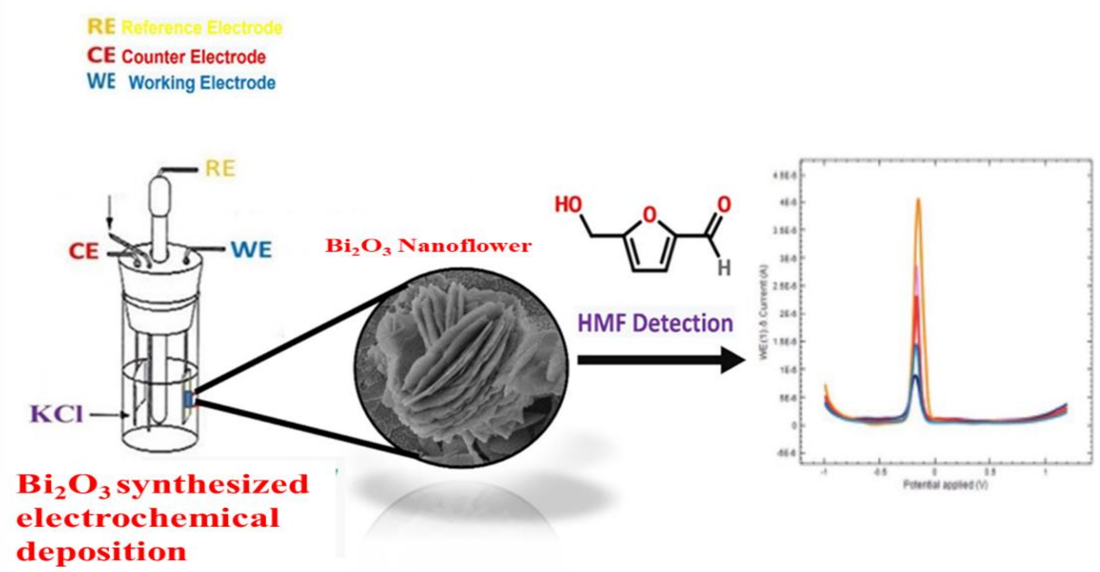


Figure 1. Systematic demonstration of HMF detection with Bi_2O_3 nanostructure electrodes.

Material and Method

Electrochemical experiments were conducted at room temperature with a BAS 100B/W electrochemical workstation connected to a three-electrode cell (C3 Cell Stand, BAS). The working electrode indium tin oxide (ITO)-coated quartz substrate with a sheet resistance of 10 Ω cm^{-2} was used as the working electrode for optical measurements. The reference electrode was an Ag/AgCl (3 M NaCl) for all electrochemical experiments, and a platinum wire was used as the counter electrode. Deionized water (i.e., >18 MΩ) was used in all experiments. Dissolved O_2 gas, 1 mM $Bi(NO_3)_3$, pH 1.5 At room temperature, electrochemical Bi_2O_3 nanostructure deposition was executed. For 30 minutes, maintain a steady voltage of +300 mV. The Bi_2O_3 working electrode was dried at room temperature, and the film was cured for roughly one minute with O_2 gas. The Bi_2O_3 modification was applied electrochemically to ensure that the surfaces generated by the potential controlled electrolysis process of nanostructured Bi_2O_3 films on ITO substrates at a constant voltage (+300 mV) had a high surface area (Figure 1). Scanning electron microscopy measurements (SEM) in the analysis were performed in ambient conditions with a Zeiss Sigma 300 instrument. AFM imaging was performed in the air using a Hitachi 5100N instrument to take surface topography and 3D images. X-ray diffraction patterns were acquired using a PANalytical Empyrean. Absorption measurements were performed using a Shimadzu UV-3101 UV-vis-nearIR spectrometer at room temperature.

Results and Discussion

Figure 2 show the SEM image taken after electrochemical Bi_2O_3 nanoflower deposition and Bi_2O_3 nanostructures electrodeposited on ITO electrodes consist of nanoflower. This observation shows that the deposition potential (+300 mV) and concentration, which provides a significant effect in the morphology-controlled synthesis of Bi_2O_3 nanostructures, remain Bi_2O_3 constant throughout the electrochemical treatment. These results also show that the surface area is increased as much as possible by coating the Bi_2O_3 films.

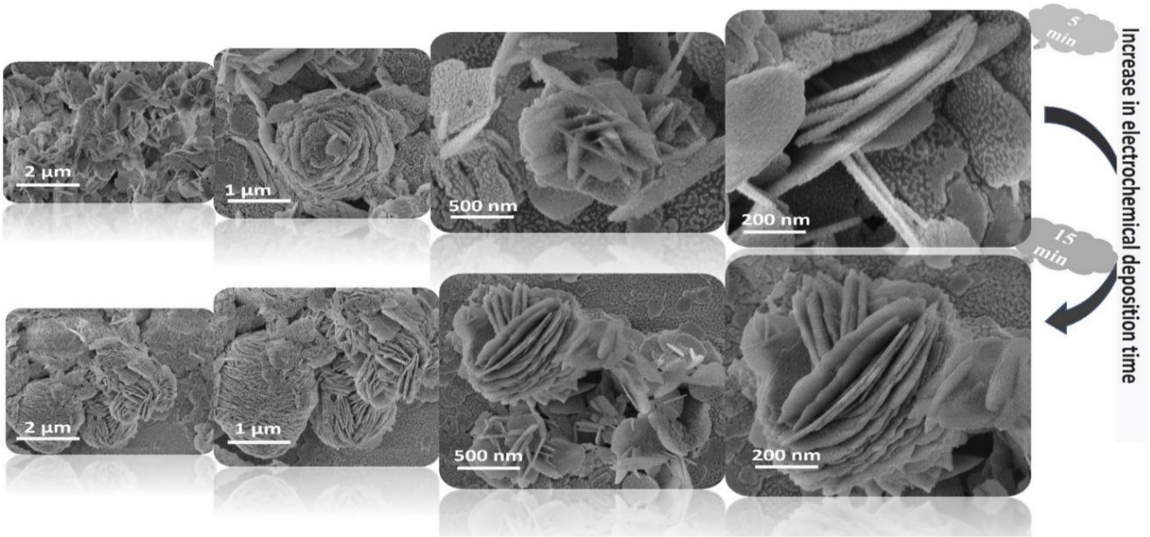


Figure 2. SEM images of Bi_2O_3 nanostructures obtained at different deposition times on the ITO electrodes for 5 min and 15 min

The observation of a single and very strong (212) peak belonging to the Bi_2O_3 phase indicates that it has a preferential electrochemical growth orientation. In the XRD diffractogram of the electrodeposited Bi_2O_3 at 2θ=11.56, 2θ=40.09 (212), 2θ=55.02 (421) and other peaks of the ITO substrate as the working electrode (Figure 3) are clearly seen the observation of a single and very strong (212) peak belonging to the Bi_2O_3 phase indicates that it has a preferential electrochemical growth orientation (Yang&Lin, 2020). It is clearly seen in the XRD spectra that the peak intensities of Bi_2O_3 increase with the increase in deposition time. AFM data of Bi_2O_3 are given in Figure 3. In the AFM data, as in the 3D images of Bi_2O_3 thin films are homogeneously completely coated on the ITO electrodes, while Bi_2O_3 shows morphological properties like a nanoflower.

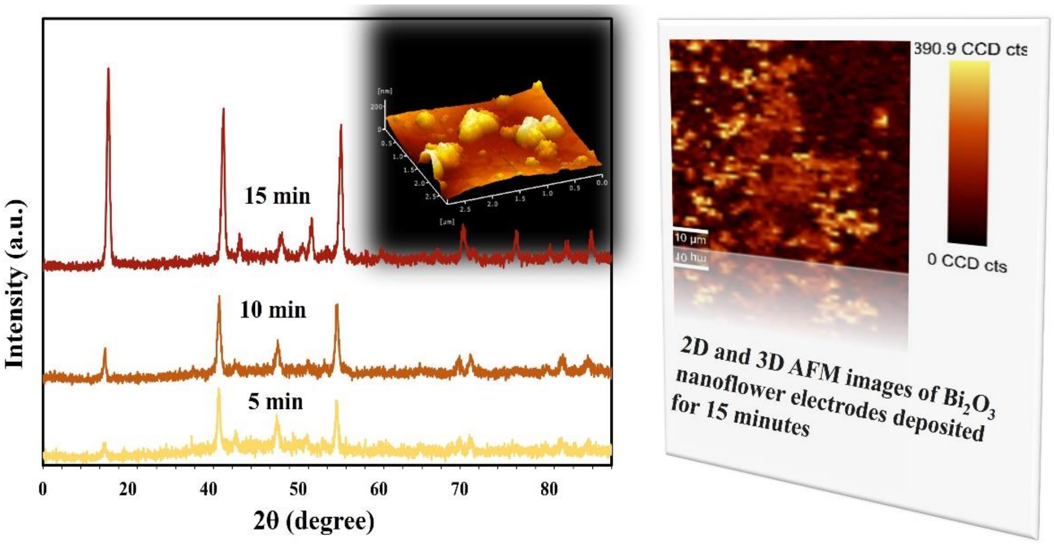


Figure 3. X-ray diffractions of Bi_2O_3 nanostructured films obtained as a result of electrodeposition on ITO electrodes for 5, 10, 15 min. Radiation source: Cu-Kα and 2D and 3D AFM images of Bi_2O_3 nanoflower electrodes deposited for 15 minutes

Spectroscopic examination was carried out using UV-Vis spectroscopy techniques. Figure 4 shows UV spectra Bi_2O_3 nanostructured electrodes at different deposition times. Depending on the increase in deposition time, Bi_2O_3 nanoflower films obtained by electrodeposition for 5, 10 and 15 minutes show absorption in the light region from approximately 312 nm to 314 nm as the deposition time increases.

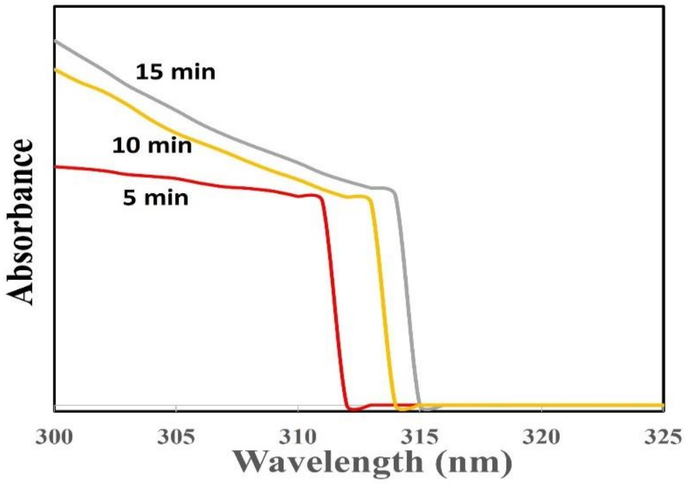


Figure 4. Absorption spectra of Bi_2O_3 nanostructured films obtained as a result of electrodeposition on ITO electrodes for 5, 10, 15 min

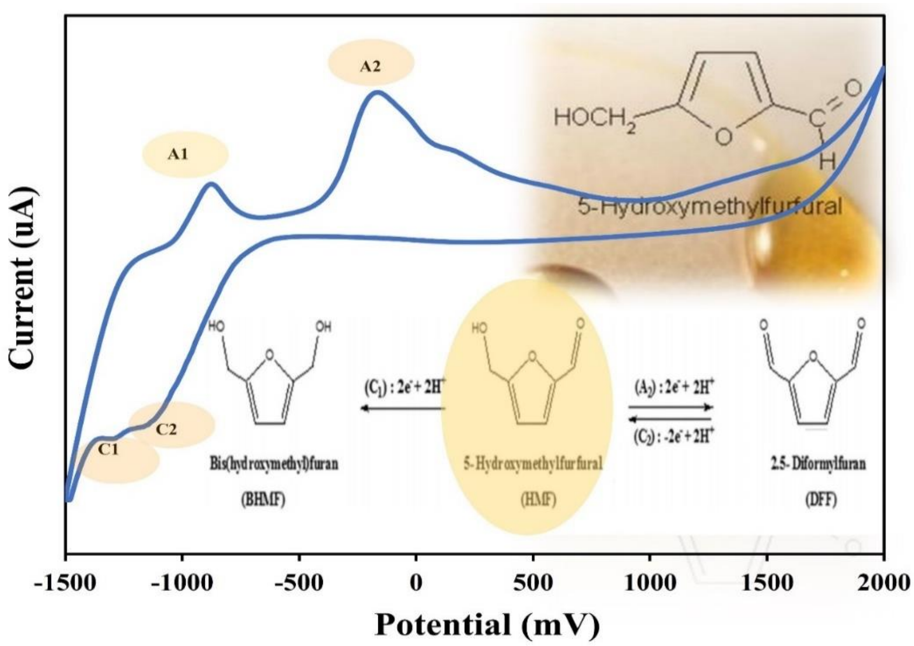


Figure 5. Cyclic voltammograms of the Bi_2O_3 electrode in 0.016 M Na_2SO_4 solution containing 0.14 g L^{-1} 5-hydroxymethylfurfural. pH:7, v = 100 mV s^{-1} T = 25 °C

To identify the redox couple A2/C2, voltammograms of HMF intermediates (DFF,HMFCAand FDCA) were plotted under the same conditions (Figure 5). Examination of these figures showed that only the electroreduction of the DFF gave two cathodic peaks towards−0.9 and−1.6 V in coincidence with the peaks C2 and C1, respectively. In order to attain a good analytical signal, the potential scan was limited between 0 and−2 V. The cathodic peak C1 was investigated under different experimental parameters. To determine the process that limits the reduction reaction of 1.26 g L^{-1} HMF at pH=7 on the Bi_2O_3 electrode, voltammograms were plotted at different potential scan rates between 100 and 300 mV s^{-1} (Figure 6). The current of the peak C1 increased with the potential scan rate.

The effect of temperature on the Bi_2O_3 electrode response was examined at different temperatures using 0.016 M Na_2SO_4 solutions (adjusted at pH= 7 containing 0.14 g L^{-1} HMF. An overlay of cyclic voltammograms with a scan rate of $100 mVs^{-1}$ is shown in Figure 6. As can be observed, the CV currents Increase with temperature. The current is multiplied by a factor of 2.01 when the temperature increases from 25 to 50 °C. This significant catalytic effect is due to the important solubility and advanced mass/charge transfer of reactive species around the surface of the electrode at elevated temperatures.

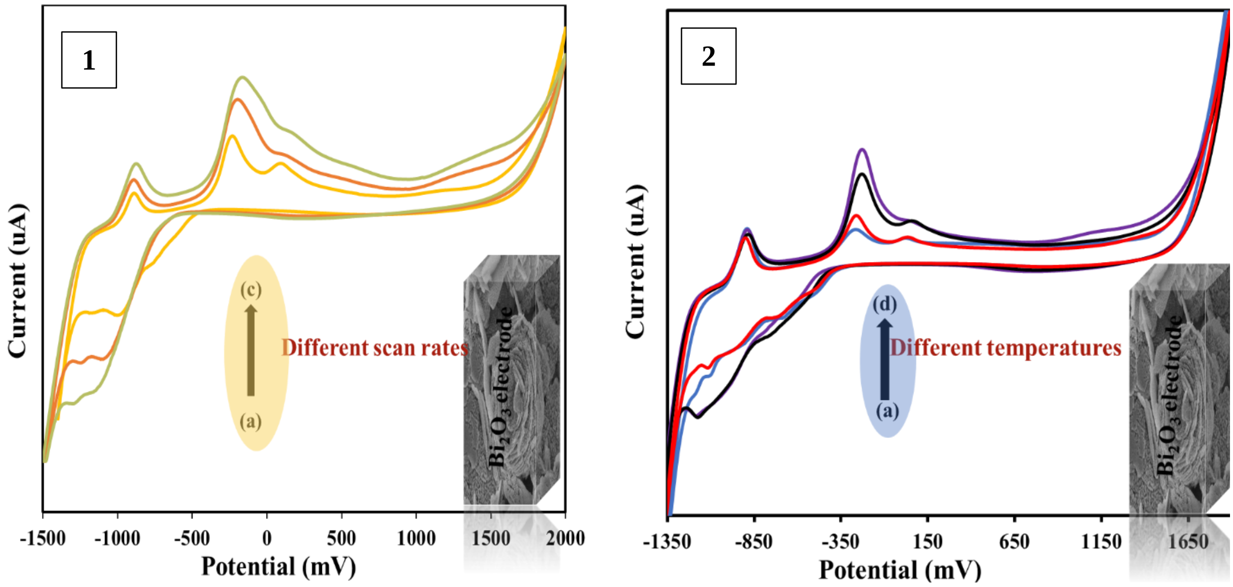
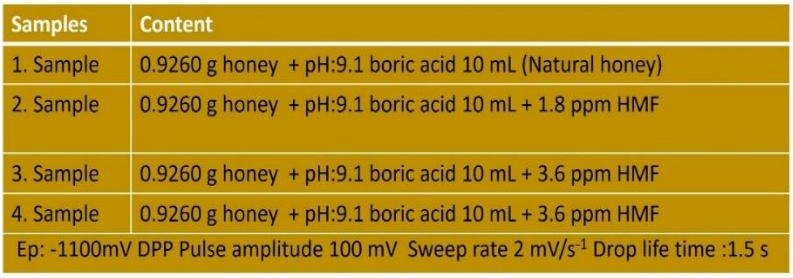


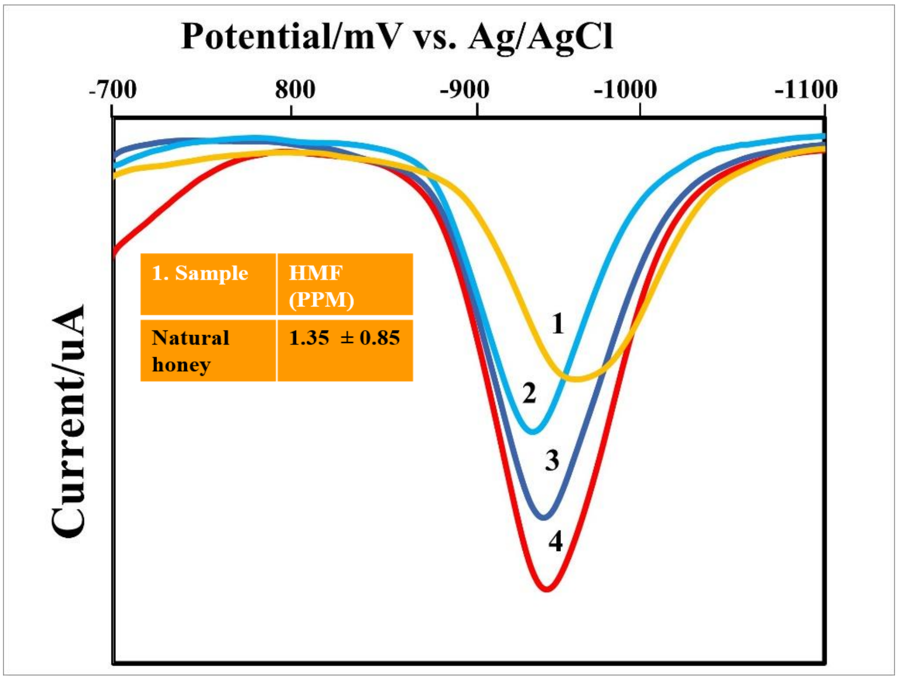
Figure 6. (1) Cyclic voltammograms of Bi_2O_3 electrode in 0.016 M Na_2SO_4 solution containing 1.4 g L^{-1} 5 hydroxymethylfurfural recorded at different scan rates. (a) 100; (b) 200; (c) 300; T = 25 °C and (2) Cyclic voltammograms of Bi_2O_3 electrode in 0.016 M Na_2SO_4 solution containing 0.14 g L^{-1} 5-hydroxymethylfurfural recorded at different temperatures. (a) 25; (b) 35; (c) 50°C and v = 100 mV s^{-1}

The HMF concentration in the honey samples was determined using the polarograms produced with a borate medium (Table 1). As HMF concentration decreased between the honey samples, measurement ambiguity increased, which derives from the low ambiguity in measuring high currents and the high ambiguity in measuring low currents. Polarograms of samples 1, 2, 3 and 4 were taken in Borate medium with the increase in current density well-defined HMF signals (Figure 7) openly demonstrate.

Table 1. Sample contents for Differential Pulse Polarography (DPP)



Samples	Content
1. Sample	0.9260 g honey + pH:9.1 boric acid 10 mL (Natural honey)
2. Sample	0.9260 g honey + pH:9.1 boric acid 10 mL + 1.8 ppm HMF
3. Sample	0.9260 g honey + pH:9.1 boric acid 10 mL + 3.6 ppm HMF
4. Sample	0.9260 g honey + pH:9.1 boric acid 10 mL + 3.6 ppm HMF
Ep: -1100mV DPP Pulse amplitude 100 mV Sweep rate 2 mV/s^{-1} Drop life time :1.5 s	



1. Sample	HMF (PPM)
Natural honey	1.35 ± 0.85

Figure 7. Sample 4 polarograms using Differential Puls Polarography (DPP) and standard addition method with Bi_2O_3 electrode. Pulse amplitude: 100 mV; sweep rate: 2 mV s; drop life time: 1.5 s. Curve 1: 10 mL of 0.5 M borate solution (pH9.1) plus 1 mL Sample 1 solution (0.9260 g honey); curves 2 to 4: successive HMF standard additions; final standard molar concentration (HMF)

Conclusion

A simple and sensitive electrochemical sensor based on bismuth oxide nanoflower that was coated onto a Bi_2O_3 nanoflower electrode was prepared and used for hydroxymethylfurfural (HMF) detection. It was observed that bismuth film electrode greatly accelerated the electron transfer rate and showed excellent electrochemical activity for the oxidation of HMF compared to bare ITO electrode. The effects of HMF concentration, scan rate and temperature on the responses of Bi_2O_3 for the detection of HMF were optimized. The presence of HMF in food has been strictly restricted by regulations due to its toxic effects on health, so the development of simple and rapid analytical methods for detection of HMF is of great importance. As a result, it was observed that, Bi_2O_3 based electrochemical sensor increased the sensitivity and paved the way for accurate and repeatable measurements for detection of HMF. Bi_2O_3 based electrochemical sensor provides a cost-effective route for the electrochemical detection of HMF. Therefore, it is believed that Bi_2O_3 nanoflower based electrochemical sensor can also be applied to other food samples and represents an alternative method for HMF detection in the future.

Statement of Conflict of Interest

The author(s) should declare that they are no conflict of interest.

Authors' Contributions

Semanur Bayrakçı and Fatma Bayrakçeken Nişancı designed and analyzed the research, Semanur Bayrakçı and Fatma Bayrakçeken Nişancı studies arranged Semanur Bayrakçı worked on the preparation of Fatma Bayrakçeken Nişancı pictures and tables. All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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Erosion Process in Meadows and Rangelands

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ABSTRACT: Meadows and rangelands play a vital role in the sustainability of agriculture and livestock. These areas, where vegetation cover is critical for soil conservation, face environmental threats such as water and wind erosion. Climate change and improper land use accelerate these processes, increasing soil loss in meadows and rangelands. The impacts of erosion not only reduce soil fertility but also disrupt regional ecosystem balances. This paper examines the key factors contributing to erosion in meadows and rangelands and discusses physical and biological measures to prevent it. Additionally, it highlights the positive effects of strategies such as grazing management and vegetation protection on the sustainability of these areas. Based on studies conducted in Türkiye, the paper discusses the measures and policies that can be implemented to mitigate the effects of erosion. In this context, it concludes that the promotion of soil conservation and sustainable land management practices is necessary.

Keywords: Erosion, Water Erosion, Wind Erosion, Meadows, Rangelands

INTRODUCTION

Soil is the primary resource plants utilize for growth and development, providing the essential water and nutrients they need. However, globally, approximately 6 million hectares of agricultural land out of 1.2 billion hectares are eroded annually. It is reported that the formation of 1 cm of topsoil in nature takes 200-400 years (Pimentel and Burgess, 1995). Despite being considered a non-renewable resource due to its lengthy formation process, an average of 75 billion tons of soil is transported annually by water and wind erosion worldwide (Anonymous, 2023). Indeed, water and wind have been identified as the most influential factors in soil displacement (Altın et al., 2021). Furthermore, the World Soil Resources Status Report (SWSR) emphasizes that soil erosion poses a major threat, particularly in arid and semi-arid regions like the Eurasian zone, including Türkiye (Anonymous, 2015).

Türkiye, due to its topography, climate, soil conditions, and geographical location, is highly susceptible to drought and erosion. Human interventions and climate change exacerbate this situation (Rehman et al., 2015). Factors such as rapid population growth, urbanization, degradation of natural areas, and misuse of fertile agricultural, forest, and pasturelands increasingly contribute to this severity. As a result of erosion, plant nutrients and organic matter are transported along with the soil, reducing soil fertility. The soils in arid and semi-arid regions of Türkiye are naturally poor in organic matter (Küçükkaya, 2010), and the topsoil transported by erosion is typically rich in organic matter (Koralay and Kara, 2022). It has been stated that the rate of soil erosion in Türkiye exceeds the rate of soil formation by 48 times (Erpul and Saygın, 2012).

Erosion is divided into two types: geological erosion (natural erosion) and accelerated erosion. While geological erosion occurs depending on climatic and land conditions, accelerated erosion arises due to improper agricultural practices, overgrazing, deforestation, and non-agricultural activities. Globally, 80% of land sensitive to geological erosion is rangelands (Gökkuş and Koç, 1993). Additionally, it is reported that soil erosion on cultivated lands and overgrazed areas is 100-1000 times greater than geological erosion (Anonymous, 2015). Overgrazing reduces soil organic matter, compacts the soil, and ultimately increases soil erosion (Faizul et al., 1995). However, rangeland vegetation grows better in soils rich in nutrients and with adequate water.

Globally, rangelands experience more water and wind erosion than expected due to geological reasons. Uncontrolled fires, deforestation around pastures, unnecessary plowing, severe drought, overgrazing, and untimely grazing exacerbate this damage (Altın et al., 2021). Particularly in heavily grazed rangelands, deterioration in vegetation structure and soil properties occurs (Mofidi et al., 2012). This situation can lead to desertification in some years and areas due to erosion.

Erosion is classified based on the factors causing soil loss as water erosion, wind erosion, and glacial erosion. Both water and wind erosion occur depending on factors such as the amount, distribution, and frequency of precipitation; soil characteristics (e.g., soil moisture, aeration, organic matter content, structure, and texture); land features (e.g., slope degree and length); the presence of prevailing winds, the speed, frequency, duration, and timing of strong winds; and the structure of vegetation. In general, water erosion increases with annual rainfall, while wind erosion decreases as vegetation cover increases (Altın et al., 2021). Additionally, the ground cover ratio of rangelands indicates resistance to erosion; water erosion increases when the ground cover ratio falls below 30%, and both water and wind erosion increase when it falls below 10% (Marshall, 1973).

Water Erosion

Water erosion is a type of erosion that occurs as a result of precipitation and the subsequent surface runoff. When examining the map showing the distribution of water erosion across different regions of Türkiye (Figure 1), it is evident that approximately 86% of Türkiye's soils are affected by water erosion to varying degrees.

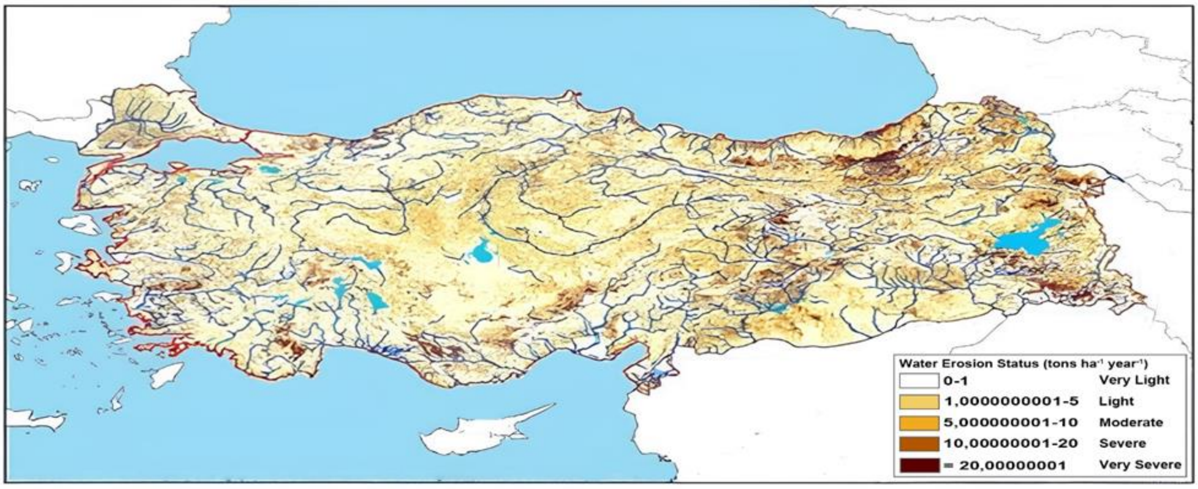

Figure 1. Türkiye Water Erosion Map (Anonymous, 2023)

In regions with an average annual total rainfall below 250 mm, the amount of rainfall is insufficient to cause erosion. Conversely, in areas receiving more than 1000 mm of rainfall annually, the land is completely covered with vegetation, protecting the soil from erosion. Regions with rainfall levels between these two values are more susceptible to water erosion. Holechek et al. (1995) stated that the most erosion-prone areas globally are those with annual rainfall between 250-1000 mm, particularly in regions with rangeland vegetation. Furthermore, even in regions with high rainfall, if the vegetation cover is destroyed, the severity of erosion can increase (Altın et al., 2021). Vegetation reduces the kinetic energy of raindrops, protects the soil, acts as a barrier against sediment flow, and thus prevents erosion (Dursun and Babalık, 2023).

In areas where the annual average total precipitation is below 250 mm, the amount of rainfall is insufficient to cause erosion, while lands receiving over 1000 mm of precipitation are entirely covered with vegetation, thereby protecting the soil from erosion. Regions with precipitation levels between these two thresholds are more susceptible to water erosion. Holechek et al. (1995) noted that the most erosion-prone regions globally are those receiving 250–1000 mm of annual precipitation, particularly areas dominated by rangeland vegetation. However, it should not be overlooked that even in regions with high precipitation, the destruction of vegetation can lead to increased erosion severity (Altın et al., 2021). Vegetation coverage enhances resistance to both water and wind erosion (Alay et al., 2016). Vegetation reduces surface runoff, diminishes the kinetic energy of raindrops, protects the soil, and acts as a barrier by reducing sediment flow, thereby preventing erosion (Dursun and Babalık, 2023).

According to the 2023 water erosion report by the General Directorate of Combating Desertification and Erosion, the amount of soil transported by water erosion in 1970 was 500 million tons per year. However, through efforts such as afforestation, erosion control, forest rehabilitation, rangeland improvement, prevention of overgrazing, and the implementation of advanced irrigation techniques in agricultural areas, this figure had decreased to 130 million tons per year by 2023 (Figure 2).

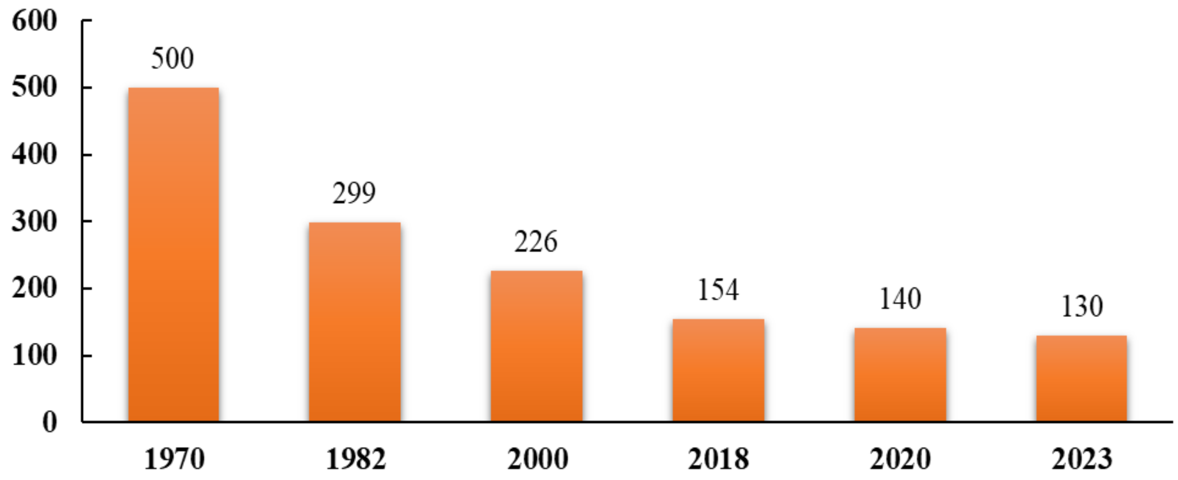

Figure 2. Soil Loss Due to Water Erosion (million tons per year) (Anonymous, 2023)

Topography (47.55%), vegetation cover (34.82%), soil properties (3.36%), and precipitation (14.26%) are significant factors influencing erosion (Figure 3). Among these, topography and vegetation cover are the most influential (Kara et al., 2018; Erdem and Türkmen, 2020). Soils with adequate vegetation cover are significantly protected from erosion, as vegetation reduces surface runoff and thereby minimizes erosion (Congo-Rwanda et al., 2016). In short, vegetation acts as a mechanical barrier against surface runoff caused by precipitation, depending on factors such as its density, coverage ratio, and height (Ibrahim et al., 2012). Key climatic factors influencing the erosion process include the duration, intensity, amount, impact force, droplet size, and angle of rainfall (Aykır and Fıçıcı, 2022). Raindrops are particularly critical in dislodging soil particles. Larger droplets create strong impacts that dislodge and scatter larger soil particles, while smaller droplets disturb finer particles. These dislodged materials are transported downslope by the combined effects of gravity and the carrying capacity of water, ultimately accumulating in lower areas (Aykır and Fıçıcı, 2022). Indeed, water erosion is frequently reported in regions with high precipitation and sloped terrains (Çelebi, 2021).

Figure 3. Factors Influencing Erosion in Türkiye (Anonymous, 2023)

A large part of Türkiye consists of sloped areas, and slope is one of the most significant causes of erosion. Each year, approximately 642 million tons of soil are transported due to water erosion in Türkiye (Erpul et al., 2020). In terms of severity classes, 60.27% of the country's land area is subject to very mild erosion, 19.13% to mild erosion, 7.93% to moderate erosion, 5.97% to severe erosion, and 6.7% to very severe erosion (Figure 4). Erosion is more severe in arid regions with steep slopes and weak vegetation cover (Koralay and Kara, 2022). The slope of the land creates significant differences in erosion rates. On steep slopes, soil material moves more rapidly downward. It has been noted that on a 10% slope, the downward splash effect of rainfall is approximately three times greater than the upward movement (Altın et al., 2021). When the slope increases fourfold, it doubles the flow velocity of water, quadruples the erosion power, increases the amount of material transported by 32 times, and raises the size of the material transported by 64 times (Heady and Child, 1994). The carrying capacity of water is dependent on the flow volume and rate, while the flow itself is influenced by the duration and intensity of rainfall.

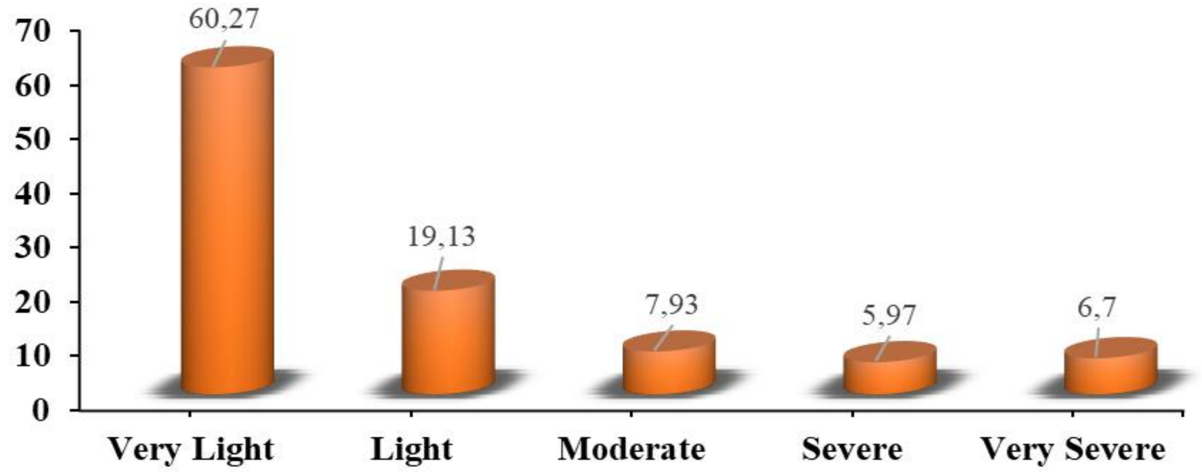

Figure 4. Distribution of Türkiye's Water Erosion Severity Classes by Land Area (%)

Depending on land use factors, 38.71% of Türkiye's soils are used for agriculture, 4.17% for forests, 53.66% for rangelands, and 3.46% for other purposes, all of which are subject to erosion (Erpul et al., 2018). This highlights that water erosion poses a significant threat, particularly to agricultural and rangeland areas (Figure 5).

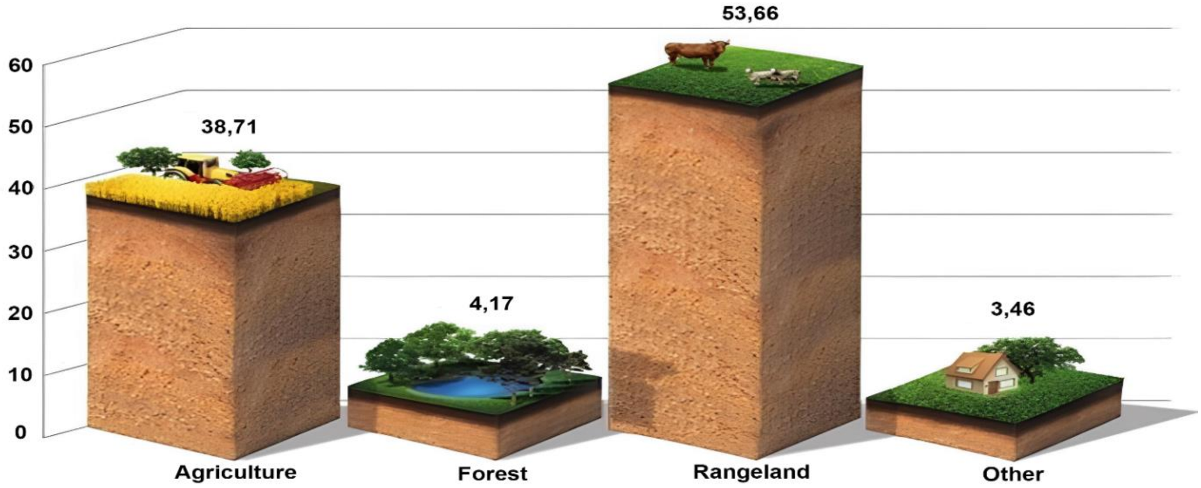

Figure 5. Distribution of Water Erosion by Land Use (%) (Anonymous, 2023)

Globally, rangelands are among the most important areas providing protection against erosion. However, as long as they are not subjected to overgrazing or other degradation processes, rangelands prevent the direct transport of soil by rainfall and wind due to their dense root systems and high vegetation cover. Bakır (1987) reported that the causes of rangeland degradation include drought, fire, invasive weed species, and excessive or early grazing. Any practice that reduces leaf area in rangelands will increase surface runoff and decrease the amount of water retained by plants, ultimately reducing the area covered by vegetation. As a result, the amount of soil transported by surface runoff will increase. Vegetation cover plays a critical role in reducing both water and wind erosion (Bilotta et al., 2007).

Wind Erosion

Wind erosion is the process by which soil particles are moved by the wind and accumulate in another area. When wind speed exceeds a certain threshold (15-25 km/h), soil particles are first displaced, followed by the transportation of light and small soil particles (Çelebi, 2021). This type of erosion is particularly prevalent in arid and semi-arid regions where precipitation is insufficient. It has been reported that 90% of Türkiye experiences arid and semi-arid climatic conditions (Akgöz et al., 2020). When examining the map showing the distribution and impact of wind erosion across different regions of Türkiye (Figure 6), it is evident that a large portion of the country is susceptible to this type of erosion.

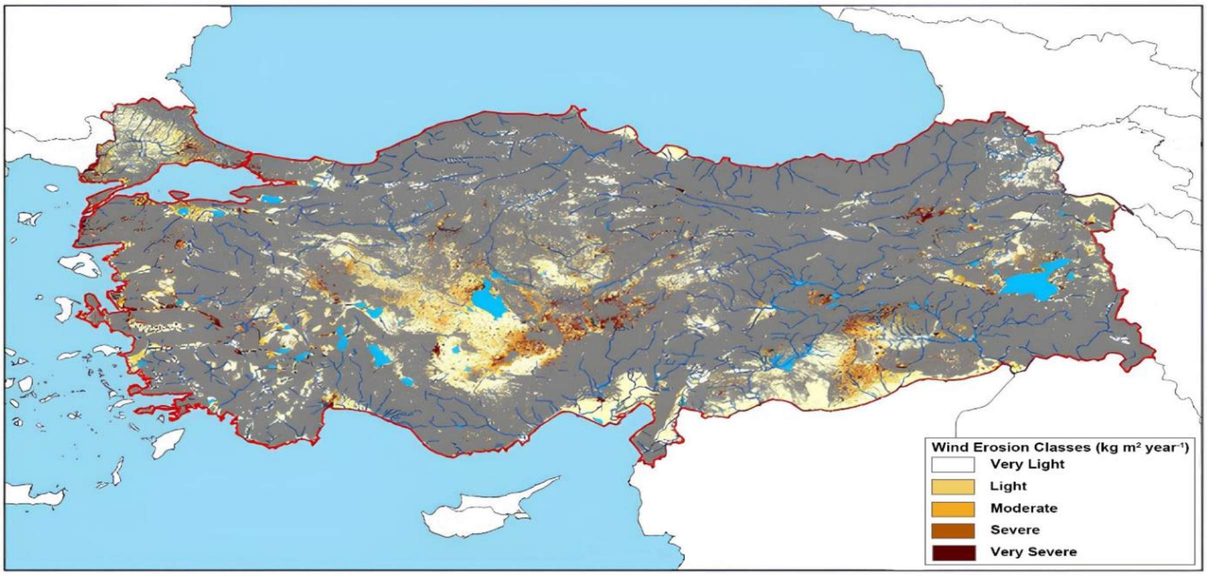

Figure 6. Wind Erosion Map of Türkiye (Anonymous, 2023)

Wind erosion is similar to water erosion in terms of its causes, consequences, and the measures that can be taken. However, the fundamental difference between the two types of erosion lies in the amount of precipitation. When precipitation is high in a region, water erosion increases, while in areas dominated by drought, wind erosion becomes more prominent. It has been reported that 99% of Türkiye's soils are affected by water erosion, while 1% is affected by wind erosion (Doğan, 2011). Due to the impact of global climate change and the increasing drought in Türkiye, it is predicted that the intensity and extent of wind erosion will expand (Karaca et al., 2008; Akgöz et al., 2020). The effects of wind erosion are particularly pronounced in areas with sandy soils and weak vegetation cover (Amiri, 2010).

During extremely dry periods dominated by strong winds, wind erosion can reach serious levels (Gökkuş and Koç, 1993). This type of erosion is expected to be more common in Türkiye's semi-arid regions (Ince et al., 2019). Approximately 85% of Türkiye's rangeland areas are located in semi-arid regions, where, despite a high diversity of grasses, production is low due to insufficient precipitation (Altın et al., 2011). Developing sustainable grazing plans is crucial to prevent the degradation of vegetation cover in rangelands (Holechek et al., 1995). Unfortunately, in 70% of Türkiye's rangelands, vegetation cover has been degraded, leaving the soil unprotected (Erkun, 1999). Improper or excessive grazing has led to vegetation loss, making these areas more susceptible to wind erosion. However, during periods with early spring and autumn rains before winter, appropriate management strategies can increase vegetation cover, preventing wind erosion damage. In addition to plant yield, factors such as the plant species' ability to cover the soil, the capacity of their roots to hold the topsoil, and their drought resistance are critical in erosion control (Erpul et al., 2020). It has been stated that wind erosion can be controlled by creating vegetation cover that covers nearly the entire soil surface, adding organic matter to improve soil structure, and reducing the exposed surface to wind by using proper tillage techniques (Altın et al., 2021).

To control wind erosion, the most effective methods include maintaining vegetation cover on the soil surface during critical periods, using windbreak fences, and leaving crop residues on the surface (Presley and Tatarko, 2009). Additionally, techniques such as strip cropping oriented perpendicular to prevailing winds and minimum tillage can increase soil resilience and reduce wind speed, thereby controlling erosion (Presley et al., 2013). In semi-arid and arid regions, where the soil surface is exposed, the presence of shrub cover is also a crucial factor in controlling wind-induced erosion. This is because shrubs reduce the amount of soil exposed to the wind (Altın et al., 2021).

Land Capability Classes and Erosion Relationship

Land capability classes are determined based on factors such as slope, drainage, erosion, and soil characteristics, all of which influence land use under the same climatic conditions. This classification is designed to address erosion and other land degradation causes (Balabanlı et al., 2005). Land capabilities are divided into eight classes, each represented by Roman numerals. The first four classes are considered suitable for cultivation, while the last four are unsuitable for farming. According to this classification, the first three classes are suitable for soil tillage, class IV is suitable for restricted soil tillage, while classes V, VI, and VII are suitable for rangeland, forests, and wildlife. Class VIII land includes areas that are unsuitable for use, such as wetlands, deserts, mountainous, and rocky terrains (Özşahin and Eroğlu, 2018). Approximately 26.6 million hectares (34.10%) of Turkey's land falls within classes I-IV, with 24.57% suitable for tilled agriculture and 9.53% suitable for restricted tillage. The remaining 65.90% of land is unsuitable for cultivated agriculture, with 60.06% of this land being suitable for rangeland, forests, and wildlife (Table 1).

Table 1. Classification of Land by Capability Classes in Türkiye

Suitable for Cultivated Agriculture			Unsuitable for Cultivated Agriculture		
Capability Class	Area (ha)	Rate (%)	Capability Class	Area (ha)	Rate (%)
I	5.086.087	6,53	V	127.934	0,16
II	6.772.873	8,69	VI	10.825.762	13,90
III	7.282.763	9,35	VII	35.836.340	46,00
IV	7.425.045	9,53	VIII	4.542.896	5,84
Total	26.566.768	34,10	Total	51.332.932	65,90

Land in classes V, VI, and VII, which are unsuitable for tillage, is suitable for rangeland, forests, and shrubland and should not be used for other purposes. However, these lands are often subjected to tillage farming or even fallow practices. These misapplications contribute to erosion and should be avoided in favor of establishing permanent vegetation cover. This is particularly critical because these lands are generally sloped and uneven, making them unsuitable for cultivation. Preserving and even enhancing the natural vegetation in these areas is vital in combating erosion. Since the early 21st century, the increasing pressure on these natural resources has led to a significant erosion problem (Lu et al., 2005), which has caused considerable damage to natural ecosystems (Issaka and Ashraf, 2017).

The Effect of Grazing on Erosion in Rangelands

There is a close relationship between surface runoff and water erosion, meaning that any process that increases surface runoff also increases the amount of erosion. In Turkey, grazing in rangelands often begins too early, and overgrazing in these areas critically reduces the number and types of plant species. Grazing during the early spring, when plants have just started growing, prevents the vegetation from reaching a level of growth sufficient for photosynthesis. As a result, these plants withdraw from the vegetation, leading to a decrease in plant density per unit area and an increase in the degree of cover and erosion severity. Additionally, overstocking the rangelands causes animals to graze plants along with their roots, while trampling damages the soil structure and makes soil particles more vulnerable to detachment. Similarly, delaying the end of grazing leads to plants entering winter in a weakened state. This prevents the plants from storing enough reserve nutrients to survive the winter, causing the vegetation to thin out and leaving the soil exposed to erosion. However, excessive grazing in the spring reduces the rate of water absorption by the soil more than heavy grazing in the autumn (Altın et al., 2021).

The type and amount of vegetation in rangelands change with grazing intensity, which in turn affects the amount of rainfall reaching the soil surface. In rangelands with dense and thick vegetation, rainfall is absorbed by the plants, while in overgrazed and sparse rangelands, the ability of plants to intercept rainfall is reduced. In short, grazing intensity has a significant impact on the infiltration of rainfall into the soil. In rangelands that are continuously and excessively grazed, animals destroy the protective plant cover and compact the soil surface. Grazing during wet conditions further exacerbates this compaction. As a result, rainfall infiltration into the soil decreases, while surface runoff and associated erosion increase. It has been reported that under light, medium, and heavy grazing conditions, the amounts of water lost through surface runoff are 11 mm, 14 mm, and 20 mm, respectively (Gökkuş and Koç, 1993). Therefore, measures that reduce surface runoff during high rainfall periods and minimize grazing damage are essential.

In rangelands in arid and semi-arid regions where proper grazing management practices are not implemented, erosion problems emerge quickly. Overgrazing changes the plant species composition, reduces the area covered by vegetation, and decreases productivity, which in turn leads to increased erosion. As vegetation decreases, the reduction in ground cover exposes the soil to the erosive effects of wind. Indeed, excessive grazing reduces plant cover and compaction damages the soil structure, leading to an increase in erosion problems (Altın et al., 2021).

Conclusion

Erosion in meadows and rangelands is a significant environmental issue that threatens both ecological balance and agricultural production. To prevent water and wind erosion, physical measures must be taken, such as protecting and increasing vegetation cover, implementing sustainable grazing plans, and reducing grazing capacity in sloping areas. While the steps taken in recent years to combat erosion in Turkey have yielded positive results, more comprehensive measures are still needed, particularly in dry and semi-arid regions. Although there has been a notable reduction in the amount of soil transported by erosion, many rangelands still require rehabilitation or erosion prevention measures.

In areas with high erosion risk, it is crucial to develop and implement land management strategies that are suitable for regional differences. The expansion of educational programs for farmers and increased government support can accelerate this process. Additionally, more effective implementation of rangeland improvement projects and the planting of plant species effective in erosion control will contribute to sustainable land management. Public awareness of the impacts of erosion, especially in rural areas, should be increased, and the government's existing erosion control policies should be effectively enforced. The protection and rehabilitation of natural vegetation is essential for successful erosion management in meadows and rangelands.

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Determining the Efficiency of Vetch Producers in Erzurum Province Using Fuzzy Data Envelopment Analysis

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ABSTRACT: This study was conducted to determine the efficiency levels of farms engaged in vetch production in Erzurum province. Vetch holds a significant position in forage crop production in Turkey and is of strategic importance for the sustainability of livestock farming. However, productivity issues and efficiency in resource utilization in vetch production directly affect the economic performance of producers. In this context, the Fuzzy Data Envelopment Analysis (FDEA) method was applied to evaluate how efficiently farms utilize their resources. Compared to traditional data envelopment analysis, FDEA provides more precise results in situations characterized by high levels of uncertainty and data ambiguity. The study utilized data collected from 55 vetch-producing farms operating in Erzurum province. These data encompassed the input and output variables of producers. Input variables included land preparation costs, sowing costs, fertilization costs, irrigation costs, and harvesting costs per decare, while the output variable was considered as vetch yield (kg/da). Symmetric triangular membership functions were used to model uncertainties, and the left and right spreads were determined for each farm. The findings revealed diversity in the efficiency levels of the farms. Many of the examined farms were evaluated as fully efficient at α-cut levels, while others exhibited low average efficiency scores. Moreover, a high positive correlation was identified between the fuzzy efficiency levels and classical efficiency levels of farms through the C-K index. The results underscore the importance of training and technical support programs to enhance the efficient use of resources by vetch producers. It was particularly emphasized that support in cost management and modern production techniques could improve producers' efficiency levels, thereby contributing to regional production efficiency. Additionally, it was recommended that efficiency levels of farms should be considered in the planning of agricultural subsidies. This study demonstrated the applicability of the FDEA method for efficiency analysis in vetch production and provided significant insights for the development of regional agricultural policies. The research highlighted that accounting for uncertainties in agricultural efficiency analyses offers policymakers and producers more realistic and practical outcomes.

Keywords: Vetch Production, Fuzzy Data Envelopment Analysis, Efficiency, C-K Index

INTRODUCTION

Vetch production serves as a fundamental feed source for livestock in regions with cold climates, such as Erzurum, and plays a significant role in the regional economy. However, maintaining production under limited resources and variable environmental conditions highlights the importance of efficiency analysis. This study examines the efficiency levels of vetch producers in Erzurum province using Fuzzy Data Envelopment Analysis (FDEA). The research aims not only to evaluate the efficiency of resources used in vetch production but also to reveal the impact of uncertainties in production processes.

Efficiency is a critical performance metric that reflects how effectively a system utilizes its available resources. This concept, which analyzes the relationship between inputs and outputs, is particularly significant in the agricultural sector for optimizing resource use. Efficiency in agricultural production not only ensures economic sustainability but also contributes to the preservation of natural resources (Coelli et al., 2005). Traditional efficiency analysis methods are based on the assumption that data are precise and complete. However, uncertainties are frequently encountered in agricultural production processes, limiting the accuracy of conventional methods.

In this context, Fuzzy Data Envelopment Analysis (FDEA), based on Zadeh's (1996) fuzzy logic theory, has been developed to address uncertainties effectively. FDEA is an extended version of the traditional Data Envelopment Analysis (DEA) method, suitable for measuring efficiency in uncertain or imprecise datasets. DEA is a non-parametric method capable of analyzing the efficiency of multiple inputs and outputs and is widely used in multi-input-multi-output production systems like agriculture (Charnes et al., 1978). However, the traditional DEA's assumption of precise data overlooks uncertainties inherent in agricultural processes, such as climate, market conditions, and human factors (Wen & Li, 2009).

The primary advantage of FDEA is its capacity to evaluate uncertain data. This method effectively models unpredictable factors frequently encountered in agricultural production, such as weather conditions, product prices, and production quantities. In vetch production, in particular, producers often make decisions based on uncertain inputs and outcomes. Therefore, FDEA offers more realistic results in such cases (Mousavi-Avval et al., 2020).

In this context, the main objective of this study is to determine how efficiently vetch producers utilize their current production resources and to perform a more realistic efficiency analysis by modeling uncertainties in the process. The results are expected to provide valuable insights for the development of regional agricultural policies and the more efficient use of resources.

Materials and Methods

The data for this study were collected from vetch-producing farms in Erzurum province. A survey method was employed to obtain economic data from the farms, and the data collected from 55 farms were prepared for analysis in Excel.

Fuzzy Data Envelopment Analysis (FDEA) was used to determine the efficiency of agricultural farms producing vetch in the Pasinler district of Erzurum. FDEA is an extension of the traditional Data Envelopment Analysis (DEA) method and is based on Zadeh's (1996) fuzzy logic and set theory. FDEA aims to provide a solution for analyzing datasets with uncertainty. Unlike traditional DEA, FDEA expresses input and output data through fuzzy set functions rather than precise values. This approach offers a more flexible structure for modeling uncertain or imprecise data (Wen & Li, 2009).

Fuzzy sets define each data point with a membership degree, which facilitates the evaluation of uncertain or incomplete data. FDEA overcomes the limitations of traditional DEA by considering uncertainties in the data, providing more realistic efficiency results. In this context, efficiency scores are calculated based on fuzzy data, and these results are expressed as fuzzy outputs that reflect uncertainties in the dataset (Wen & Li, 2009).

One of the main advantages of FDEA is its ability to offer more realistic efficiency analyses by considering uncertainties in inputs and outputs. This method has the potential to provide more accurate analyses in sectors where uncertainty is prevalent, such as agriculture, energy, and healthcare.

Input and output variables were identified, with inputs representing resource usage (land preparation costs, sowing costs, fertilization costs, irrigation costs, and harvesting costs) and outputs representing the results achieved (vetch yield in kg/da). In this context, input-oriented technical efficiency values were examined.

The fuzzy lower and upper bounds of the variables were determined using symmetric triangular membership functions, considering standard errors. After fuzzification, the lower and upper bounds were defuzzified using alpha-cut levels, and then efficiency scores were calculated with traditional DEA models. For each decision-making unit, the lower and upper bound efficiency scores were combined with the Chen-Klein index to compute the final efficiency scores. Spearman's Rank Correlation test was applied to examine the relationship between the results of traditional DEA and FDEA (Miran, 2022). These analyses were conducted using the R statistical software.

Fuzzy Data Envelopment Analysis (FDEA) is considered an extension of the traditional Data Envelopment Analysis (DEA) method. It is based on fuzzy logic and set theory (Zadeh, 1996) and provides an approach to evaluating datasets with uncertainty. In this method, input and output data are expressed as fuzzy sets rather than precise values. Each input or output variable is defined by a function that represents a fuzzy set instead of a precise value. These fuzzy sets are defined by a membership degree, which allows for reflecting uncertainty. This helps overcome the limitations of traditional DEA and more effectively addresses uncertainty and imprecision in the dataset. FDEA calculates efficiency scores by considering uncertainties in the input and output data, and these scores are obtained as fuzzy outputs that reflect the uncertain nature of the data (Wen & Li, 2009).

In fuzzy set theory, let E be a non-empty set and $Z \subseteq E$ olsun. For each $x \in E$, a membership function $\mu_Z(x): E \to [0,1]$ is defined, which shows the degree of membership of x in the set. Thus, a fuzzy set $\tilde{Z}$ on the set E is defined by the membership function $\tilde{Z}$;

$\tilde{Z} = \{(x, \mu_{\tilde{Z}}(x)): x \in X\}$ (Zadeh, 1996).

Although there are many types of membership functions in the literature, such as triangular, trapezoidal, exponential, and bell-shaped curves, it has been observed that the change in the method does not significantly affect the result, aside from the differences in the methodology (Karabacak and Kutlu 2024; Ecer, 2007). In this study, a triangular membership function has been used within the FDEA analysis to facilitate the process.

Since the FDEA method is essentially a linear programming method, the fuzzified data, which is transformed into fuzzy numbers using the triangular membership function, cannot be directly used with the FDEA method without removing the uncertainty information. Therefore, to adapt these fuzzified data to the FDEA method without eliminating the uncertainty information, the method known as the "extension principle of fuzzy numbers" proposed by Zadeh (1996) is employed, using α-cut levels. The α-cut level, as described here, is defined as a set $\widetilde{(A_\alpha)}$ consisting of elements whose membership degree is greater than or equal to α. The membership degree of the elements in a fuzzy set is expressed as follows for $\alpha \in [0,1]$ olmak üzere;

$\widetilde{A_\alpha} = \{(x, \mu_{\tilde{A}}(x) \geq \alpha): x \in X\}$ (Gündüz, 2015).

Thus, fuzzy numbers are converted into precise values within the interval $[L(\alpha), U(\alpha)]$ a for each for each α-cut level. Here, $L(\alpha)$ represents the lower bound, and $U(\alpha)$ i epresents the upper bound. At this point, by considering the lower and upper bounds, the confidence intervals for the data for each $\alpha \in [0,1]$ can be expressed as:

$A_\alpha = [L(\alpha), U(\alpha)]$ şu şekilde ifade edilir (Kao ve Liu, 2000: 429).

$A_\alpha = [L = \pi^l + \alpha(\pi^m - \pi^l), U = \pi^u - \alpha(\pi^u - \pi^m)]$

Thus, through the model developed by Kao and Liu (2000), it has been demonstrated that the DEA method can be applied to fuzzy data. In other words, for the FDEA model, let us assume that the input data is represented as xij $\tilde{x}_{ij}$ and the output data as $\tilde{y}_{rj}$ in a fuzzy form. From here, the general representation of the inputs and outputs as triangular fuzzy numbers can be expressed as follows:

$$\tilde{x}_{ij} = \left(x_{ij}^{l}, x_{ij}^{m}, x_{ij}^{u}\right), \tilde{y}_{rj} = \left(y_{rj}^{l}, y_{rj}^{m}, y_{rj}^{u}\right)$$

Research Findings and Discussion

Table 1 presents the descriptive statistics. In the data related to vetch production, the yield per decare varies between 410 kg and 490 kg. The average yield has been calculated as 475 kg/da. The costs of land preparation are determined to be an average of 167.5 TL/da. The planting costs are calculated as an average of 175.5 TL/da. Fertilization costs average 72.5 TL/da, and irrigation costs average 60.5 TL/da. The harvest costs are calculated to be an average of 110.25 TL/da.

Table 1. Descriptive Statistics for Input and Output

Output	**Minimum**	**Maksimum**	**Mean**	**Standart Sapma**
Vetch Yield (kg/da)	410	490	475	42,52
Input				
Land Preparation Cost (TL/da)	150	200	167,5	25,37
Planting Cost (TL/da)	140	210	175,5	35
Fertilization Cost (TL/da)	50	115	72,5	33,01
Irrigation Cost (TL/da)	20	90	60,5	35,14
Harvest Cost (TL/da)	100	150	110,25	26,41

Table 2 shows the efficiency values of the farms according to the α cutting levels and the averages of these values. The results indicate that the efficiency levels of the farms vary. Many of the examined farms are evaluated as fully efficient (1.000) at certain α cutting levels. However, some farms show low average efficiency values. This suggests that inputs are not being used efficiently or that outputs are improvable. Overall, it has been observed that as the α cutting level increases, the efficiency values decrease. This indicates that farms show performance differences in the face of uncertainty in a fuzzy environment. Some farms exhibit constant efficiency (1.000) at all cutting levels (e.g., Farm 1 and Farm 7). These farms maintain high performance even in uncertain conditions.

Table 2. The efficiency values of the farms at the α cutting levels

						Efficiency values at the α cutting levels							
Farm	**0**	**0,25**	**0,50**	**0,75**	**1**	**Mean**	**Farm**	**0**	**0,25**	**0,50**	**0,75**	**1**	**Mean**
1	1,000	1,000	1,000	1,000	0,695	0,939	**29**	1,000	1,000	1,000	1,000	1,000	1,000
2	1,000	0,968	0,917	0,824	0,592	0,860	**30**	1,000	0,995	0,986	0,961	0,700	0,928
3	1,000	0,938	0,838	0,647	0,326	0,750	**31**	1,000	1,000	1,000	1,000	1,000	1,000
4	1,000	1,000	1,000	1,000	0,468	0,894	**32**	1,000	1,000	1,000	1,000	1,000	1,000
5	1,000	0,938	0,838	0,647	0,326	0,750	**33**	1,000	0,950	0,867	0,730	0,459	0,801
6	1,000	1,000	1,000	1,000	0,468	0,894	**34**	1,000	0,950	0,867	0,730	0,459	0,801
7	1,000	1,000	1,000	1,000	1,000	1,000	**32**	1,000	1,000	1,000	0,000	1,000	0,800
8	1,000	1,000	1,000	1,000	0,432	0,886	**36**	1,000	0,995	0,986	0,961	0,700	0,928
9	1,000	1,000	1,000	1,000	0,727	0,945	**37**	1,000	0,999	0,996	0,988	0,919	0,981
10	0,652	0,517	0,369	0,209	0,096	0,368	**38**	1,000	1,000	0,994	0,961	0,819	0,955
11	0,432	0,353	0,265	0,173	0,070	0,259	**39**	1,000	0,999	0,996	0,988	0,919	0,981
12	1,000	1,000	1,000	0,000	1,000	0,800	**40**	1,000	1,000	1,000	1,000	1,000	1,000
13	0,781	0,609	0,426	0,233	0,071	0,424	**41**	0,484	0,407	0,320	0,220	0,101	0,306
14	1,000	0,954	0,874	0,697	0,301	0,765	**42**	1,000	1,000	1,000	1,000	0,750	0,950
15	1,000	0,916	0,787	0,566	0,213	0,696	**43**	1,000	0,914	0,783	0,561	0,275	0,707
16	1,000	1,000	1,000	1,000	0,563	0,913	**44**	0,244	0,214	0,174	0,125	0,063	0,164
17	1,000	1,000	1,000	1,000	1,000	1,000	**45**	1,000	0,950	0,852	0,697	0,421	0,784
18	1,000	1,000	1,000	1,000	0,188	0,837	**46**	1,000	0,998	0,991	0,971	0,800	0,952
19	1,000	1,000	1,000	0,000	1,000	0,800	**47**	1,000	0,999	0,996	0,988	0,919	0,981
20	1,000	1,000	1,000	1,000	1,000	1,000	**48**	1,000	1,000	0,994	0,961	0,819	0,955
21	1,000	0,987	0,959	0,892	0,701	0,908	**49**	1,000	0,999	0,996	0,988	0,919	0,981
22	1,000	1,000	1,000	1,000	1,000	1,000	**50**	1,000	1,000	1,000	1,000	1,000	1,000
23	1,000	1,000	1,000	1,000	0,500	0,900	**51**	1,000	1,000	1,000	1,000	1,000	1,000
24	1,000	1,000	1,000	1,000	1,000	1,000	**52**	0,484	0,407	0,320	0,220	0,101	0,307
25	1,000	1,000	1,000	0,000	1,000	0,800	**53**	1,000	0,914	0,783	0,561	0,275	0,707
26	1,000	0,987	0,959	0,892	0,701	0,908	**54**	0,244	0,214	0,174	0,125	0,063	0,164
27	1,000	1,000	1,000	1,000	1,000	1,000	**55**	1,000	0,950	0,852	0,697	0,421	0,784
28	1,000	1,000	1,000	1,000	0,500	0,900							

Table 3 compares the Chen-Klein Index and classical Data Envelopment Analysis (DEA) efficiency scores for the farms. The results show that there are some differences between the efficiency values calculated by the two methods. The Chen-Klein Index values are generally higher than the classical DEA scores. For example, the Chen-Klein Index for Farm 2 is 0.860, while the classical DEA score is 0.592. This difference can be explained by the Chen-Klein method's ability to account for uncertainties and fuzzy environments. While classical DEA relies on a deterministic relationship between inputs and outputs, the Chen-Klein method evaluates uncertainties more flexibly. According to the Chen-Klein Index results, the number of farms with perfect efficiency (1.000) is higher (e.g., Farms 7, 17, 20, 22, 24, and 27). On the other hand, some farms, such as Farm 11 and Farm 44, have low efficiency scores according to both the Chen-Klein Index and classical DEA. Some farms (e.g., Farm 13) show moderate efficiency with the Chen-Klein Index.

Table 3. Efficiency Scores of Farms Based on the Chen-Klein Index and Classical Data Envelopment Analysis (DEA)

Farm	Chen-Klein İndex	Classical Data Envelopment	**Farm**	Chen-Klein İndex	Classical Data Envelopment
1	0,939	0,695	**29**	1,000	1,000
2	0,860	0,592	**30**	0,928	0,700
3	0,750	0,326	**31**	1,000	1,000
4	0,894	0,468	**32**	1,000	1,000
5	0,750	0,326	**33**	0,801	0,459
6	0,894	0,468	**34**	0,801	0,459
7	1,000	1,000	**32**	0,800	1,000
8	0,886	0,432	**36**	0,928	0,700
9	0,945	0,727	**37**	0,981	0,919
10	0,368	0,096	**38**	0,955	0,819
11	0,259	0,070	**39**	0,981	0,919
12	0,800	1,000	**40**	1,000	1,000
13	0,424	0,071	**41**	0,306	0,101
14	0,765	0,301	**42**	0,950	0,750
15	0,696	0,213	**43**	0,707	0,275
16	0,913	0,563	**44**	0,164	0,063
17	1,000	1,000	**45**	0,784	0,421
18	0,837	0,188	**46**	0,952	0,800
19	0,800	1,000	**47**	0,981	0,919
20	1,000	1,000	**48**	0,955	0,819
21	0,908	0,701	**49**	0,981	0,919
22	1,000	1,000	**50**	1,000	1,000
23	0,900	0,500	**51**	1,000	1,000
24	1,000	1,000	**52**	0,307	0,101
25	0,800	1,000	**53**	0,707	0,275
26	0,908	0,701	**54**	0,164	0,063
27	1,000	1,000	**55**	0,784	0,421
28	0,900	0,500			

Spearman Rho: 0.8360646, p<0,001

The Spearman's Rho coefficient was obtained as 0.836, indicating a very strong and positive correlation between the two variables (Chen-Klein Index and Classical DEA). Upon examining Figure 1, it can be observed that the two indices generally follow parallel trends, but the Classical DEA Efficiency Scores deviate significantly from the Chen-Klein Index in some farms, reaching much lower values. This discrepancy is particularly noticeable in farms with lower efficiency scores.

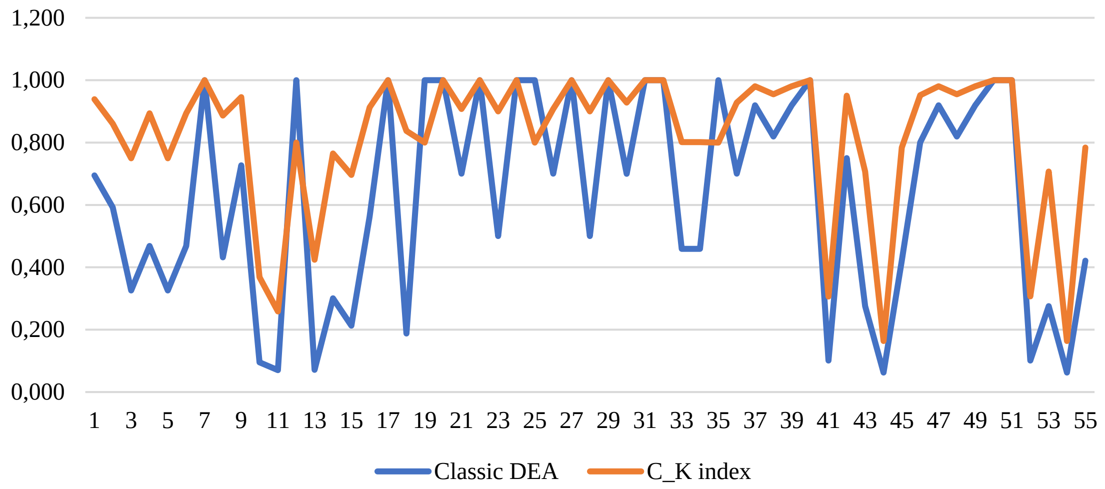

Figure 1. The variation between the Chen-Klein Index and Classical DEA Efficiency Scores of the farms.

Table 4 shows the distribution of farms' efficiency levels according to the Chen-Klein (C-K) Index. According to the data, 12.73% of the farms have an efficiency score below 0.5, indicating that their efficiency levels are quite low. Among the farms with medium-level efficiency, there is only one farm in the 0.51-0.70 range, which constitutes 1.82% of the farms. The farms with higher efficiency levels are concentrated in the 0.71-0.90 range, which includes 20 farms, accounting for 36.36% of the total. In the highest efficiency range of 0.91-1, 27 farms are located, representing 49.09% of the total. This suggests that nearly half of the farms have achieved a high level of efficiency.

Table 4. Distribution of Farms' Efficiency Ranges According to the C-K Index

Efficiency Range	Frequency	Distribution (%)
<0,5	7	12,73
0,51-0,70	1	1,82
0,71-0,90	20	36,36
0,91-1	27	49,09

Conclusion and Recommendations

In this study, the efficiency levels of farms were compared using the Chen-Klein (C-K) Index and Fuzzy Data Envelopment Analysis (FDEA). The results revealed both the similarities and differences between the two methods. It was found that both methods provide valuable insights for efficiency analysis, with FDEA proving to be more effective in certain situations. The C-K Index stands out as a stable and balanced method for evaluating the overall efficiency levels of farms. According to the C-K Index, most farms have an efficiency score in the 0.91-1 range, indicating that a large portion of the farms operate at high efficiency levels. Based on the table, 27 farms (49.09%) are in this high-efficiency range, while 7 farms (12.73%) have low efficiency scores below 0.5. The group with the highest efficiency levels represents nearly half of the total farms, while 20 farms (36.36%) show medium efficiency levels. The low-efficiency farms make up only 12.73% of the sample. This distribution suggests that while the majority of farms operate at high efficiency levels, there are still some with low efficiency.

In the agricultural sector, where uncertainties and data gaps are common, the use of FDEA is recommended. This method, in particular, allows for a more accurate evaluation of low-efficiency farms. Decision-makers in the agricultural sector can use the results obtained from these methods to assess the effectiveness of support policies, optimize resource allocation, and develop strategies to improve efficiency levels. It is recommended to develop targeted support programs for low-efficiency farms. Specifically, policies and training programs aimed at improving the performance of farms with efficiency scores below 0.5 can be implemented.

In conclusion, both methods are valuable for determining the efficiency levels of agricultural farms. However, due to FDEA's superior handling of uncertainties, it is particularly recommended for situations where data is incomplete or uncertain. These methods will contribute to the more effective implementation of agricultural policies and the efficient allocation of resources.

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International Conference on
Food, Agriculture and Animal Sciences
19-22 December 2024, Erzurum, TÜRKİYE

An Overview of Automatic Milking Systems and Their Impact on Milk Production, Composition, and Udder Health

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ABSTRACT: The milking of animals is an activity that consumes the highest labor requirement on dairy farms. Automatic milking systems (AMS) are one of the important technological innovations that increase productivity, reduce labor and support sustainability in modern dairy farms. AMSs are designed to perform all stages of the entire milking process and to milk without human intervention. The principle of robotic milking starts with the cows voluntarily entering the milking parlor and each teat being recognized by automatic sensors. After cleaning the teats, milking is carried out by means of high-precision equipment. Recently, AMS is becoming more widespread among farmers, especially in Europe. Compared to conventional milking systems (CMS), AMS has been reported to reduce milking labor significantly. Milk frequency is reported to be 2.4 and 2.6/day and milk yield is higher. There are controversial results on milk fat and protein content, but the majority of studies suggest that milk fat and protein content either decrease or remain the same as a result of more frequent milking. On the other hand, the free fatty acid composition is reported to be higher with AMS. In AMS, a brush attached to the robot arm cleans all teats, but the majority of researchers agree that the cleaning success of AMS is lower compared to CMS, especially if the teats are too dirty. There are also conflicting results on the SCC of AMS compared to CMS, but the majority of researchers report higher or similar milk SCC with AMS. The aim of this study is to present the general features of automatic milking systems and to examine the effects of these systems on parameters such as milk yield, milking labor, milk composition, udder health, somatic cell count

Keywords: Automatic Milking System, Milk Yield, Milk Quality, Milking Labor, Udder Health

INTRODUCTION

Milk is defined as a complete foodstuff with its protein, fat and mineral substances and has a very important place in human nutrition (Gasmalla et al., 2017). The use of milk obtained from mammals as human food dates back to ancient times. With the increase in the world population and the demand for milk, the dairy sector is growing and developing day by day. Today, it is estimated that there are approximately 240 million people working in the dairy sector, 150 million dairy production farms and 1 billion people make a living from this sector (Anonymous, 2017). Many different animal species are used for milk production, but the highest production is provided by cattle. In 2022, total world milk production was reported as 930 million tons and 81% of this production was provided by cattle (Anonymous, 2024). New technologies are being developed and put into practice every day in order to reduce the cost of the product produced in the dairy cattle sector and to increase productivity. The milking of animals is an activity that accounts for 25-35% of the labor requirement on dairy farms and is a significant time-consuming activity (de Koning, 2010). In order to reduce the labor force and time loss in milking, various studies were carried out and automatic milking systems (AMS) were developed in the Netherlands in 1992. Since its development, the demand for AMS has been quite high in countries, especially in Europe, where labor is expensive and where there are a lot of large companies with intensive production. Barkema et al. (2015) reported that the number of enterprises using AMS in the world was 25 thousand in 2015. In 2020, this number was estimated to be over 50 thousand (Simões Filho et al., 2020) and it is predicted that by 2025, 50 per cent of dairy farms in north-western Europe will have AMS (Cogato et al., 2021).

Automatic milking systems are systems designed to carry out the milking process flawlessly without compromising animal welfare, taking into account the health of the animals and the product produced. A wide range of studies have been carried out to investigate the effects of AMS on animal health, animal behavior, animal welfare, herd management, milk yield and quality, and increasing labor efficiency. This review discusses the working principles and effects of AMS on milk yield, milk quality, udder health, milk hygiene, and milking labor by evaluating the studies conducted on this topic.

Milking Process

Automatic milking systems are designed to perform all stages of the whole milking process and to achieve a perfect milking. In order to carry out these activities, AMS are equipped with various elements. These elements are the parlor, the udder detection device, the robot arm to apply the teat cups, the udder cleaning device including sensors and software, and the milker (De Koning et al., 2002).

In AMS, cows voluntarily come to the milking machine and the milking process takes place. Firstly, the cow coming to the milking machine is recognized by the system through the magnetic necklace on its neck. If a sufficient amount of time has elapsed since the last time the cow was milked, the cow is accepted into the milking parlor, if not enough time has passed, the system does not allow the cow to enter (Mihina et al., 2012). Milking parlors can be single stall or multiple stalls and the number of cows milked varies according to the number of stalls. In single stall systems, there is only one milking robot, while in multi-stall systems, a single robot can pass to other stalls and perform the milking process. In machines with one stall, an average of 55-65 cows can be milked daily (Brouček and Tongel, 2015). Figure 1 shows a milking parlor in an automatic milking system.

Figure 1. Milking Parlor in Automatic Milking Systems (Photo by Ann-Christine Ek, Finland)

The cow entering the milking parlor is fed by the system through the feeders at the front of the parlor and the cow is calmed down. Through these feeds, cows are encouraged to come to the machine throughout the day (Molfino, 2018). These rations should be desirable for the cows (Madsen et al., 2010). The amount of ration to be given to each cow can be determined by the owner according to the lactation period or milk yield of the cow and recorded by the system and feeding is made in accordance with this information when the cow enters the parlor. When the cow starts to feed, the robotic arm determines the position of the teats by ultrasound, laser or image analysis (Artmann, 1997). The system records the positions of the teats for each cow and can use this information in subsequent milking (Demir and Öztürk, 2010). Before the milking process starts, the teats are cleaned by means of cylindrical rotating brushes and water. The brushes also stimulate the nerves and are effective in the milk reduction. In another method used for teat cleaning before milking in AMS, there is an extra milking cup-like equipment in the system. This nozzle is attached to each teat individually by the arm and the teats are cleaned with pressurized water and air pressure (Figure 2). In another teat cleaning system, utilized in AMSs the teats are cleaned in the teat cups.

Figure 2. Cleaning Teats Using a Brush and Water in an AMS

After cleaning, the cylindrical brushes or the cups used for cleaning are retracted by the system, the milking cups are attached to the teats and the milking process is started. In AMS, it is very important that the milking cups are properly attached to the teats. Disruptions in this process can lead to milk leakage (Persson Walleret al., 2003) as teat stimulation causes milk to start leaking (Gygax et al., 2007). Milk leakage creates a favourable environment for microbial growth around the teat opening and is a significant risk factor for mastitis. (Stefanowska et al., 2000; Waage et al., 2001). If the distance between the teats is too close or too far, it may cause problems in attaching the milking cups (Jacobs and Siegford, 2012). In case any of the cows has a blind teat, this information is entered into the system by the owner and this teat is not milked in the subsequent milking processes. The process of attaching the milking cups takes 12 seconds on average and the milking process is started after all the milking cups are attached (Jiang et al., 2017). Each teat cups have its own sensors and the milk flow rate is detected and the teats are removed when milking is finished. During milking, some physical characteristics of cows (weight, milk yield per teat and milking time of each teat, etc.) and quality characteristics of milk (temperature, color, conductivity, fat and protein content, somatic cell count, etc.) are instantaneously detected and recorded by the system (De Koning, 2002).

Milking Labor

Milking is a daily ritual that consumes around 31% of the time spent working on dairy cattle farms (Hogan et al., 2022). Relieving farm operators from daily milking tasks may be the most appealing initial factor in AMS (Jacobs and Siegford, 2012). An AMS allows for more frequent milking events without the need for human labour (de Koning et al., 2002). A survey study conducted on 530 AMS owners in Canada has revealed that average employment (full- and part-timers together) fell by 20% when AMS was introduced and the time spent for milking related activities has also decreased significantly as compared to conventional milking systems (Tse et al., 2018). Similarly, Örs and Oğuz (2018) reported that the farms using AMS have 21.72% lower labor costs than the farms using conventional milking systems.

Milk Yield and Composition

In enterprises where automatic milking system is used, milking interval varies depending on many factors such as breed, machine type etc. One of the most important features of automatic milking is that animals can visit the milking parlor voluntarily. This causes the diversity in the milking interval to increase. In some farms, milking is done 3 times a day, while in others the time between milking reaches 12 hours (Mollenhorst et al., 2011). It has been found that factors such as cow factor, milking time and variation in milking interval have significant effects on milk production in AMS (Hogeveen et al., 2001). In many studies examining the effects of milking frequency on milk yield, it was reported that milk yield increased with increasing milking frequency. Wiking (2022) reported an 18% increase in milk yield with AMS compared to twice daily milking, with mean milking intervals varying between 2.4 and 2.6. Likewise, other studies have reported a 2-12% increase in milk yield with AMS compared to conventional twice-daily milking systems (Svennersten-Sjaunja, 2007; Jacobs and Siegford, 2012; Cotago et al., 20-21). Cow stress is one of the factors adversely affecting milk yield and animal welfare. The welfare of animals is significantly increased in automatic milking systems (Maršálek et al., 2012). The milking process, which takes a long time and is labor intensive in cattle farms, is generally very stressful for animals and milking persons as well. Especially in case of aggressive behavior of the employees performing the milking process, milk yield in cows decreases and the amount of milk remaining in the udder increases. Blood cortisol level increases in cows that are stressed during milking and this causes a decrease in milk yield (Tancin and Tancinova, 2008; Maršálek et al., 2012). Since the milking process takes place without human intervention in AMS, such stress factors in cows are eliminated and losses in milk yield can be prevented. The study by Piwczyński et al. (2020) found that on farms that switched from traditional milking to automatic milking, cow milk yield increased by 1078 kg in the first lactation and by 1182 kg in the second lactation. Likewise, Tse et al (2018) reported that in a survey of 530 farms using AMS, 81 per cent of owners reported higher milk yields.

Automatic milking systems usually allow cows to be milked more than 2 times a day. More frequent milking can increase the amount of milk production, but may slightly reduce the proportion of milk components. More frequent milking prevents milk from accumulating in the udder for a long time. Milk that sits for a long time can cause more condensation of fat globules in the udder. In automatic milking systems, therefore, a slight decrease in milk fat can be observed. Most studies in the literature reported a decrease in milk fat and protein content, although some studies reported an increase in milk constituents. Soberon et al (2011) reported a decrease in milk fat and protein with an increase in milking frequency. Similarly, a study in Israel reported that milk from cows milked with AMS had lower fat content than cows in conventional milking systems, but no difference in milk protein content (Shoshani and Chaffer, 2002). A 0.2% reduction in milk fat with AMS was reported by Rotz et al. (2003). Brzozowski et al. (2020) suggested that the decrease in milk protein/fat ratio observed with AMS could be mainly due to the increase in milk yields. It has also been reported that the content of free fatty acids (FFA) in the milk collected from farms milking with AMS has increased (de Koning et al., 2004). Elevated levels of FFA in milk are undesirable as they impart an acidic taste to products made with this milk. It has been reported that an increase in the frequency of milking and a shortening of the milking interval in AMS systems leads to an increase in the FFA content in milk (Wikinng et al., 2006; Jacobs and Siegford, 2012).

Udder Health and Milk Quality

Milking systems used in dairy farms play a key role in milk yield, milk quality and labour saving as well as animal health and welfare. Milking hygiene has a very important effect on udder health in cows, especially in case of over milking, pathogens can enter the udder canal during the milking process (Hovinen and Pyörälä, 2011). In addition, over milking increases the risk of mastitis by causing discomfort and tissue damage in the teat (Krawczel et al., 2017). In traditional milking methods, the teat cups are attached to the cow and the milking cups remain on all teats until the milking is completed and continue to vacuum the teats. In AMS, the milking cups are removed from the milked teats and the teat tissue is prevented from being affected by over-milking. The SCC in milk is used as a criterion to reveal udder health and to diagnose subclinical mastitis (Coşkun et al., 2023). In AMSs, herd health can be closely monitored as SCC monitoring is performed at each milking for early detection of mastitis. Bausewein et al. (2022) reported that the sensitivity of robotic milking systems in detecting clinical mastitis was between 31-78%.

Various results have been reported on the effects of AMS on somatic cell count. Salovuo et al. (2005) and Oudshoorn and de Boer (2006) reported that SCC did not change in automatic milking systems. In addition, De Koning et al. (2003) and Johansson et al. (2017) reported an increase in the number of milk SCC with AMS, while Bentley et al. (2013); Tousova et al. (2014) reported a decrease in the amount of SCC. The effects of AMS on milk SCC undoubtedly depend on the milking management of the enterprise before the installation of AMS, but there are some points to be considered in milking with AMS. In AMS, the udder is not dried after washing and milking is started immediately, which is among the reasons why the bacterial load in the udder remains high (Jacobs and Siegford, 2012). The lack of human factor in milking and the fact that the system applies the same cleaning application to all teats regardless of their dirtiness. In addition, differences in the position and structure of the teats are one of the reasons for the increase in SCC, as the teats with unusual shapes may not be cleaned properly by the robot. Especially in very dirty teats, milking may start without adequate cleaning. Hvaale et al. (2002) determined in their study conducted in enterprises milked with AMS that the average 10-20% of udder cleaning per cow was unsuccessful. In a study conducted by Klungel et al. (2000), milk samples were taken from the milk tanks in enterprises that switched to automatic milking. It was reported that while the rate of milk tanks with SCC ≥ 250 thousand cells/ml was 27.4% before the establishment of AMS, this rate increased to 39.1% after AMS establishment. In the same study, the proportion of milk tanks with total bacterial count ≥ 50 cfu/ml was 4.1% before AMS, while this rate increased to 16.1% after the establishment. Similarly, Hiitiö et al. (2017) reported that the SCC count of cows in enterprises with AMS was higher than those with conventional milking systems. Moreover, Van der Vorst et al. (2002) reported that milk tank SCC increased significantly in the first 1-2 years following the installation of AMS, but this number decreased over time.

Conclusion

Automatic milking systems are spreading rapidly around the world. Many researchers agree that milk yield increases and milking labor is significantly reduced with AMS. However, there are controversial results on milk composition and udder health. AMS appears to have a reducing effect on milk fat and protein, although some studies suggest otherwise. This effect is thought to be due to more frequent milking. The effects of AMS on udder health and milk hygiene undoubtedly depend on the milking management of the farms prior to AMS. However, based on the evaluation of the studies on the subject, AMS seems to have some disadvantages compared to CMS in terms of teat cleaning and milk hygiene. In order to ensure high milk quality and better udder health on the farm, it is recommended that farmers using AMS keep their farm clean.

Funding

This research was conducted without any external funding

Statement of Conflict of Interest

The authors declare that they have no conflict of interest.

Authors' Contributions

VFÖ, designed the study, ZÇ worked on the preparation of figures. Both authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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Evaluation of Oats in Terms of Human Nutrition

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ABSTRACT: Oats (*Avena sativa*) are a highly nutritious and versatile cereal grain widely utilized in human diets. Rich in protein, dietary fiber, and essential micronutrients, oats stand out for their health benefits and functional properties. This study examines the various roles of oats in modern diets and provides a detailed overview of their use in breakfast products, baked goods, plant-based milk alternatives, infant formulas, functional foods, gluten-free diets, and sports nutrition. The beta-glucan content in oats contributes to cardiovascular health, weight management, and diabetes control by lowering cholesterol, regulating blood sugar, and enhancing satiety. Moreover, their prebiotic properties improve gut health and foster a balanced microbiota. With a low carbon footprint, oats also align with environmental sustainability efforts. By synthesizing findings from academic research, this comprehensive review highlights the importance of oats in promoting public health and supporting sustainable food systems. The results underscore the potential of oats as a fundamental component in a variety of dietary practices.

Keywords: Oat, *Avena sativa*, Human Nutrition, Beneficial

INTRODUCTION

Oats (*Avena sativa*) are a highly nutritious cereal crop that have drawn attention from traditional agricultural practices to the modern food industry due to their wide range of applications. With a rich content of protein, dietary fiber, vitamins, and minerals, oats stand out as a unique food option both for healthy eating and the production of functional foods (Whitehead et al., 2014). Consumed as a staple food for centuries, oats have recently attracted the intense interest of dietitians and food scientists, gaining increased prominence in the context of healthy living trends (Slavin, 2013).

Notably, oats' beta-glucan content supports cardiovascular health and contributes to cholesterol reduction (EFSA, 2011). In addition, their low glycemic index and satiety-inducing properties play a crucial role in diabetes management and weight control (Wolever & Jenkins, 1993). Beyond these aspects, the prebiotic effects of oats improve gut health by supporting the gut microbiota, thereby enhancing overall health status (Slavin, 2013). As a versatile cereal, oats serve as an energy and protein source in sports nutrition and as a wheat alternative in gluten-free diets.

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In the modern food industry, oats are incorporated into a wide variety of products, ranging from breakfast cereals and infant formulas to plant-based milks and energy bars. From an environmental sustainability perspective, oats are notable for their low carbon footprint as a crop (Röös et al., 2020). Understanding the role of oats in human nutrition and exploring their diverse applications is important for improving individual health and establishing a sustainable food system. In this study, the various dietary uses of oats will be examined in detail, supported by scientific literature to provide a comprehensive evaluation.

Nutritional Composition and Components

Unlike other grains, oats are notably rich in protein, dietary fiber, vitamins, and minerals. With a protein content ranging between 10% and 24%, oats are considered a valuable plant-based protein source (Butt et al., 2008). Oat protein is rich in essential amino acids such as lysine and possesses a high biological value. This characteristic makes oats particularly suitable for supporting vegetarian and vegan diets.

The most notable component is β-glucan, which lies at the core of oats' positive health effects. β-glucan constitutes a large portion of the soluble fiber in oats, and its health impacts have been extensively studied. On average, β-glucan makes up about 3–8% of the dry weight of oats (Whitehead et al., 2014). This compound forms a gel-like structure in the gastrointestinal tract, slowing down digestion, inhibiting the reabsorption of bile acids, and thereby contributing to the reduction of cholesterol levels.

Oats are also an important source of vitamins and minerals. In addition to B vitamins (thiamin, riboflavin, niacin), they contain vitamin E. Minerals such as magnesium, zinc, phosphorus, iron, and calcium further enhance the nutritional profile of oats. These vitamins and minerals are known to support energy metabolism, strengthen the immune system, and maintain bone health (Peterson, 2001).

Furthermore, oats contain phenolic compounds and avenanthramides—unique polyphenols with antioxidant, anti-inflammatory, and antiproliferative properties (Chen et al., 2007). These properties make oats a functional food, playing a significant role in the prevention of chronic diseases such as cardiovascular conditions and certain types of cancer.

Health Effects

Oats are widely recognized in the field of nutrition for their positive health effects, which range from regulating cholesterol levels and improving gut health to strengthening the immune system. This section details the health benefits of oats in light of various research findings and academic studies.

Cholesterol and Cardiovascular Health

The role of oats in regulating cholesterol levels is well documented. β-glucan, at the core of oats' effect on cholesterol, forms a gel-like structure in the intestine that binds bile acids and reduces their absorption. As a result, the liver uses more cholesterol to produce bile acids, leading to lower blood cholesterol levels. Ripsin et al. (1992) reported that oats can reduce LDL ("bad") cholesterol by about 5–10%.

The U.S. Food and Drug Administration (FDA) permits health claims for oat-based products that support cholesterol reduction. According to the FDA, consuming 3 grams of β-glucan per day is sufficient to lower the risk of cardiovascular disease. Likewise, the European Food Safety Authority (EFSA, 2011) confirms oats' ability to improve cardiovascular health when consumed regularly.

Blood Sugar Control

Oats have a low glycemic index, which positively influences glycemic control. This attribute is linked to their β-glucan content. By delaying gastric emptying and slowing carbohydrate digestion, β-glucan prevents sudden postprandial spikes in blood sugar levels. Wood et al. (2007) found that regular oat consumption improves insulin sensitivity and enhances glycemic control in individuals with type 2 diabetes.

In addition, oats can support weight management by increasing satiety. Due to the high viscosity of β-glucan, the stomach contents become more dense, prolonging feelings of fullness (Beck et al., 2009). This effect can help prevent overeating and reduce the risk of obesity.

Gut Health

As a fiber-rich food, oats offer numerous benefits for gut health. They regulate bowel movements, preventing constipation, and their prebiotic properties promote the growth of beneficial gut bacteria. Slavin (2013) noted that oat fiber consumption increases microbial diversity in the gut, which in turn can positively influence overall health, including immune function.

Oats may also help reduce inflammation in the gut. For individuals with inflammatory bowel conditions, oat fiber provides a protective effect on the intestinal mucosa. Regular oat consumption supports general digestive health and helps maintain a balanced gut microbiota.

Antioxidant Activity

Oats contain unique polyphenols known as avenanthramides, which possess antioxidant properties that neutralize harmful free radicals in the body. Chen et al. (2007) demonstrated that avenanthramides can reduce the risk of cardiovascular disease and help prevent inflammation.

Antioxidants also support skin health by reducing oxidative stress, thereby slowing signs of aging. Oats are used in cosmetic products, and oat baths are known to alleviate the symptoms of eczema and other skin conditions.

Immune System Support

The positive effects of oats on the immune system are largely attributed to their β-glucan content. β-glucan activates immune cells, increasing resistance to infections. Volman et al. (2008) reported that β-glucan provides protection against respiratory infections and enhances immune function.

More recent studies suggest that oats may also play a role in cancer prevention. Phytochemicals found in oats can activate immune cells and inhibit tumor growth. These findings highlight oats' potential both as a preventive food and as a functional dietary supplement that supports the immune system.

Applications of Oats in Human Nutrition

Oats (*Avena sativa*) have become an indispensable food in human nutrition thanks to their rich nutritional profile and functional properties. Beyond their traditional uses, oats have found a variety of applications in the modern food industry for the production of functional foods and within healthy lifestyle trends. This text provides a detailed examination of the various ways oats are utilized in human nutrition, supported by academic references.

Breakfast Products

Oats are most commonly consumed in breakfast products. Oatmeal and granola provide prolonged satiety and balanced energy levels due to their high fiber and complex carbohydrate content. The ability of beta-glucan to delay gastric emptying increases the popularity of oat-based breakfast foods (Whitehead et al., 2014). When eaten at breakfast, oats play a significant role in diabetes management by regulating blood sugar levels (Wolever & Jenkins, 1993) and also support mental performance through steady energy release (Slavin, 2013).

Oat-based breakfast products can be diversified by combining them with nuts and dried fruits to enhance their nutritional value, offering consumers a broader variety of nutrients. This makes oats an indispensable component of modern dietary trends (Beck et al., 2009).

Baked Goods and Snacks

In bakery products, the use of oat flour or whole oats enhances their nutritional quality. Oat-based breads, cookies, and cakes offer a healthy alternative due to their high protein and fiber content. By substituting wheat flour with oat flour in gluten-free baked goods, it becomes possible to develop products suitable for individuals with celiac disease.

Additionally, energy bars and protein snacks are other important products that leverage oats to meet the energy needs of active individuals. Their fiber and protein content promotes satiety, while also providing sustained energy (Slavin, 2013). Using oats in formulations with reduced sugar content makes it possible to diversify the range of healthy snack options.

Plant-Based Milk Alternatives

Within the plant-based milk market, oat milk is a popular choice for individuals with lactose intolerance and for vegans. The natural fiber content in oats lends a creamy texture to these milk alternatives (Meydani, 2009). Moreover, the low carbon footprint of oats makes oat milk an environmentally friendly option (Röös et al., 2020). Oat milk’s ability to produce foam makes it a common choice in specialty coffee beverages like lattes.

Infant Formulas

The soft texture and high nutritional value of oats make them suitable for use in infant formulas. Oat-based formulas enriched with iron, magnesium, and B vitamins support infants’ growth and development (Pulido et al., 2009). For individuals at risk of celiac disease, oat-based infant formulas also serve as a suitable alternative.

Functional Foods

The functional food industry benefits from the beta-glucan content in oats, which helps lower cholesterol levels. By reducing LDL cholesterol, beta-glucan supports cardiovascular health (EFSA, 2011). Probiotic cereals and prebiotic snacks are other key products that capitalize on oats (Ripsin et al., 1992).

In the functional foods category, the presence of phytochemicals in oats that may reduce cancer risk expands their application. These products support a balanced gut microbiota, thereby playing a multifaceted role in overall health management.

Use in Gluten-Free Diets

As oats are naturally gluten-free, they provide a valuable alternative for individuals with celiac disease and those adhering to gluten-free diets. However, due to the risk of contamination with gluten, it is recommended to choose certified gluten-free oat products. Oat-based gluten-free breads and cakes contribute to a healthy variety within the diet.

Sports Nutrition

Oats serve as a high-quality carbohydrate source rich in energy and nutrients, making them ideal for athletes. Consuming oats before or after exercise supports muscle repair and provides sustained energy. Oat-based protein powders and energy bars are widely used by athletes. The amino acid profile of oats helps support muscle mass and reduce muscle fatigue.

Medical and Dietetic Uses

Dietitians and healthcare professionals often recommend oats for managing diabetes, hypertension, and cholesterol. Due to their soluble fiber content, oats effectively control postprandial glucose levels (Wood et al., 2007). Furthermore, oat-based products stand out for their beneficial effects on gut health, thereby gaining attention in the medical and dietetic fields.

Conclusion

Oats hold a unique and versatile position in both traditional and modern food industries with regard to human nutrition. Thanks to their high fiber, beta-glucan, and protein content, oats offer numerous health benefits. From breakfast products to functional foods, from plant-based milks to sports nutrition, this cereal is widely utilized and stands out for its suitability in gluten-free diets.

Scientific research has demonstrated that oats can have positive effects on diabetes, cardiovascular diseases, obesity, and gut health. Moreover, as a sustainable food choice, they provide significant advantages in terms of environmental impact. Oats are poised to maintain their importance in the fields of nutrition science and food technology well into the future. In order to foster healthier individuals and communities, it is recommended that oats be incorporated more widely into daily diets.

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Evaluation of Oats in terms of Animal Nutrition

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ABSTRACT: Oat (*Avena sativa*) is a prominent component in animal feed due to its high nutritional value, digestibility, and adaptability. Its high fiber content and fatty acid composition support energy and digestive health, particularly in ruminants, while also benefiting monogastric animals and poultry. The β-glucan found in oats regulates gut microbiota, enhancing immunity and reducing inflammation. As an economical feed source, oats improve feed utilization and animal performance when combined with other grains. In poultry, oats have been observed to contribute to intestinal mucosa development and growth performance. This study emphasizes the importance of incorporating oats into balanced formulations for different animal species and highlights their significance in animal nutrition.

Keywords: Oat, *Avena sativa*, Animal Nutrition

INTRODUCTION

Oat (*Avena sativa*) stands out as a significant cereal in animal nutrition due to its high nutritional value, digestibility, and adaptability potential. Its use in the animal feed industry, often combined with other cereals, provides a cost-effective alternative. The energy-providing properties and support for digestive system health make oats an essential feed ingredient for various animal species (Karaman et al., 2020; Yılmaz & Yücel, 2020).

The high fiber content of oats makes it a key component in ruminant feed rations. Additionally, its fatty acid composition plays an effective role in meeting energy requirements (Kara & Demir, 2021). Compared to other cereals, oats have lower starch but higher fiber content. While this characteristic supports rumen functions in ruminants, it may limit its use in poultry diets (Dilmen, 1956).

Studies on the role of oats in animal nutrition have particularly focused on the positive effects of its β-glucan content on digestive health and feed utilization. Oat β-glucan has been reported to support gut microbiota, reduce inflammation, and improve animal health (Gürbüz, 2005; Hall, 2020). Furthermore, the presence of B-group vitamins and minerals makes oats a balanced component for animal health and performance (Yılmaz & Yücel, 2020).

In addition to its nutritional benefits, the use of oats in feed formulations offers economic advantages. Its ability to adapt easily to local conditions can reduce costs, especially in regions with limited agricultural resources. The high fiber and protein content make oats a suitable component for combination with various feed ingredients (Karaman, Akgün & Türkay, 2020; White & Edwards, 2019). However, balancing oats appropriately with other raw materials in feed formulations is critical to achieving optimal feed performance (Kara & Demir, 2021).

Nutritional Values of Oats

Oats are a highly valuable feed source in animal nutrition, notable for their rich nutrient content. One hundred grams of oats provide approximately 389 kcal of energy and contain 12-15% crude protein (Yılmaz & Yücel, 2020). Oats have a balanced composition of carbohydrates, proteins, fats, vitamins, and minerals. Its fat content is higher than that of other cereals, enhancing its energy density. Notably, it is rich in unsaturated fatty acids such as butyric acid and oleic acid (Karaman, Akgün & Türkay, 2020).

The fiber content of oats is also remarkable. Soluble fibers, particularly β-glucan, support digestive health in animals. These digestible fibers positively influence gut microbiota, improving both feed utilization and intestinal health (Gürbüz, 2005; Hall, 2020). Additionally, oats are rich in B-group vitamins (B1, B2, B6) and vitamin E, which support energy metabolism and overall health in animals. Minerals such as iron, magnesium, phosphorus, and potassium further contribute to its value as a key feed ingredient (Kara & Demir, 2021).

The nutritional benefits of oats vary depending on the animal species. For instance, it is preferred as an energy source for ruminants, while it enhances feed utilization efficiency in poultry. In monogastric animals like pigs, oats exhibit gut health-improving effects (Dilmen, 1956; Smith & Jones, 2021). Given these attributes, the balanced inclusion of oats in feed rations is of critical importance (Cherney & Marten, 1982).

Oats in Ruminant Nutrition

In ruminant nutrition, oats can be utilized as both roughage and concentrate feed. Its high fiber content supports rumen health, helping to prevent metabolic disorders such as acidosis. Studies have demonstrated the positive effects of oats on feed intake, milk yield, and meat quality in ruminants (Karaman et al., 2020; White & Edwards, 2019). The low starch content of oats optimizes rumen fermentation when used as an energy source, reducing the adverse effects often associated with high-starch feeds (Yılmaz & Yücel, 2020).

The inclusion of oats in ruminant rations is crucial for maintaining energy and protein balance. Combining oats with other cereals enriches the nutritional content of feed rations while enhancing animal performance. Oat straw, in particular, supports chewing activity in ruminants, improving feed efficiency (Kara & Demir, 2021). Additionally, the antioxidant content of oats may contribute to improved milk and meat quality (Dilmen, 1956).

Oats in Monogastric and Poultry Nutrition

For monogastric animals and poultry, oats are typically used in concentrate feed formulations. The high fiber content of oats supports gut health in monogastric animals, such as pigs, while also improving feed utilization efficiency. For instance, oat bran is known to regulate gut microbiota and enhance digestive system performance in pigs (Gürbüz, 2005). Furthermore, the β-glucan content of oats offers positive effects on the immune system (Yılmaz & Yücel, 2020; Zhou & Yu, 2004).

In poultry nutrition, oats serve as a complementary component in feed formulations. However, their high fiber content may limit their inclusion in large quantities. Despite this, balancing oats with other feed ingredients can enhance gut health and feed efficiency. For example, Alzueta et al. (2001) demonstrated the positive effects of oats on intestinal mucosa development and nutrient digestion. Their study highlighted the performance-enhancing effects of incorporating oats into broiler chicken diets.

Research has shown that oats improve feed utilization and growth performance in poultry (Kara & Demir, 2021; Smith & Jones, 2021; Veldman et al., 1993). By improving gut health and nutrient absorption, oats contribute to better overall productivity in monogastric animals and poultry.

Conclusion

This study has highlighted the significant contributions of oats to animal nutrition and their benefits across different animal species. Oats provide a critical component in animal feed as both an energy and fiber source. In particular, they support rumen health in ruminants, exhibit gut microbiota-improving effects in monogastric animals, and enhance growth performance in poultry. Additionally, the economic and easily accessible nature of oats makes them an attractive option for feed formulations.

In the future, further research focusing on genotype selection, cultivation techniques, and processing methods will be necessary to unlock the full potential of oats in the feed industry. Such advancements can help optimize the nutritional benefits of oats and expand their applications across diverse animal nutrition systems.

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Experimental Applications of Natural and Technological Drugs with Honey Bees: Status, Opportunities and Challenges

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ABSTRACT: Honey bees are important pollinators whose environmental importance is not discussed, and they are creatures whose culture varieties are widely grown to obtain more than one valuable product. Beekeeping is a field of study that requires considerable attention due to both workload and easy effects from environmental factors. The intensive coexistence in culture and the preference of yield-based breeds increase the frequency of various bee diseases. These diseases and their control can be quite difficult with the effects of climate change. Existing bee diseases can be caused by more than one microorganism group such as parasites (*Varroa*), fungi (*Nosemosis*), bacteria (European and American foulbrood) and viruses (Deformed Wing Virus). Although there are various chemicals for the control of microbial diseases, these chemicals can cause problems such as environmental damage or residues in bee products, and even there are completely banned chemicals (OTC etc.). The utilization or development of resistant strains in the context of combating these diseases may prove an efficacious solution. Nevertheless, it may prove inadequate, necessitate a considerable investment of time, or result in yield loss. An alternative method of control is the deployment of natural or technological (micro or nano technological) products that are completely harmless or do not leave residues. The application of these products should be done directly in the field and with bee colonies rather than in laboratory conditions. In this case, it is quite easy to apply to honey bees in colonies in hives and it can be practical to get the results. However, environmental conditions (wind, rain, amount of flowers and nectar, etc.) and uncontrolled parameters can produce results far from standard work. In order to address these challenges, it may be effective to utilise micro-hives, which can be deployed in isolated areas and which can accommodate different seasonal replications. Furthermore, the extensive use of statistical analysis may prove beneficial.

Keywords: Honey Bee, Beekeeping, Bee Diseases, Technological drugs

INTRODUCTION

Honey bees (*Apis mellifera*) play a pivotal role in both ecological stability and economic prosperity. Ecologically, they are indispensable pollinators, supporting the reproduction of countless flowering plants and maintaining biodiversity across ecosystems (Ahmed, 2023). Their pollination activities not only ensure the survival of wild plant species but also maintain habitats for numerous other organisms, making them critical contributors to ecological balance (Potts et al., 2016). Furthermore, *A. mellifera* serve as bioindicators, reflecting the health of their environments and highlighting issues such as pollution and habitat degradation (Quigley et al., 2019). Economically, *A. mellifera* significantly enhance agricultural productivity by pollinating crops essential for global food security (Malav et al., 2022). Their contributions extend beyond the farm, fueling industries reliant on high-quality fruits, vegetables and oilseeds while also underpinning the beekeeping sector, which produces valuable commodities such as honey, beeswax and royal jelly (Genç & Dodoloğlu, 2017).

The history of combating bee diseases and pest control is closely intertwined with the evolution of beekeeping practices and scientific advancements. In the early days of apiculture, beekeepers relied on simple, natural methods to maintain colony health. Smoking, for example, was used not only to calm bees during hive inspections but also as a rudimentary measure to ward off pests (Langstroth, 2004). Other traditional remedies, such as the use of herbs and plant extracts, were employed based on empirical knowledge passed down through generations.

As beekeeping became more systematic in the late 19th and early 20th centuries, the identification of specific diseases and pests such as American foulbrood (*Paenibacillus larvae*) and tracheal mites (*Acarapis woodi*) spurred efforts to develop targeted treatments (Genç & Dodoloğlu, 2017). Early interventions often involved mechanical approaches, like destroying infected hives, to prevent the spread of pathogens (Rossi et al., 2018). However, these methods were labor-intensive and economically unsustainable for large-scale operations.

The mid-20th century marked a turning point with the introduction of synthetic chemicals for pest control. Coumaphos, fluvalinate, flumethrin, formamidine and amitraz became widely used to combat Varroa destructor mites and other threats (Mitton et al., 2022). These chemicals were effective in the short term but came with significant drawbacks, including the development of resistance in pests, the potential toxicity to bees and the contamination of hive products such as honey and wax (Lodesani & Costa, 2005). Increasing awareness of these issues in the late 20th century led to a shift in focus towards safer and more sustainable solutions.

The concept of Integrated Pest Management (IPM) emerged as a cornerstone of modern beekeeping. IPM combines chemical treatments with cultural practices, biological controls and mechanical interventions to reduce dependence on harmful pesticides. Natural substances such as oxalic acid, formic acid and essential oils gained popularity because of their lower environmental impact and reduced risk to bee health (Bava et al., 2023).

Today, research focuses on developing innovative solutions, including biotechnological and nanotechnological interventions, to address the growing challenges posed by bee diseases and pests. This evolution reflects the ongoing quest for sustainable and effective methods to protect *A. mellifera* health.

Natural and Organic Drugs in Beekeeping

Natural and organic compounds are increasingly being used in beekeeping as sustainable and environmentally friendly alternatives to synthetic treatments (Cengiz, 2012). These remedies are derived from natural sources such as plants, minerals and organic acids. The remedies are valued for their lower toxicity, minimal environmental impact and reduced likelihood of contaminating hive products like honey and wax.

Nowadays, as organic feeding becomes increasingly important, synthetic acaricides used in *Varroa* control are being replaced by organic acids, which are natural components of honey (Wehling et al., 2003). In the control of *Varroa* mites, the use of organic compounds that have no toxic effects on humans and bees can be an effective solution to this serious problem. Organic acids such as oxalic acid, formic acid and lactic acid are the most commonly used organic compounds against the *Varroa* parasite today. When applied at the appropriate time and dose, these organic acids do not cause queen losses in colonies or have negative effects on adult bees and brood populations (Milani, 1999; Goodwin et al., 2002).

Oxalic acid, which is naturally found in many plants, only kills *Varroa* on adult bees (Qadir et al., 2021) and is not effective on closed brood cells. For this reason, its use in early spring and late autumn, when closed brood cells are the least, gives successful results. It is reported that this use provides 90-95% success (Nanetti, 1999; Paradin et al., 2000). In case of high doses and multiple repetitions of oxalic acid, it can cause loss of queen and adult bees in the colony (Gerogorc and Planic, 2001). Formic acid has been used in *Varroa* control in other European countries, especially in Germany, since 1980. It is stated that the effectiveness of the acid varies between 60-92% depending on the application method (Imdorf et al., 1997). In order to see the desired effect in *Varroa* control with formic acid, the application temperature is important and the high or low environmental temperature is effective in success. In order to achieve the desired success, the air temperature should be between 10-25 ºC (Akyol & Özkök, 2005). Since lactic acid does not affect the closed brood cells, it gives successful results in *Varroa* control in the early spring and late autumn periods when the brood population in the colony is at its lowest (Imdorf & Kilchenmann, 1990).

Essential oils have gained popularity as natural alternatives the control of *Varroa destructor* mites in *A. mellifera* colonies due to their effectiveness, safety and minimal environmental impact (Bava et al., 2023). Among these, thymol, derived from thyme plants, is the most widely used. Thymol disrupts mite activity and reproduction, often incorporated into commercial formulations like Apiguard. Its vapor action works well at warmer temperatures, making it effective during active beekeeping seasons (Giacomelli et al., 2016).

Other essential oils, such as menthol, eucalyptus and camphor, also show potential against *Varroa* mites. Menthol is particularly effective against tracheal mites, while eucalyptus and camphor oils act as repellents or fumigants to reduce mite loads (Singh, 2014). Essential oils are commonly used in treated pads, strips or sugar syrups to enhance their dispersion within the hive. Essential oils like thymol, lemongrass and eucalyptus have antifungal properties that help control *Nosema apis* and *N. ceranae* infections (Topal et al., 2020).

Technological Drugs and Approaches in Beekeeping

Recent advances in science and technology have revolutionized the development of drugs and strategies to protect *A. mellifera* from pests, diseases and environmental challenges. These technological approaches aim to provide more precise, effective and sustainable solutions, reducing the reliance on traditional chemical treatments and addressing the growing threats to bee health.

Biotechnology has introduced novel methods for managing *A. mellifera* health, such as RNA interference (RNAi). RNAi works by silencing specific genes in pests like *Varroa destructor*, disrupting their biological functions and ultimately leading to their death (McGruddy et al., 2024). This approach is highly specific, targeting only the pest while leaving *A. mellifera* and other beneficial organisms unharmed. Additionally, research into genetically engineered bees with enhanced resistance to diseases and environmental stressors is gaining momentum, offering a potential long-term solution to colony losses (Guichard et al., 2023).

Nanotechnology offers innovative tools for drug delivery and pest control. Nanoparticles are used to encapsulate and deliver active ingredients such as acaricides or antimicrobial agents directly to target areas within the hive (Gamal Eldin et al., 2024). These systems allow for controlled release, minimizing dosage and reducing side effects on bees and the environment. Nanotechnology is also being used to combat diseases such as *Nosema*, American and European foulbrood (Santos et al., 2014; Özüiçli et al., 2023).

Technological advancements have led to the development of smart hives equipped with sensors to monitor environmental conditions, colony health, and hive activity in real-time. These systems collect data on temperature, humidity, brood development and foraging behavior, providing beekeepers with actionable insights. Early detection of anomalies, such as pest infestations or diseases, allows for timely and targeted treatments, reducing colony losses and improving management efficiency (Zheng et al., 2024).

Modern drug formulations are being designed to enhance specificity and efficacy while reducing side effects. For instance, slow-release strips impregnated with acaricides or essential oils ensure sustained mite control with minimal exposure to bees. Similarly, probiotics tailored for *A. mellifera* are being developed to improve gut health and enhance immunity, particularly after exposure to antibiotics or pesticides.

Opportunities in Beekeeping Research Today

Beekeeping research is flourishing as the global awareness of the critical role bees play in ecosystems and agriculture continues to grow. One of the most promising areas is the development of sustainable pest management solutions.

Another significant opportunity lies in the study of *A. mellifera* genetics and breeding programmes. Advances in genomics and molecular biology allow researchers to identify and propagate traits that enhance disease resistance, productivity and adaptability to climate change. Breeding efforts now focus not only on increasing honey yields but also on creating bees that are resilient in diverse environments and sustainable for local ecosystems.

The impacts of climate change on *A. mellifera* populations present another urgent research frontier. Scientists are investigating how shifting temperatures, altered blooming periods, and extreme weather events affect bee behavior, physiology and colony health. By understanding these impacts, researchers can develop mitigation strategies, such as adaptive foraging models and climate-resilient beekeeping practices.

Research into bee products and their applications offers expanding opportunities in both human and animal health. Studies on the bioactive compounds in honey, propolis, royal jelly and bee venom. These items are uncovering their potential uses in medicine, nutrition and even industrial applications. Similarly, there is increasing interest in how bee-derived products can contribute to sustainable agriculture and livestock management, such as their potential role as natural antibiotics or growth enhancers.

Finally, the integration of technology into beekeeping is revolutionizing the field. Smart hives equipped with sensors and artificial intelligence enable real-time monitoring of hive health, temperature, humidity and bee activity. These tools not only improve management practices but also provide rich datasets for researchers to analyze trends and predict colony outcomes. This intersection of traditional beekeeping and modern technology ensures a more efficient and sustainable future for apiculture.

Beekeeping research today is a vibrant, interdisciplinary field with numerous opportunities to address global challenges. By harnessing scientific advancements and fostering collaboration across sectors, the potential to enhance the health and sustainability of bee populations and their ecosystems is immense.

Challenges in Beekeeping Research

While natural, organic, and technological approaches in beekeeping offer promising solutions for managing pests, diseases and environmental stressors, they also present a number of challenges. These difficulties must be addressed to fully realize the potential of these innovations and ensure their successful implementation in apiculture.

One of the primary challenges is the variability in effectiveness of natural and organic treatments. Factors such as environmental conditions, colony size and the specific pest or disease being targeted can significantly influence the efficacy of these methods. For example, essential oils and organic acids require precise dosing and application to achieve desired results without harming bees or leaving residues in hive products. In addition, these natural remedies may not provide immediate or complete control, requiring repeated applications or integration with other methods.

The adoption of technological approaches also faces hurdles, particularly for small-scale and traditional beekeepers. Advanced technologies like smart hives, RNA interference, and nanotechnology-based treatments often involve high initial costs, complex maintenance, and the need for specialized knowledge. These factors can limit accessibility and scalability, especially in developing regions where resources and technical expertise may be scarce.

Another significant issue is the potential for unintended side effects. Even natural and organic compounds can disrupt hive dynamics if misused. For instance, excessive use of essential oils might alter bees' behavior or interfere with queen pheromones, while improper application of organic acids can harm brood or adult bees. Similarly, technological solutions like nanoparticle-based drugs must be carefully tested to ensure they do not pose long-term risks to bees, other pollinators or the environment.

Regulatory and market challenges also present obstacles. The approval process for new natural and technological treatments can be lengthy and costly, delaying their availability to beekeepers. Furthermore, some beekeepers may hesitate to adopt these methods due to a lack of clear evidence or education about their benefits and limitations. Misinformation or skepticism about emerging technologies can further slow adoption rates.

Another difficulty is the need for extensive research and development. Many natural and technological approaches are still in experimental stages, requiring extensive studies to optimize their application and assess their long-term impacts. Limited funding and resources for apicultural research can hinder progress, especially in addressing region-specific challenges such as local pests, diseases and environmental conditions.

Finally, climatic and ecological variations can complicate the implementation of these approaches. The effectiveness of treatments like organic acids and essential oils may fluctuate with temperature, humidity, and other climatic factors. Additionally, changes in agricultural practices, pesticide use and habitat availability can influence the success of natural and technological solutions.

Conclusion

Natural, organic and technological approaches represent a transformative shift in beekeeping, offering innovative solutions to address the pressing challenges facing by *A. mellifera* populations. These methods have significant potential to improve colony health, increase productivity and reduce the environmental and health risks associated with conventional chemical treatments.

Despite the difficulties, the opportunities presented by these approaches far outweigh the challenges. They offer not only immediate solutions to pest and disease management, but also long-term strategies to enhance the resilience of *A. mellifera* colonies in the face of climate change and environmental pressures. By embracing these advancements, the beekeeping industry can safeguard *A. mellifera* populations, support biodiversity and ensure the continuation of vital pollination services critical to global ecosystems and agriculture. Natural, organic and technological approaches will play a key role in shaping the future of sustainable beekeeping.

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Pesticides or Nanoplastics More Dangerous?

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ABSTRACT: In recent years, threats to the environment and human health have become increasingly complex, and most of these threats are caused by human activities. Pesticides and nanoplastics, two important environmental pollutants, are at the forefront of these threats. Both have the potential to cause serious health problems worldwide, and in this article, the dangers of both pollutants will be compared. Pesticides have been known and widely used as pest control tools for many years, while nanoplastics have emerged as a newly discovered but rapidly spreading pollutant, making it necessary to make an in-depth assessment on this subject. Pesticides are chemical substances used in agriculture to kill or control pests. These chemicals aim to increase crop productivity by killing insects, weeds, fungi and other pests. However, the effects of pesticides on the environment have been investigated for many years, and many negative results have emerged. Pesticides damage ecosystems by seeping into nature through soil, water and air, and can have toxic effects on living things, including humans, by entering the food chain. People exposed to pesticides, especially farmers, can face serious health problems. These problems include cancer, neurological diseases, reproductive disorders and immune system diseases. The dangers of pesticides are further deepened by the negative effects they create on biodiversity. These chemicals used in agricultural areas not only kill the targeted pests, but can also affect beneficial insects and other living things. Thus, the ecosystem balance is disrupted and nature becomes more vulnerable to pests that develop resistance to pesticides. This situation can lead to the use of stronger and more harmful chemicals, causing a vicious circle.

Keywords: Health, Environment, Soil, Pesticide, Nanoplastic, Microplastic

INTRODUCTION

Micro and nano plastics are tiny plastic contaminants of emerging global concern with a wide range of ecological and health implications. Known as micro(nano) plastics (MNPs) with distinctive size (<5 mm), color, shape, particle density, gravity, and peculiar sources. Depending on their sources, plastic particles may be classified as either primary or secondary MNPs. MNPs are plastic particles manufactured with specific characteristics for use in a variety of applications, such as exfoliating scrubs, drugs, and industrial pellets, as well as those used as raw materials in the production of plastic items (Junaid et al. 2023).

People have taken the precaution of using yield enhancers in certain areas to boost agricultural production because of the possibility of the global population outstripping food production. Xenobiotics have been extensively used by farmers to increase yield and protect against harmful organisms in agricultural areas (Arslan et al., 2017). As a result of repeated and uncontrolled applications, not only target species acquire resistance and develop a high survival rate against these chemicals but non-target useful species are also affected (Arslan et al., 2017). Chemicals can reach water resources and aquatic environments as a result of rainfall and agricultural runoff, which may lead to toxic effects for both human and aquatic life. This chemical contamination causes the death of aquatic animals and enters the food chain (Arslan et al., 2017).

Despite the regulatory restrictions for the use of pesticides, the use of pesticides has gradually increased because of their low cost and broad spectrum. The high levels of chemicals contained in the runoff from agricultural, industrial, and commercial industries flow into the water sources and lead to the pollution of aquatic life. Currently, developed countries have remarked acute toxications of pesticide in wildlife such as fish. Pesticide pollutions in lakes and rivers are harmful for wild population of fish. Thus, wildlife poisoning surveillance programs should be established for understanding the side effects of pesticides. For these programs, first, the investigation of side effects of commonly used pesticides is necessary in fish While fish are directly exposed to these chemicals, humans and animals are indirectly exposed via the food chain.

A study examined the release of microplastics (MPs) and phthalates (PAEs) from tea bags into the tea, how these substances can enter the human body, and their potential health effects. The study analyzed 45 tea bag samples from different Iranian and German brands, quantifying the amount, size, and shape of the microplastics and phthalates. According to the findings, an average of 412.32 microplastic particles were detected in Iranian tea bags, and 147.28 microplastic particles were found in German tea bags. The most common size range for microplastics was 100–250 µm, with fibers being the most common shape, and the particles were transparent in color. Polyethylene (PE) and nylon were identified as the most common microplastic polymer types in tea bags. Additionally, an average of 2.87 mg/g of phthalates was found in Iranian tea bags, and 2.37 mg/g in German tea bags. The most prominent phthalates in tea bags were Diethylhexyl phthalate (DEHP) and diisobutyl phthalate (DiBP). The study revealed that microplastics and phthalates leach into the tea as it is brewed, and that drinking 200-400 mL of tea daily could result in the ingestion of between 648 and 1,296 microplastic particles. DEHP, in particular, has been identified as a potential cancer risk for children, adolescents, and adults. This suggests that long-term exposure to these substances could have adverse health effects. In conclusion, the study emphasizes that the high levels of microplastics and phthalates in tea bags pose health risks, and consumers should be cautious (Kashfi et al. 2023).

The study by Rita Kihnna et al. (2024) on microplastics and nanoplastics highlights the dangers of these materials to the environment and human health. Approximately 40% of the plastic produced worldwide is used for packaging, and up to five trillion plastic bags are consumed every year. However, inadequate disposal and persistence of plastic waste in nature seriously threaten the environment and health. Large pieces of plastic gradually turn into microplastics (MPs) and nanoplastics (NPs), and these small particles can be transported in water, land, and the atmosphere, entering living organisms in various ways, especially by ingestion, inhalation, and skin contact. Long-term exposure to MPs and NPs can lead to health problems such as chronic inflammation, autoimmune diseases, atherosclerosis, and cancer. Therefore, it is essential to develop sustainable strategies to reduce plastic pollution in the environment and its harm to human health. These strategies include reducing plastic use, material substitution, filtration, recycling, and technological innovation. Furthermore, solving this global problem requires interdisciplinary cooperation in the fields of medicine, public health, environmental science, economics, and policy.

The review by Soutmitra et al. (2024) addresses the growing concerns regarding microplastics (MPs) and nanoplastics (NPs) in soil and their potential impact on the environment and human health. MPs and NPs can enter the soil through various pathways, such as agricultural activities, sewage sludge applications, and atmospheric deposition. Once in the soil, they can accumulate in the upper layers, affecting soil structure, water retention capacity, and nutrient availability. In addition, these plastics can transport harmful substances such as heavy metals and persistent organic pollutants, which can have serious consequences for ecosystems. MPs and NPs can also lead to the release of chemicals and additives, causing food web contamination and groundwater pollution, which pose risks to public health. The presence of these plastics in soil ecosystems can negatively affect soil microorganisms, altering plant growth and nutrient availability. Although, in some cases, they may assist in soil remediation, MPs and NPs generally harm soil ecology and increase public health risks through the food chain and groundwater contamination.

The review by Mariateresa Russo et al. (2023) covers global micro- and nanoplastics pollution and the risks they pose to human health, harmful chemical elements, pollutant carriers, and physical damage. Here are a few key findings from the study: Microplastics in soil interfere with water and nutrient uptake by adhering to crop seeds and root surfaces or accumulating in the vascular systems. Additionally, micro- and nanoplastics cause oxidative damage in plants, disrupting metabolic processes and releasing chemical additives that lead to cytotoxic and genotoxic effects in plants. Microplastics alter both the biotic and abiotic conditions of the soil, negatively affecting the supply of water and nutrients to crops. Finally, the combined toxicity of different microplastics in soil can lead to more significant adverse effects on plants. Furthermore, ingested plastics cause numerous problems in the human body, such as antibiotic resistance, neurological complications, microbial toxicity, metabolic syndrome, genotoxicity, reduced uterine arterioles, inflammation, oxidative stress, and chronic diseases.

This study highlights the importance of toxicological and epidemiological research to investigate the potential effects of microplastics (MPs) on human health by examining their amount and size in the most commonly consumed fruits and vegetables. The study aims to examine the number and size (<10 μm) of MPs in fruits and vegetables most frequently consumed by humans (apples, pears, broccoli, lettuce, carrots, and potatoes) and to correlate these with daily intake levels. The study demonstrated that average MP (microplastic) concentrations in fruits and vegetables range from 1-4 μm, with approximately 190,000-196,000 particles/g fresh weight and 51,000-126,000 particles/g fresh weight, respectively. This study also confirmed the accumulation of micro- and nanoplastics (MNPs) in edible plant tissues obtained from real-world market sources. In light of these results, it is considered of urgent importance to conduct toxicological and epidemiological studies to further investigate the potential effects of MPs on human health (Conti et al 2020).

In a review by Pingfan Zhou et al. (2023), nanoplastics (NPs) can rapidly accumulate in soil, posing serious threats to ecosystems and human health. However, the environmental behavior and toxicity of NPs in the soil-plant system are not yet fully understood. This review examines the interactions of NPs with plants, their uptake mechanisms, and phytotoxicity. NPs can be absorbed by plant roots and transported through the xylem to all parts of the plant, including edible portions, which may pose a risk to human health. Additionally, NPs affect plants' ability to transport water and nutrients, inhibiting photosynthesis and other biochemical processes, which negatively impacts plant growth and development. The combined effects of NPs with other soil contaminants highlight the potential for more severe toxic consequences.

Carmen Freire et al. (2023) conducted a study aimed at determining how the risk of depression and suicide changes in agricultural workers and rural individuals exposed to pesticides. The 11 depression and 14 suicide studies in the MEDLINE database over 15 years showed that previous pesticide poisoning increased the risk of depression by 2.08 to 5.95 times, while suicide rates increased by 60% to 161% in areas with high pesticide use. Furthermore, agricultural labor was associated with a higher risk of suicide compared to other occupational groups (OR between 1.30 and 4.13). Chlorpyrifos use was found to increase suicide rates by 137%. However, these associations are still based on limited evidence, and the authors emphasized the need for more extensive research.

Mehjin AM AL-Ani et al. (2019) aimed to determine the environmental effects of pesticides and their negative impacts on soil health. For this purpose, they investigated the effects of commonly used pesticides (Glyphosate, Alpha-cypermethrin, and Malathion) on soil microorganisms. The pesticides were added to the soil at different concentrations (0, 50, 100, 200 ppm) and incubated at 30 °C. The study observed the effects of these pesticides on the microorganisms over a period of 7 weeks, assessing bacteria, fungi, actinomycetes, and microbial activities. The results showed that all pesticides significantly reduced both the number of microorganisms and microbial activities. The effect was inversely proportional to the pesticide type and application concentration; in particular, soil samples treated with 200 ppm Malathion exhibited the lowest microbial activity and microorganism count. These findings confirm the environmental impacts of pesticides and their negative consequences on soil health.

Wei Zhou et al. conducted a comprehensive review of the impacts of chemical pesticide use on the environment and human health. The review emphasizes that the widespread use of pesticides presents significant health risks, particularly for infants and children. Worldwide, there are 385 million cases of unintentional pesticide poisoning each year, 11,000 of which result in death. Approximately 44% of farmers are poisoned by pesticides annually. Pesticides can have adverse effects on the nervous system, leading to cancer, diabetes, respiratory disorders, neurological diseases, and reproductive issues. Highly toxic pesticides, such as organochlorines and organophosphates, increase the risk of diseases like cancer, Parkinson's, and Alzheimer's. Furthermore, exposure to pesticides is linked to diabetes and respiratory problems. The negative impact of pesticides on reproductive health is also a significant concern. These findings underscore the need for safer practices and stricter regulatory measures to reduce pesticide use. Additionally, adopting more sustainable pest control methods is crucial.

Material and Method

In this review, scientific studies are compared comparatively. Nanoplastics are plastic particles that are smaller than 100 nanometers in size and are formed as a result of the breakdown of plastic materials. These particles accumulate rapidly in seas, lakes, soil and the atmosphere, and can be digested by microorganisms and living things. The small size of nanoplastics can make them extremely dangerous for surrounding ecosystems and humans. The human body can take these small particles and allow them to reach the internal organs, bloodstream and even the brain.

Although the effects of nanoplastics on human health are not yet fully understood, research shows that these substances can cause inflammation, cellular damage and genetic changes in the body. Nanoplastics, which especially carry the risk of accumulating in organs such as the brain, liver and kidney, can lead to serious health problems such as neurological diseases and cancer. In addition, in terms of environmental effects, these small plastic particles can be consumed by fish and other aquatic creatures in aquatic ecosystems, which can have devastating effects on biodiversity.

Another important danger of nanoplastics is that the chemical components of plastics spread into the environment over time. When nanoplastics combine with toxic substances, the entry of these harmful chemicals into nature and the food chain can pose an additional risk to human health. The fact that plastics are not long-lasting and biodegradable makes them a permanent threat to the environment.

Although both pesticides and nanoplastics are substances that pollute the environment and harm human health, their effects are felt in different dimensions and ways. The dangers of pesticides have been known for a long time and have been directly linked to various health problems. These chemicals have permanent effects by biologically accumulating in nature and living things. However, many countries have enacted laws and regulations to control the effects of pesticides and have limited the use of these chemicals. These measures have reduced the effects of pesticides to some extent. On the other hand, nanoplastics are a newer environmental problem and research in this area is still in its infancy. It is thought that nanoplastics can spread more quickly in ecosystems and penetrate biological systems, especially due to their small size. This may make them a greater threat in the long term. However, the long-term consequences of the effects of nanoplastics are still unknown, making them quite uncertain and potentially much more dangerous.

Result and Discussion

In recent years, threats to the environment and human health have become increasingly complex, many of which are caused by human activities. Pesticides, which have been used effectively for many years to protect agricultural crops from pests and to increase income, are now creating increasingly serious problems for soil and the environment, in addition to the harm they cause to human health. Pesticides degrade soil health by reducing microbial diversity, making it difficult for plants to absorb nutrients due to changes in pH levels, and increasing plant stress factors through heightened soil toxicity. Furthermore, pesticides contribute to water pollution and the contamination of groundwater and surface water, threatening ecosystems and drinking water sources. These issues pose significant risks to human health and will become a major threat to agricultural sustainability and profitable production in the future. To protect human health and promote environmental sustainability effectively, it is essential to make practices such as biological control, integrated pest management (IPM), natural and organic agriculture, increasing plant resilience, agroecological methods, cultural practices, physical methods, pest detection and monitoring technologies, soil health protection, and education and awareness-raising more widespread.

Additionally, nanoplastics, which have become one of the leading environmental pollutants in recent decades, are formed from various sources in our environment. Many factors, such as the slow degradation of larger plastics, industrial processes, water and air pollution, agricultural practices, recycling activities, and personal care products, contribute to the formation and spread of nanoplastics. This spread poses significant dangers by reaching plants and ecosystems through soil and waterways, particularly in agricultural areas. Plants can absorb nanoplastics through their roots, and these microplastics can negatively affect plant growth by inhibiting water and nutrient uptake. Moreover, nanoplastics can interact with microorganisms in the soil, reducing biodiversity and soil fertility. Nanoplastics deposited on agricultural products can enter the food chain, causing potential harm to human health. Therefore, the presence of nanoplastics in agricultural areas represents a serious threat to both the environment and public health.

Conclusion

Pesticides and nanoplastics are two different threats that pose serious harm to the environment and human health, but both are significant environmental problems worldwide. Although the harmful effects of pesticides have been known for a long time, it can be said that nanoplastics pose an increasingly greater threat. While pesticides accumulate in nature and harm ecosystems, nanoplastics, as a newly discovered and rapidly spreading threat, have the potential to cause wider environmental and health effects.

In conclusion, the long-term effects of nanoplastics make them a more uncertain but potentially more dangerous threat. Therefore, more research and effective policies need to be developed at the global level to understand the effects of both pollutants and to combat these threats. However, many studies conducted over the years have shown that pesticides are more dangerous synthetics globally.

Considering the place pesticides hold in the global economy, it becomes clear that they are more dangerous and need to be fought more.

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Association between Kappa-Casein Gene Polymorphism and Milk Protein Yield in Brown Swiss Cattle Breed: A Meta-Analysis

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ABSTRACT: Kappa-casein is a major consideration milk protein genes, influencing the technical qualities of milk and the quality of dairy products. Milk composition in dairy cattle is a quantitative feature affected by environmental and genetic factors. In several fields of animal research, quantitative summaries of literature data are frequently required. In these circumstances, meta-analyses must be utilized to analyze summary data. This study aimed to use meta-analysis to identify polymorphisms in the k-CN gene associated with protein content in Brown Swiss breeds. Statistical analysis to identify heterogeneity between studies and overall estimations was carried out with Stata 11.2 software. The random effects model was utilized to generate 95% confidence intervals. The analysis included articles that met the relevant conditions. (AA versus. AB), (AA vs. BB), and (AB vs. BB) used as genetic models. The findings of this study show that there was greater heterogeneity among studies indicating increased genetic variability. The association analysis does not show a significant relationship between kappa-casein gene polymorphisms and milk protein yield (P>0.05).

Keywords: Meta-analysis, Protein, Kappa Casein, Polymorphisms

INTRODUCTION

Milk is a fundamental product produced by various animals, including cows, sheep, goats, horses, buffaloes, and camels, and is consumed regularly (Scholz-Ahrens et al., 2020). Milk's chemical components, such as protein, fat, carbs, vitamins, and minerals, are crucial in human nutrition (Kliem et al., 2013). Bovine milk constituents are quantitative characteristics influenced by environmental and genetic factors (Dogru, 2015). Genetic polymorphism of cow milk proteins has been extensively investigated due to its significant role in breeding strategies, as well as in studies on population structure and the conservation of natural genetic diversity among indigenous breeds. Additionally, milk protein polymorphism has been shown to have a substantial impact on both qualitative and quantitative milk traits in numerous studies (Dogru, 2015). Casein, the primary class of milk proteins, accounts for approximately 80% of the total protein content in milk and is composed of αS1-, αS2-, β-, and κ-casein isoforms (Eigel et al., 1984).

Today, as in all disciplines, the number of scientific inquiries on cattle is steadily increasing. These days, a vast amount of independent research has been done on every topic in any field, with varying conclusions. Glass (1976) proposed the procedure of integrating and synthesizing research into a single study, which he called "meta-analysis," as a novel way to arrange, analyze, and reach new conclusions and interpretations. Simultaneously, important information is also provided by the meta-analysis study about whether the results found in individual studies are a sign of random or chance. Therefore, the increase in sample size is also an increase in the statistical significance level of the study (Sağlam and Yüksel, 2007). The current meta-analysis has some advantages (1) The information was collected from a variety of published studies and languages; (2) The meta-analysis was performed using allele-additive models; (3) To confirm the main findings, we conducted a sensitivity analysis and eliminated one study. On the other hand, this meta-analysis had several limitations: (1) The limitations of the studies in the review, which could be a source of variability in the overall results; (2) The precision of the results may be reduced by the small sample sizes of these studies; (3) we found a high heterogeneity among studies under all three alleles models; and (4) Several factors including other SNPs and genes may influence milk production characteristics. A current study was conducted to analyze the relationship between kappa-casein gene polymorphisms and milk protein by systematic review and meta-analysis.

Material and Method

The κ-casein gene polymorphism and its association with protein yield in Brown Swiss cattle were investigated for the current review study using the databases of Google Scholar, ResearchGate, Wiley, Springer, PubMed, and Elsevier. The Stata 11.2 program was used to conduct statistical analyses following the inclusion and extraction of data. In this investigation, estimates were made using both fixed-effect and random-effect models. Studies were evaluated by forest plot, and statistical I^2 was used to find interstudy heterogeneity. The fixed-effects model makes the assumption that the actual treatment effect is the same in every research and In the random-effects model, the true effect estimate differs from research to study. To measure the abilities between the groups, standard deviation and standardized mean differences (SMDs) were computed at 95% CI (Confidence Interval). To measure abilities across the three genetic models for each attribute, standard deviation, and SMDs were computed at 95% CI.

Statistical Analysis

In this investigation, estimates were made using both fixed-effect and random-effect models. Studies were evaluated by forest plot, and statistical I^2 was used to find interstudy heterogeneity. While the random-effects model assumes that the genuine effect estimate differs for every study, the fixed-effects model assumes that the true effect of treatment is the same for every study. Stata 11.2 software was used to analyze the data, and 95% confidence intervals were used to assess the relationship between κ-casein gene polymorphisms and protein yield. When there were less than ten included studies, the Hedges technique was applied to determine the standardized mean difference (SMD).

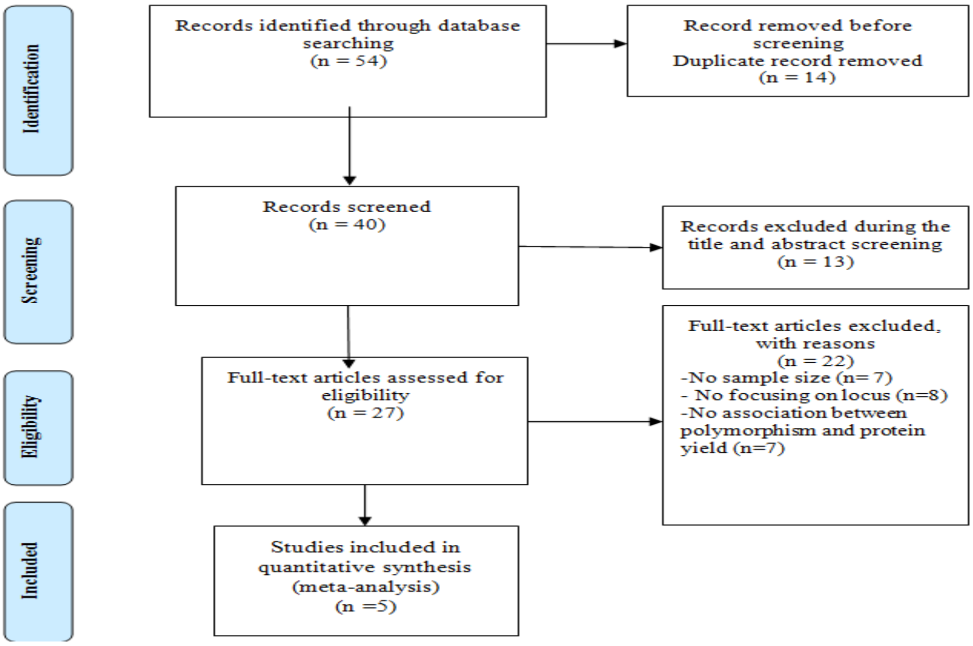

Figure 1. The inclusion and exclusion criteria are displayed in the PRISMA flow diagram

Results and Discussion

Lipids and proteins in an analysis of the findings from 5 studies, a higher degree of heterogeneity was found in the study which indicated higher genetic variability. As illustrated by the forest plot figure 1, the I^2 statistic for all meta-analyses conducted under 3 co-dominant models, where the I^2 was higher than 50%, thus random effects and lower than 50% fixed effect models were employed to analyze data. For the AA vs AB model, heterogeneity was ($I^2\%$ = 28.7%) with an overall standardized mean difference (0.07), and the heterogeneity statistic was found non-significant ($P > 0.05$). For the AA vs. BB model, heterogeneity was ($I^2\%$ = 54.6%) with an overall standardized mean difference (0.09), and the heterogeneity statistic was found to be significant ($P < 0.05$). In the AB vs BB model, didn’t found heterogeneity ($I^2\%$) and overall standardized mean difference (-0.03), and the heterogeneity statistic found non-significant ($P > 0.05$).

When the confidence interval of the effect size did not touch the vertical line, it indicated a significant difference between genotypes in the association meta-analysis results, as represented by the vertical dashed line with a diamond. Figure 2 illustrates the analysis of studies on milk protein yield. The relationship between the additive model (AA vs. AB) and protein yield was found to be non-significant (P>0.05), and the overall confidence interval of the effect size touched the line. Similarly, figure 3 illustrates the study of (AA vs. BB). The relationship between the additive model (AA vs. AB) and protein yield was found to be non-significant (P> 0.05), and the overall confidence interval of the effect size touched the line. Finally, the association between cattle with the additive model (AB vs BB) was found non-significant. In overall results, the association between the κ-casein gene and milk protein yield was found non-significant in the Brown Swiss. Differences in sample size, environmental effects, and breeds studied especially genotype-environment interactions, may be the main reason for non-significant. In the discussion, the relationship between protein yield and κ-casein gene genotypic models (AA vs. AB) was found non-significant (P>0.05), and similar results were reported by (Ladyka et al., 2022; Chrenek et al., 2003). They also found that polymorphism of κ-casein gen had no significant effect on milk protein. Likewise, in the analysis of (AA vs. BB) as shown in figure 3. The overall confidence interval of the effect size touched the line and the association between the additive model (AA vs. BB) and protein yield indicated non-significant (P>0.05). This result is consistent with the studies (Ladyka et al., 2021; Pishchan et al., 2021). The analysis of (AB vs. BB) is shown in figure 4. The overall confidence interval of the effect size touched the line and the association between the additive model (AB vs. BB) and protein yield indicated non-significant (P>0.05). This result is consistent with the studies (Ladyka et al., 2021; Ladyka et al., 2022, Pishchan et al 2021).

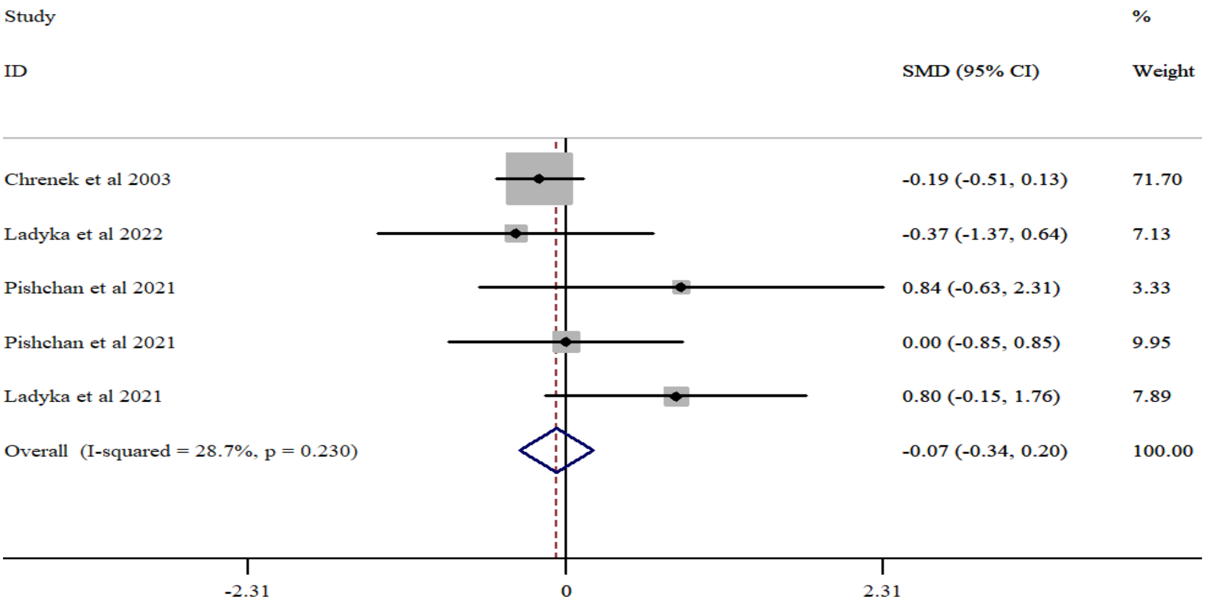

Figure 2. κ-casein forest plot allele models for polymorphisms and milk protein output (AA vs. AB). Each study's weight is shown by the circle, its confidence interval is shown by the horizontal line, and a summary of the findings is shown by the diamond at the bottom of the figure

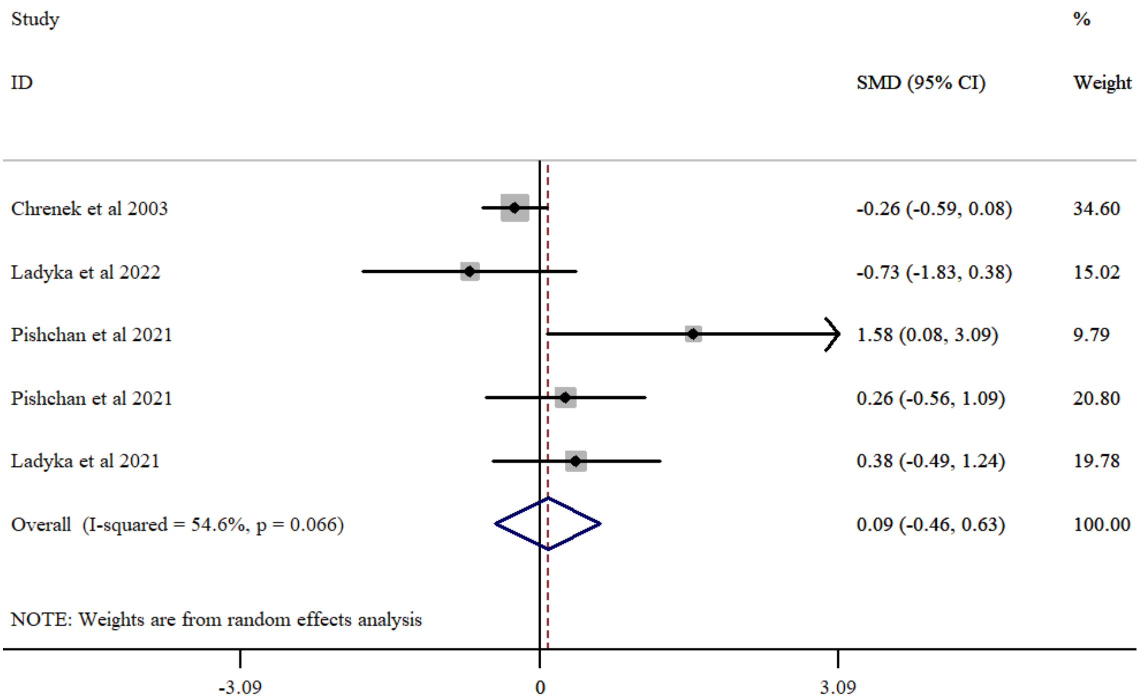

Figure 3. The κ-casein polymorphisms and milk protein yield (AA vs. BB) alleles model is represented by a forest plot. Each study's weight is represented by a circle; each study's confidence interval is shown by a horizontal line; and a summary of the findings is shown by the diamond at the bottom of the plot

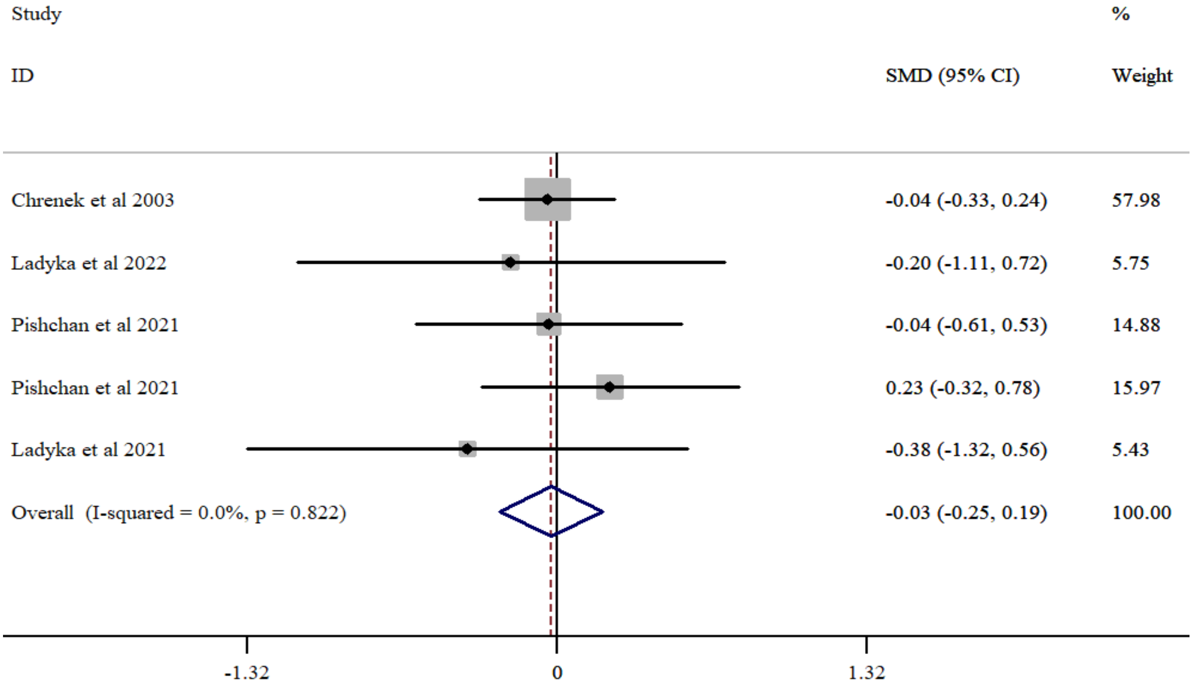

Figure 4. κ-casein forest plot allele models for polymorphisms and milk protein yield (AB vs. BB). Each study's weight is shown by the circle, its confidence interval is shown by the horizontal line, and a summary of the findings is shown by the diamond at the bottom of the figure

Conclusion

Consequently, research on the association between κ-casein gene polymorphisms of all co-dominance models and milk protein in Brown Swiss cattle, undertaken between 2003 and 2022, was determined to be non-significant. Higher genetic variability was suggested by a greater degree of heterogeneity among the investigations. Therefore, more research should be done to determine the κ-casein gene's polymorphism and how it affects the amount of milk protein produced.

Acknowledgement

Not applicable

Funding

No specific grant from a public, private, or nonprofit funding organization was obtained for this study.

Statement of Conflict of Interest

We certify that there is no conflict of interest with any financial organization regarding the material discussed in the manuscript.

Authors' Contributions

MO, ZM, and KE conceptualized the study, while ZM, KE, and ES were responsible for data collection and organization for analysis. MO conducted the statistical analysis, and the manuscript was written by MO, KE, and ZM.

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Association between Kappa-Casein Gene Polymorphism and Milk Fat Yield in Brown Swiss Cattle Breed: A Meta-Analysis

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ABSTRACT: Focused on genes that influence phenotypes and have economic significance, genetic research in livestock may be useful for breeding initiatives. Through a systematic review and meta-analysis, this study sought to determine how Kappa-Casein gene polymorphisms and milk fat yield in Brown Swiss cattle relate to one another. A meta-analysis is a technique that estimates or evaluates the common effect size by combining and reevaluating the findings of at least two research. The articles that satisfied the specified criteria were included in the analysis, which included a total of seven research from 2003 to 2022. Data was analyzed using three co-dominant models: AA vs AB, AA versus BB, and AB versus BB. 95% confidence intervals were calculated based on study heterogeneity and the Random effects model. The statistical stability of total estimates was evaluated using I^2 tests in Stata 11.2 software. The study discovered no significant connection between kappa-casein gene polymorphisms and milk fat output (P>0.05).

Keywords: Meta-Analysis, Fat, Kappa-Casein, Polymorphisms

INTRODUCTION

In dairy cows, the primary goal of selection is to improve both productivity and milk composition. Breeding programs can be made more efficient by using molecular approaches and identifying the basic genes that influence productivity qualities in livestock. Milk fat contains essential fatty acids and is a major source of energy, and the quality of dairy products is associated with the presence of bioactive lipids (Michalski et al., 2002; Bauman and Griinari, 2003; Wiking et al., 2004). Milk fat concentration are varies among ruminant animals, and dairy scientists and nutritionists often face challenges in understanding milk fat variation at the farm level (Daley et al., 2022). Significant research has been published on factors that influence milk composition, such as genetics (Andersson-Eklund and Rendel, 1993; Abdallah and McDaniel, 2000; Stoop et al. 2008).

The kappa-casein (κ-CN) gene polymorphism is analyzed using two allelic variants: A and B, which occur in all cow breeds. Variant B of the κ-casein gene causes two point mutations at positions 136 and 148, resulting in amino acid substitutions of Tyr-Iso and Ala-Asp (Suprovych and Mokhnachova, 2017). Nowadays, the study of cow milk productivity in relation to alleles or genotypes of specific genes important for bovine productivity is timely and relevant. This allows us to generate accurate forecasts regarding cows' lifetime milk productivity (Ladyka et al., 2021; Pishchan et al., 2021).

Systematic reviews and meta-analyses are commonly used in various fields, including animal science, as part of the investigation process. They synthesize available evidence and can aid in designing new research. Determining the necessity of the research can be established (Borenstein et al., 2009; Motmain et al., 2022). Meta-analysis is a statistical test or approach that combines the findings of several research into a single estimate (Ozdemir & Ozdemir, 2023). A primary objective of meta-analysis is to yield accurate and reliable results by increasing the sample size through the integration of multiple studies, thereby reducing the confidence interval of the measurements and addressing issues arising from the conflicting outcomes of previous research (Field, 2005).

A meta-analysis improves the precision of effect estimates while also establishing new hypotheses (Lean et al., 2009; Ozdemir et al., 2018). The current meta-analysis has some advantages (1) The information was collected from a variety of published studies and languages; (2) The meta-analysis was performed using allele-additive models; (3) We removed a single study in a sensitivity analysis to validate the overall results. On the other hand, this meta-analysis had several limitations: (1) The limitations of the studies in the review, which could be a source of variability in the overall results; (2) The precision of the results may be reduced by the small sample sizes of these studies; (3) we found a high heterogeneity among studies under all three alleles models; and (4) Several factors, including genetics and the environment, can influence milk output.

Material and Method

A comprehensive search of scientific journals was conducted to identify potential meta-analyses of polymorphism κ-CN gene and its ampact on milk fat yield in Brown Swiss dairy cattle. Radom effect model and fixed effect model are used for statistical analysis. Model selection was dependent on whether the effects of the studies were homogeneous or heterogeneous; when the study effects were homogeneous, a fixed model was employed; if the study effects were heterogeneous, a random model was used. The Hedges method and Q statistic were employed to determine heterogeneity between trials, with the I^2 index being utilized for additional quantification. The writers extracted data separately, and the data was collected using Microsoft Excel. Mistakes or errors in studies and data collecting are resolved through communication amongst them. Totally 7 studies found about polymorphism of κ-CN gene and associated with milk fat yield, and selected for this analysis. Key information, including the author's name, publication year, country of study, sample size, genotypes, breed, and milk fat production (kg), was extracted from the included studies.

Statistical Analysis

Random-effects and fixed-effects models were employed in this analysis to estimate outcomes. The statistical measure I^2 was utilized to evaluate inter-study heterogeneity, and the results were visualized through a forest plot. The fixed-effects model assumes that the true treatment effect is consistent across all studies, whereas the random-effects model accounts for variability in the true effect estimates among studies. Data analysis was conducted using Stata software (version 11.2), with the association between κ-CN gene polymorphisms and fat yield evaluated using 95% confidence intervals. Given that the number of studies included in the meta-analysis was fewer than 10 (Figure 1), the standardized mean difference (SMD) was calculated using Hedges' method.

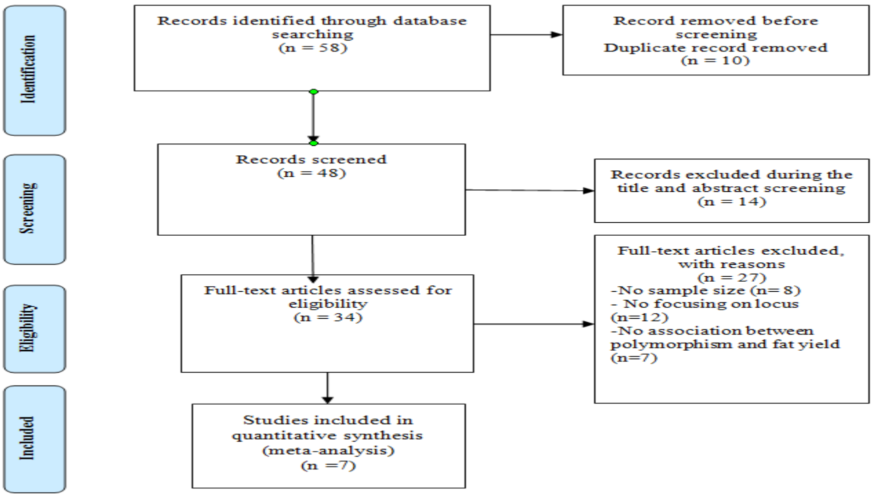

Figure 1. The PRISMA flow diagram illustrating the inclusion and exclusion criteria

Results and Discussion

Lipids and proteins are fundamental constituents of milk, playing a crucial role in determining its nutritional value and the technical properties of its derivatives. For instance, cheese yield is strongly influenced by the concentration of milk casein, while the concentration and composition of milk fat are critical determinants of milk and cheese quality. Previous research, including studies by Molee et al. (2015) and Mahmoudi et al. (2023), has suggested that key genetic factors may influence these milk characteristics. The association analyses conducted in these studies revealed a high degree of heterogeneity, reflecting substantial genetic variability associated with these traits. The included number of investigated studies and the results of heterogeneity statistic for bias in publications, and also the I^2 statistical test for heterogeneity between studies in the meta-analysis presented in figure 2,3,4. As illustrated by the forest plot, the I^2 statistic for all meta-analyses conducted under 3 co-dominant models, where the I^2 was higher than 50%, thus random effects and lower than 50% fixed effect models were employed to analyze data. For the AA vs. AB model, SMD estimates among genotypes indicated substantial heterogeneity (I^2% = 74.8 %) with an overall standardized mean difference (0.03), and the heterogeneity statistic was found to be significant ($P <0.05$). For the AA vs. BB model, SMD estimates among genotypes indicated substantial heterogeneity (I^2% = 68.3 %) with an overall standardized mean difference (0.02), and the heterogeneity statistic was found to be significant ($P <0.05$). For AB vs BB model, SMD estimates among genotypes indicated substantial heterogeneity (I^2% = 34.5.3 %) with over all standardized mean difference (0.02), and the heterogeneity statistic was found non-significant ($P >0.05$).

The results of the meta-analysis are depicted by a vertical dashed line marked with a diamond. A significant difference between genotypes was observed when the confidence interval of the effect size did not overlap with the line. In the analysis of milk fat yield studies, as shown in Figure 2, the overall confidence interval of the effect size intersected with the line, indicating that the association between the additive model (AA vs. AB) and fat yield was non-significant ($P > 0.05$). Likewise, In the analysis of (AA vs. BB) as shown in figure 3. The overall confidence interval of the effect size touches the line and the association between the additive model (AA vs. AB) and fat yield indicated non-significant ($P> 0.05$). Finally, the association between cattle with the additive model (AB vs. BB) was found non-significant as shown figure 4. In overall results, the association between the κ-CN gene and milk fat yield was found non-significant in the Brown Swiss. The primary explanation may lie in variations in sample size, environmental influences, and the breeds examined, particularly the interactions between genotype and environment. In cattle, milk components are quantitative traits shaped by both genetic and environmental factors. Milk fat content serves as a critical indicator of milk quality due to its nutritional significance and its technological relevance in dairy production. Among ruminants, fat is the most variable milk component, with its concentration differing considerably between individual cows (Daley et al., 2022).

Based on the findings of the meta-analysis conducted in this review. In the analysis of milk fat yield studies as shown in figure 1. the overall confidence interval of the effect size touched the line and the association between the additive model (AA vs. AB) and fat yield indicated non-significant ($P > 0.05$). These findings are in agreement with (Chrenek et al., 2003; Ladyka et al., 2022; Doğru et al., 2015). They found that κ-CN gene polymorphisms were not associated with milk fat in the Brown Swiss cattle. Likewise, in the analysis of (AA vs. BB) as shown in figure 3. The overall confidence interval of the effect size touches the line and the association between additive model (AA vs. BB) and fat yield indicated non-significant (P>0.05). This result is consistent with the studies (Ladyka et al., 2021; Özdemir et al., 2005; Pishchan et al., 2021). Finally, the association between cattle with additive model (AB vs. BB) found non-significant. At overall results the assoication between κ-CN gene and milk fat yield found non-significant in the Brown Swiss cattle. The primary factors may include variations in sample size, environmental influences, breeds studied, and, notably, genotype-environment interactions. Furthermore, several findings reported by other authors contrast with the results of this study.

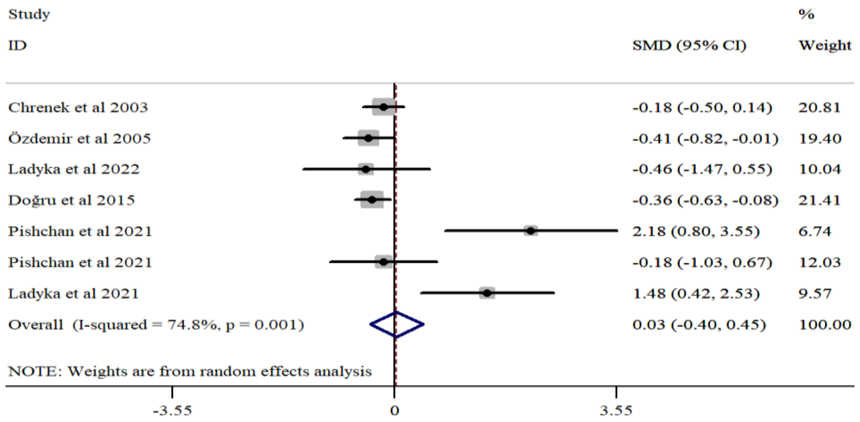

Figure 2. The forest plot for κ-CN polymorphisms and milk fat yield (AA vs. AB alleles model) illustrates the results of the analysis. Circles depict the relative weight of each study, while horizontal lines represent the confidence intervals for individual studies. The diamond at the bottom of the plot provides a summary estimate of the overall results.

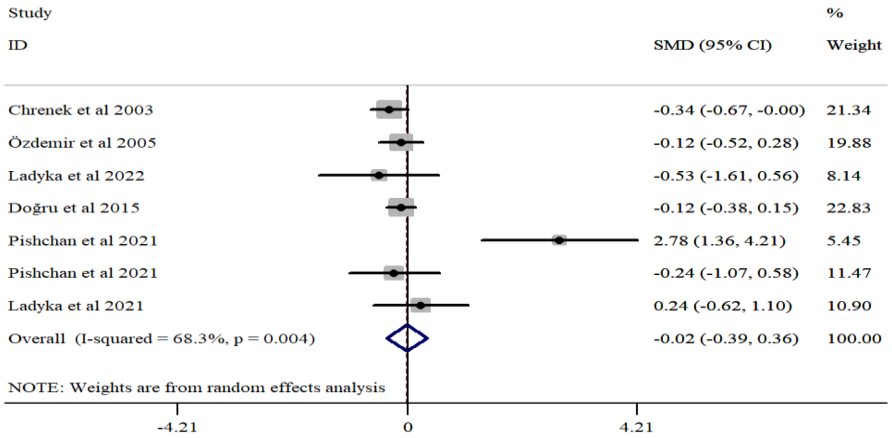

Figure 3. The forest plot for κ-CN polymorphisms and milk fat yield (AA vs. BB alleles model) presents the analysis results. Circles indicate the relative weight of each study, while horizontal lines represent the confidence intervals for individual studies. The diamond at the bottom of the plot summarizes the overall results.

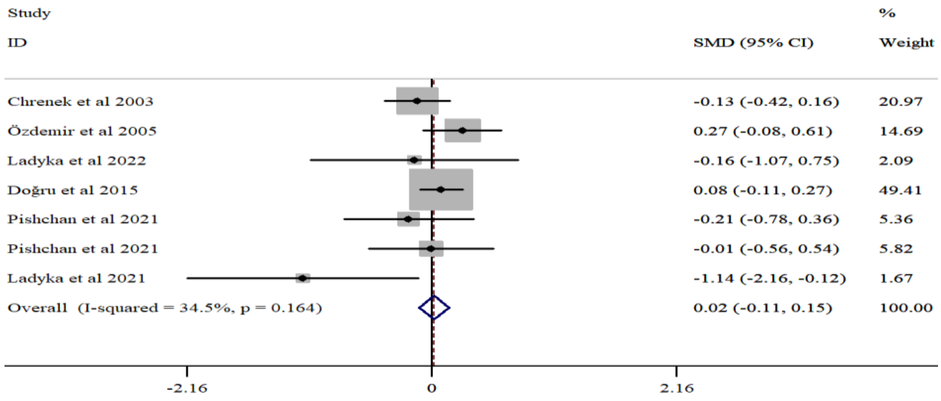

Figure 4. Forest plot for κ-CN Polymorphisms and milk fat yield (AB vs BB) alleles model. The circle represents the weight of each study; the horizontal line is indicative of the confidence interval for each study; the Diamond located at the bottom of the plot represents a summary of the results

Conclusion

This study conducted a comprehensive meta-analysis to investigate the association between κ-CN gene polymorphisms and milk fat yield. The findings indicated a non-significant relationship between these polymorphisms and milk fat yield. However, substantial heterogeneity was observed among the included studies, suggesting considerable genetic variability. Consequently, further research is warranted to better characterize the polymorphisms of the κ-CN gene and their potential impact on milk fat yield.

Milk is a fundamental product produced by various animals, including cows, sheep, goats, horses, buffaloes, and camels, and is consumed regularly (Scholz-Ahrens et al., 2020). Milk's chemical components, such as protein, fat, carbs, vitamins, and minerals, are crucial in human nutrition (Kliem et al., 2013). Bovine milk constituents are quantitative characteristics influenced by environmental and genetic factors (Dogru, 2015). Genetic polymorphism of cow milk proteins has been extensively investigated due to its significant role in breeding strategies, as well as in studies on population structure and the conservation of natural genetic diversity among indigenous breeds. Additionally, milk protein polymorphism has been shown to have a substantial impact on both qualitative and quantitative milk traits in numerous studies (Dogru, 2015). Casein, the primary class of milk proteins, accounts for approximately 80% of the total protein content in milk and is composed of αS1-, αS2-, β-, and κ-casein isoforms (Eigel et al., 1984).

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Statement of Conflict of Interest

As authors, we declare that there is no conflict of interest.

Authors' Contributions

MO, ZM, and KE designed the study, and ZM, KE, and ES collected the all data and arranged it for the analysis. MO performed the statistical analysis and MO, KE, and ZM wrote the paper.

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Phosphate Solubilising Fungi (PSF) Microorganisms

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ABSTRACT: Phosphate solubilizing microorganisms are microorganisms that convert insoluble phosphate compounds in the soil that cannot be taken up directly by plants into soluble form and make them available to plants. Among these microorganisms, bacteria (*Pseudomonas*, *Bacillus*) and fungi (*Aspergillus*, *Penicillium*) stand out. These microorganisms play an important role in environmentally friendly agricultural practices as they support natural biological processes. Phosphate solubilizing fungi are microorganisms that make soil soluble phosphorus available to plants. Phosphorus is an important nutrient for plant growth, but is not usually found in soluble form in nature. Phosphate-solubilizing fungi convert phosphates into simpler, soluble forms, making it easier for plants to take up this nutrient. This process can help reduce fertilizer use in agriculture and promote environmentally friendly farming practices. Furthermore, these fungi can improve the overall health of plants and increase soil fertility.

Keywords: Phosphate, Fungi, Microorganisms, Phosphate Solubilize

1. Definition and Importance of Phosphate Solubilizing Microorganisms

Phosphate solubilizing microorganisms (PSM) are important microorganisms that convert insoluble phosphate compounds in soil into a form that can be taken up by plants (Shi et al., 2022). These microorganisms increase the availability of phosphorus for plants by secreting organic acids and phosphatase enzymes. PSMs are microorganisms that convert insoluble phosphate compounds in soil into plant-available form using organic acids, phosphatase enzymes and other biochemical mechanisms (Rawat et al., 2022). PSMs are among the plant growth-promoting bacteria (PGPR) and play a critical role in increasing agricultural productivity by supporting plant growth (Doğan et al., 2024). These microorganisms play a vital role in agroecosystems, as most of the phosphorus in soil is in insoluble forms. Phosphorus is one of the most important macronutrients for plant growth after nitrogen and potassium. It is involved in many critical processes such as photosynthesis, energy transfer, cell division and root development. However, plants often experience phosphorus deficiency due to its low solubility and immobility (Grzebisz et al., 2024).

Furthermore, the use of phosphate solubilizing microorganisms supports sustainable agricultural practices by reducing the environmental impact of chemical fertilizers. These microorganisms improve the physical and chemical structure of the soil, resulting in healthier and more productive plant growth (Fu et al., 2024). Finally, the potential of PSMs in biotechnological applications makes it possible for them to be used more widely in agriculture in the future. Phosphate solubilizing microorganisms include fungi (e.g. *Aspergillus* and *Penicillium* species) and bacteria (Bacillus, Pseudomonas and Rhizobium species). These organisms secrete organic acids, such as citric, malic, lactic and gluconic acid, which make insoluble phosphates soluble (Kaur et al., 2016). Bacteria such as Bacillus megaterium and Pseudomonas fluorescens are particularly notable for their phosphate solubilizing capacity. These microorganisms both support plant growth and improve overall soil health by increasing soil microbial diversity (Ng et al., 2022).

2. Biological Functions of Phosphate Solubilizing Fungi

Phosphate solubilizing fungi are organisms that fulfill an important biological function, especially in agriculture. These fungi dissolve undissolved phosphates in the soil and make them available to plants. Phosphate is an important nutrient for plant growth and these organisms ensure that this nutrient is utilized efficiently (Rawat et al., 2021). Recent studies on phosphate solubility, biological functions of fungi and their role in ecosystems have revealed how important these organisms are for sustainability in agriculture. Phosphate solubilization is the process by which inorganic phosphate in soil is liberated in soluble form, usually as monohydrate phosphate or phosphoric acid (Hedley and McLaughlin, 2005). This process is carried out by microorganisms capable of phosphate solubilization. Phosphate solubilization is an important contribution of fungi to soil. Phosphate solubilization mechanisms are usually realized through the production of organic acids. These acids dissolve phosphate minerals in the soil, converting them into soluble phosphate that plants can use. Some phosphate solubilization mechanisms may also involve transport systems that allow fungi to take phosphate directly into their cells (Khan et al., 2014).

3. Phosphate Solubilizing Fungi and Sustainability in Agriculture

In agriculture, the limited availability of phosphate in soil can negatively affect plant growth. In particular, the biodegradability of phosphate can help reduce the use of phosphate fertilizers, resulting in less chemical burden on the ecosystem. The role of phosphate-solubilizing fungi in making phosphate available to plants has great potential for sustainability in agriculture. These fungi can reduce the use of chemical fertilizers while increasing soil fertility. In this way, environmental pollution and soil erosion can be prevented (Singh et al., 2020).

4. Biodiversity of Phosphate Solubilizing Fungi

There are many species of fungi capable of phosphate solubilization. The biodiversity of these fungi results from their ability to adapt to different soil conditions and plant species. Different species of these fungi can use different mechanisms for organic acid production, pH lowering and phosphate biodegradation. Furthermore, some of these fungi form mycorrhizal associations, facilitating the transport of phosphate to plants. Mycorrhizal associations are a symbiotic cooperation between plant roots and fungi. These relationships increase phosphate uptake by plants, while at the same time giving fungi access to nutrient sources (Etesami et al., 2021). Phosphate solubilizing fungi provide many different services in ecosystems. These fungi increase soil fertility, while also contributing to the cycling of organic matter. Together with other soil-dwelling microorganisms, these fungi can improve soil health by supporting biodiversity. Furthermore, phosphate solubilizing fungi have important ecosystem functions, such as regulating soil pH and reducing the effects of toxic metals. These properties are critical to ensure a healthier and more efficient production process in agriculture (Rawat et al., 2021; Wahab et al., 2023).

5. Organic and İnorganic Phosphate Solubilization Routes

Phosphate solubilization processes allow phosphate to become soluble in soil, which is critical for plant growth. Phosphate is an important source of nutrients for plants, and the dissolution of phosphates in undissolved form in soil is essential for plants to be able to take up this nutrient. These solubilization processes are carried out by biological organisms, particularly microorganisms with the ability to solubilize phosphate. These microorganisms include bacteria, fungi and some algae. Phosphate solubilization mechanisms are generally classified into two main groups: organic and inorganic (Khan et al., 2014).

5.1. Inorganic Phosphate Solubilization Pathways

Inorganic phosphate solubilization encompasses the processes by which minerals present in soil become soluble. This process involves the conversion of phosphate from its insoluble form, usually bound to the phosphate minerals apatite, to soluble forms of phosphate that can be taken up by plants. Inorganic phosphate solubilization occurs by several different mechanisms (Emami Karvani and Chitsaz Esfahani, 2021).

5.1.1. Production of Organic Acids

The most common mechanism for the dissolution of inorganic phosphate is the production of organic acids. Microorganisms with phosphate-solubilizing capacity lower the pH of the soil, allowing phosphate to dissolve. These microorganisms accelerate the dissolution of phosphate minerals by producing organic acids (e.g. citric acid, malic acid, lactic acid). The acids bind to the surfaces of phosphate minerals, allowing them to dissolve. These acids also help to make minerals bioavailable (Amarasinghe et al., 2022).

5.1.2. Phosphate Binding Proteins and Enzymes

Some microorganisms produce enzymes that solubilize phosphate. Phosphate solubilizing enzymes help dissolve phosphate into biologically active form. These enzymes enable the release and dissolution of phosphate, making it possible for plants to take up these phosphates. Phosphate solubilization mechanisms are activated by the production of these enzymes, making phosphate bioavailable (Zhu et al., 2018).

5.2. Organic Phosphate Solubilization Pathways

Organic phosphate solubilization mechanisms refer to the processes involved in the solubilization of organic phosphate compounds present in soil. Organic phosphates are phosphate compounds that are utilized by plant roots and microorganisms in the soil and are usually secreted by microorganisms. The dissolution of organic phosphates allows the phosphate present in the soil to be used efficiently. Organic phosphate solubilization mechanisms include (Lazo et al., 2017).

5.2.1. Enzymatic Solubility

The dissolution of organic phosphate is mediated by phosphate hydrolase enzymes produced by microorganisms. These enzymes break down organic phosphate compounds, releasing phosphate in soluble form. In particular, the breakdown of phosphate-binding organic compounds leads to increased levels of plant-available phosphate in the soil. Microorganisms can solubilize organic phosphates by cutting phosphate ester bonds (Rawat et al., 2021).

5.2.2. Mycorrhizal Relationships

Symbiotic relationships with mycorrhizal fungi play an important role in the solubilization of organic phosphates. By interacting with plant roots, mycorrhizal fungi are able to dissolve organic forms of phosphate and transport it to the plant. This process allows plants to take up phosphate more efficiently and also supports the mycorrhizal fungus' food supply. Such symbiotic relationships accelerate the phosphate cycle and improve soil health (Etesami et al., 2021).

6. Common Phosphate Solubilizing Fungal Species (*Aspergillus*, *Penicillium*, etc.)

Fungal species with phosphate solubilizing capacity are of great importance, especially in agriculture, to solubilize phosphate and allow plants to efficiently take up this nutrient. These fungi dissolve phosphate minerals in the soil, allowing plants to utilize phosphate more efficiently. Common phosphate solubilizing fungi include *Aspergillus* and *Penicillium* species. Recent studies on the biological properties, phosphate solubilization mechanisms and agricultural applications of these fungi have revealed the potential of these organisms to increase agricultural productivity (Metha et al., 2019).

6.1. Phosphate Solubilization Capacity of *Aspergillus* Genus

The genus *Aspergillus* is one of the most important fungal species with phosphate-solubilizing capacity. Many species of this genus dissolve insoluble phosphates in the soil, making them available to plants. *A. niger* is one of the best-known phosphate solubilizing fungi. *A. niger* dissolves phosphate by producing organic acids. Citric acid in particular plays an important role in the phosphate solubilizing capacity of this fungus. Responsive mechanisms include pH lowering, release of organic acids and production of enzymes that enable the biodegradation of some minerals (Behera, 2020).

Research on the phosphate solubilization mechanisms of *Aspergillus* species suggests that these species can be used as biological fertilizers in agricultural applications. Fungi of the genus *Aspergillus* may help reduce fertilizer use by increasing phosphate uptake by plants, especially in low phosphate soils. Furthermore, these fungi facilitate phosphate uptake by plants through mycorrhizal associations, allowing the development of more sustainable practices in agriculture (Ahmad et al., 2022).

6.2. Phosphate Solubilization Capacity of *Penicillium* Genus

The genus *Penicillium* is also an important group of fungi with phosphate solubilizing capacity. *Penicillium* species are frequently encountered in studies on phosphate solubilization. These fungi produce organic acids that are usually involved in the solubilization of phosphate minerals in soil (Wakelin et al., 2004). The solubilizing capacity of *Penicillium* species is based on the release of phosphate through the creation of an acidic environment, similar to *Aspergillus* species (de Oliveira Mendes et al., 2014).

One of the most well-known characteristics of *Penicillium* species is their high phosphate solubilizing capacity, especially in low pH environments. This facilitates the liberation of phosphate, especially in acidic soils. Fungi of the genus *Penicillium* not only produce organic acids in phosphate solubilization processes, but also bind to phosphate minerals, helping to make these minerals bioavailable. These species often take an active role as part of the soil microbiome, releasing phosphate, which is essential for the healthy growth of plants (Wang et al., 2023).

6.3. Use of *Aspergillus* and *Penicillium* Species in Agriculture

The use of fungi with phosphate solubilizing capacity in agricultural applications is an important step in the development of environmentally friendly fertilizers and more efficient farming methods. Fungal species such as *Aspergillus* and *Penicillium* biodegrade phosphate, allowing plants to utilize this nutrient more efficiently. Using these fungi as biological fertilizers in agriculture can reduce the use of chemical fertilizers and minimize their environmental impact. Furthermore, phosphate solubilizing microorganisms can improve soil health, increase microorganism diversity and regulate soil structure (Altaf et al., 2018). The potential of phosphate solubilizing fungi to increase agricultural productivity has been demonstrated by many recent studies. For example, one study compared the phosphate solubilization capacities of *Penicillium* and *Aspergillus* species and showed that these species support yield increases in agricultural crops. The use of these fungi can contribute to solving environmental problems, especially those caused by the overuse of phosphate fertilizers (Srinivasan et al., 2020).

6.4. Other Phosphate Solubilizing Breeds

The genus *Trichoderma* is another important group of fungi with phosphate solubilizing capacity. These species solubilize phosphate through the production of organic acids. Furthermore, by taking part in mycorrhizal associations, *Trichoderma* species can increase phosphate uptake by plants and strengthen their resistance to diseases. *Trichoderma* harzianum is one of the best known species in this group. The phosphate solubilization mechanisms of *Trichoderma* species involve the production of citric acid and malic acid, which liberate phosphate (Bononi et al., 2020). The genus *Mucor* is another group of fungi with phosphate solubilizing capacity. *Mucor* species produce enzymes that specifically help release phosphate in biodegradable form. These fungi allow phosphate to be dissolved through organic acids, helping to release phosphate that plants can use. The phosphate solubilization mechanisms of *Mucor* species are associated with pH lowering and organic acid production (Elfiati et al., 2021). The genus *Fusarium* is a group of fungi, some species of which have the capacity to solubilize phosphate. These species are usually present as part of the soil microflora and solubilize phosphate through the production of organic acids. *Fusarium* species actively display phosphate solubilizing capacity, especially in low pH environments, and can be used as biological fertilizers for plants (Sudiana et al., 2020). Fungi of the genus *Rhizopus* also show phosphate solubilizing ability. These fungi dissolve phosphate through the production of organic acids. *Rhizopus* species can increase phosphate uptake by plants, often by forming mycorrhizal associations. These species can work efficiently and increase phosphate solubilizing capacity, especially in acidic soils (Vera-Morales et al., 2023). The genus *Mortierella* is another important group of fungi with phosphate solubilizing capacity. *Mortierella* species can dissolve phosphate by producing organic acids. Furthermore, these fungi can improve soil health by increasing soil biodiversity. Fungi of the genus *Mortierella* are particularly effective in solubilizing organic phosphates and provide a source of nutrients for plants (Sang et al., 2022). The genus *Alternaria* is another type of fungus capable of phosphate solubilization. In addition to having phosphate solubilizing capacity, species of this genus can form symbiotic relationships with plants, helping to increase their phosphate uptake. Phosphate solubilization mechanisms of *Alternaria* species include organic acid production and pH reduction (Spagnoletti et al., 2017) (Table 1).

Table 1. Phosphate solubilizing fungi

	Name of PSM species	**Plant species**	**Positive Effects on plants**	**References**
Phosphate solubilising fungi (PSF)	*Trichoderma* spp.	*Glycine max*	Promotion in growth, enhanced P-uptake efficiency	Bononi et al (2020)
	Penicillium bilaii	*Triticum aestivum* L.	Increase yield, higher spike density	Ram et al (2015)
	Talaromyces aurantiacus and *Aspergillus neoniger*	*Moso bamboo (Phyllostachys edulis (Carrière) J. Houz.)*	Release of soluble P by decomposing recalcitrant P-bearing compounds	Zhang et al (2018)
	Aspergillus terreus, *Penicillium pinophilum*	*Sorghum bicolor*	Improve P-uptake and dry matter yield	Steiner et al (2016)
	Aspergillus and *Penicillium* sp.	*Phaseolus vulgaris* L	Increase number of leaves and root fresh weight	Elias et al (2016b)
	Acremonium (TB1), *Aspergillus* (TM7), *Hymenella (TM1)* and *Neosartorya* (TM8)	*Zea mays*	Improve growth and yield as well as P uptake efficiency.	Ichriani et al (2018)
	Penicillium bilaji and Penicillium spp.	*Zea mays*	Increase plant height, number of leaves per plant, dry matter production, cob length, grain weight per cob, 1000 grain weight, grain yield and tissue nutrient content	Patil et al (2012)
AMF (up regulation	*Funneliformis mosseae,* *Rhizophagus intraradices* *Claroideoglomus etunicatum*	*Glycine max* L.	Improve plant growth	Adeyemi et al. (2021a)

	Funneliformis mosseae	*Medicago sativa*	Improvement in growth, increased secretion of organic acids and enhanced soil fertility	An et al. (2022)
	Glomus spp.	*Allium cepa* L.	Increased yield	El-Sherbeny et al. (2022)
	R. clarus *C. etunicatum*	*Acmella oleracea*	Increase in growth, biomass, phenolic content	Vieira et al. (2021)
	Archaeospora, Claroideoglomus, Funneliformis, Diversispora,	*Acaena elongata* L.	Elongation and overall growth of plants	Vazquez-Santos et al. (2021)
	Claroideoglomus etunicatum	*Acacia gummifera* *Retama monosperma*	Higher yield, increase growth and enhance tolerance to salt stress	Fakhech et al. (2021)

7. Other Characteristics and Application Areas of Phosphate Solubilization Fungi

Aspergillus and *Penicillium* species are not only noted for their phosphate solubilizing properties, but also for other biological functions. These fungal species contribute to the cycling of organic matter in the soil, break down toxic substances and form symbiotic relationships with plants to help transport nutrients. Furthermore, some *Penicillium* and *Aspergillus* species can also provide protection against disease-causing pathogens and can therefore be used as biological control agents (Boro et al., 2022). In conclusion, phosphate solubilizing fungi, especially *Aspergillus* and *Penicillium* species, have great potential for sustainability and environmentally friendly practices in agriculture. The phosphate solubilization mechanisms of these fungi can prevent environmental pollution and improve soil fertility by reducing the use of phosphate fertilizers. Moreover, the use of these fungi as biological fertilizers stands out as an important strategy to increase agricultural productivity (Dukare et al., 2021).

7.1. Effect of PSF on soil fertility

Phosphate is an essential nutrient for energy production, cell structure and genetic material of plants. However, most of the phosphate in the soil is bound in such a way that it cannot be taken up by plants. Phosphate minerals are present in soil in insoluble forms, making it difficult for plants to take up this nutrient. This is where microorganisms with phosphate solubilizing capacity come in. These microorganisms make it possible for plants to take up this nutrient, especially by releasing phosphate in biodegradable form (da Silva et al., 2017).

Phosphate solubilizing fungi, through organic acids and some enzymes, dissolve insoluble phosphates in soil and convert them into phosphate form that plants can use. These fungi play an active role as part of the soil microbiome. Fungal genera such as *Aspergillus*, *Penicillium*, *Trichoderma* are known for their phosphate solubilizing mechanisms and their impact on soil is multifaceted. Studies have shown that PSFs improve soil health by increasing the diversity of microorganisms in the soil, as well as increasing phosphate uptake by plants and increasing yields (Fu et al., 2024).

The contribution of phosphate solubilizing fungi to soil fertility can generally be explained by several main mechanisms:

Organic Acid Production: PSFs produce organic acids such as citric acid, malic acid and lactic acid to dissolve phosphate. These acids dissolve phosphates in the soil, allowing plants to utilize this mineral (Nasr et al., 2021).

Increased Microbial Diversity: By increasing the diversity of the soil microbiome, PSFs also improve the bioavailability of other nutrients. This helps to improve soil health overall (Idbella et al., 2024).

Symbiotic Relationships: PSFs form mycorrhizal relationships with plants, allowing for more efficient uptake of phosphate as well as other nutrients by plants (Sun et al., 2024).

7.2. Contribution of Phosphate Solubilizing Fungi to Soil Microbial Population

Phosphate solubilizing fungi (PSF) play an important role in the soil ecosystem. These fungal species not only increase phosphate uptake by plants, but also improve the diversity and health of the soil microbial population. Soil microorganisms are essential components of soil health and fertility, as they play a critical role in organic matter transformation, nutrient cycling and plant access to nutrients. PSFs contribute to the interactions of these microorganisms, increasing soil biodiversity and thus improving soil health (Prasad et al., 2021).

Phosphate solubilizing fungi interact with microorganisms in soil in many different ways. These interactions alter the structure of the soil microbial population by affecting the biochemical activities of microorganisms. While PSFs release organic acids into the soil to dissolve phosphate, they also establish symbiotic relationships with other microorganisms in the soil. These relationships can increase the diversity of the microorganism community and improve soil health. Fungal species such as *Aspergillus*, *Penicillium*, and *Trichoderma* contribute to these interactions (Macías-Rodríguez et al., 2020). PSFs provide an important mechanism to increase the diversity of the soil microbiome. The action of phosphate-solubilizing fungi can change the microflora structure of the soil. These fungal species increase plant uptake of this nutrient by solubilizing phosphate, while at the same time supporting the growth of soil microorganisms. Species such as *Trichoderma harzianum* interact with bacterial and fungal communities in the soil, increasing microbial diversity. This diversity helps improve soil health and plant access to nutrients (de Azevedo Silva et al., 2021).

Phosphate solubilizing fungi are microorganisms that can solubilize insoluble phosphates naturally present in soil. Plants usually take up phosphate in the soil in soluble form, but much of this phosphate is present in the soil in insoluble form. PSFs dissolve these phosphates, allowing plants to take up more phosphate. This mechanism has the potential to use PSFs as biological fertilizers. The use of PSFs in biotechnology allows to reduce the use of chemical fertilizers and minimize environmental impacts (Kour et al., 2020). PSFs can increase agricultural productivity by improving plant growth, especially in low phosphate soils. Various fungal species produce organic acids, which dissolve phosphate. This soluble phosphate becomes bioavailable to plants. Furthermore, PSFs improve the soil microbiome, increase soil biodiversity and generally improve soil health (Wang et al., 2021). The biotechnological potential of PSFs is not limited to providing phosphate for plants. These fungal species establish symbiotic relationships with other microorganisms in the soil, promoting biological interactions, which in turn improves soil health. In particular, PSFs have the ability to compete against pathogens and can be used as part of biological pest control methods. Some PSF species produce antibiotics and enzymes, which increases the potential to use them as biological control agents (Mitra et al., 2020).

The use of PSFs in microbial biotechnology also offers an important strategy to produce natural fertilizers and maintain soil health. The overuse of chemical fertilizers can degrade soil structure, lead to water pollution and cause negative impacts on the ecosystem. The use of PSFs can help reduce reliance on these chemical fertilizers while improving soil health (van der Putten et al., 2016).

8. Recent studies on PSF

Phosphate solubilizing fungi (PSF) have become an important area of research in biotechnology. These fungal species solubilize phosphate in soil and the environment, allowing plants to take up this nutrient more efficiently. In addition, PSFs offer great potential for sustainable agricultural practices, biofertilizers and environmentally friendly agricultural methods. The use of PSFs in biotechnology aims to make agricultural production systems more efficient and environmentally friendly (Singh et al., 2018). This article reviews recent developments and research findings on the use of PSFs in biotechnological applications. Genetic engineering is another method used to further enhance the biotechnological potential of PSFs. Genetic modification techniques can increase the phosphate solubilizing capacity of

PSFs and make them more efficient. Furthermore, these techniques can make PSFs more resilient, enabling them to fight more effectively against environmental stress conditions. For example, some research is working on genetically modifying PSFs to make them produce more organic acids and solubilize more phosphate (Fu et al., 2024).

9. Future Perspectives

The potential of PSFs in biotechnology is great and increasingly being explored. In the future, more effective use of these fungal species could increase sustainability in the agricultural sector and solve environmental problems. In particular, the use of phosphate solubilizing fungi as biological fertilizers could be an important step in protecting soil health by replacing chemical fertilizers. Furthermore, genetic modification of these fungi to make them more efficient could further strengthen the role of PSFs in the biotechnological field. The effect of PSFs on soil fertility has been proven by many studies and it has been shown that they can play an important role in increasing agricultural productivity. The production of organic acids in the soil by phosphate solubilizing fungi and the biological interactions of microorganisms increase the availability of phosphate to plants, thereby increasing yields. Furthermore, the use of these fungi as environmentally friendly fertilizers has great potential to increase the sustainability of agriculture.

The integration of PSFs into agricultural production systems to improve soil health and increase productivity could be an important biotechnological and environmental development. In the future, further research and wider use of these fungal species as biological fertilizers could reduce dependence on phosphate fertilizers in the agricultural sector and have positive impacts on the environment.

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Phosphate Forms and Sources in Soils

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ABSTRACT: Phosphate is one of the essential nutrients required for healthy plant growth. It plays a critical role in fundamental biological processes such as energy production, cell division and synthesis of genetic material. In agriculture, phosphate is widely used as a fertilizer to increase productivity. However, phosphate resources are limited and its overuse can lead to environmental problems. Phosphate deficiency inhibits plant growth and causes yield losses, so efficient and sustainable use of phosphate is crucial. The future of phosphate will be shaped by innovative technologies and sustainable management strategies. The limited availability of phosphate resources necessitates the efficient use and recovery of this resource. New research and technologies have great potential to reduce the environmental impacts of phosphate and increase agricultural productivity.

Keywords: Phosphate, Soil, Phosphate Form, Phosphate Source

1. Introduction

Phosphate forms in soil are one of the important factors affecting phosphorus uptake by plants. Phosphorus is a vital nutrient for plants and is required for many biological functions such as energy transfer, photosynthesis, DNA and RNA synthesis (Khan et al., 2023). However, most forms of phosphate present in soil cannot be directly utilized by plants. This varies depending on the solubility of phosphate in the soil solution and the chemical properties of the soil (Chien et al., 2011). Phosphorus is present in soil in two main forms, organic and inorganic. Inorganic phosphate is present in the soil solution in the form of soluble phosphate ions (H_2PO_4- and HPO_4^{2}-) and can be taken up directly by plants. However, in acidic soils with low pH, phosphate combines with iron (Fe) and aluminum (Al) to form compounds with low solubility, making it difficult for plants to take up phosphate. Organic phosphates, however, are found in organic matter, especially in plant and animal waste, and are mineralized by microorganisms, making them accessible to plants (Siebielec et al., 2018). Soil pH, microorganism activities and soil organic matter content are important factors affecting the bioavailability of phosphate. Furthermore, the fact that phosphate binds with various minerals in the soil and becomes less soluble directly affects the efficiency and environmental impact of phosphorus fertilizers (Timofeeva et al., 2022).

The formation and bioavailability of phosphate in soils is an important research topic for improving the efficiency of phosphorus fertilizers and developing sustainable agricultural practices. In this context, the development of soil management strategies to improve the bioavailability of phosphate is critical to ensure both agricultural productivity and environmental sustainability. The forms of phosphate in soil and its availability to plants is an important research topic in the fields of agronomy and soil science. Phosphorus is an essential nutrient for plants and plays a critical role in many biological processes such as photosynthesis, energy transfer and cell division. However, most forms of phosphate in soil are not directly available to plants, making it difficult to manage soil fertility and fertilization strategies. The different forms of phosphate in soil vary depending on environmental conditions, especially pH level, soil organic matter content and microorganisms (Kruse et al., 2015).

The presence of phosphate in different forms in soil and the effects on the bioavailability of these forms is a critical issue for the development of more efficient strategies for the use of phosphorus fertilizers and the implementation of sustainable agricultural practices. In this context, the study of the various forms of phosphate present in soil constitutes an important research area, especially to increase the efficiency of phosphate fertilizers and minimize their environmental impacts.

2. General Forms of Phosphate in Soil

Phosphate is present in soil in organic and inorganic forms. Inorganic phosphate is the form that can be taken up directly by plants and is usually present in soil solution as soluble phosphate ions. These forms contain phosphate ions such as H_2PO_4- and HPO_4^2- and can be taken up directly by plants. However, the presence of this soluble form of phosphate in soil is limited because they can often react with minerals such as calcium, iron and aluminum, losing their solubility (Vance et al., 2003).

Calcium phosphates are commonly found in neutral and alkaline soils and often form phosphate compounds with low bioavailability for plants. In alkaline soils, calcium phosphates form soluble forms that limit accessibility for plants (Hedley et al., 1982). Iron and aluminum phosphates are more common in acidic soils and these compounds also show low bioavailability for plants. Phosphates in this form lose their solubility in acidic conditions by combining with iron and aluminum oxides (Shen et al., 2011).

Organic phosphates are derived from plant and animal waste, humus and other organic matter. Phosphates in this form cannot be taken up directly by plants, but are mineralized by microorganisms, making them accessible to plants. Organic phosphates are an important source of phosphorus in soil and are continuously cycled by microorganism activities (Turner et al., 2007).

3. Phosphate Sources

Phosphate resources can be divided into two groups: domestic and external sources. Indigenous Phosphate Sources: Natural sources of phosphate in soil are phosphate minerals and organic matter. Phosphate minerals, especially calcium phosphates such as apatite, are among the native phosphate sources. However, the bioavailability of these minerals is generally low because they take time to be converted into soluble forms of phosphate. Furthermore, phosphate in organic matter is not available until it is mineralized by microorganisms (Bünemann, 2015). Artificial Phosphate Sources: Phosphate fertilizers are widely used in agriculture to overcome phosphate deficiency. Superphosphate, triple superphosphate and ammonium phosphate are phosphate fertilizers that make phosphate more readily available to plants. However, long-term use of phosphate fertilizers can lead to acidic conditions in the soil, causing phosphate to be lost in soluble form (Achat et al., 2010). Environmental Impacts of Phosphate Resources: Phosphate is also an environmental concern. Excess phosphate use can enter water bodies and lead to eutrophication. This can lead to degradation of aquatic ecosystems, algal blooms and oxygen depletion (Brush et al., 2020). Therefore, phosphate utilization needs to be managed in a sustainable manner.

4. Distribution and Accessibility of Inorganic Phosphate Forms in Soils

The major form of inorganic phosphate present in soil solution is soluble phosphate ions ($H_2PO_4^-$ and HPO_4^{2-}). These phosphates can be taken up directly by plants. However, the solubility of phosphate in soil is often controlled by pH and its interactions with mineral compounds present in the soil. Especially in acidic soils, phosphate combines with iron (Fe) and aluminum (Al) to form low-solubility phosphate compounds. These compounds become inaccessible to plants and the bioavailability of phosphate is reduced. Iron and aluminum phosphates formed in acidic conditions bind most of the phosphate and prevent plants from utilizing phosphate in this form (Rahman et al., 2018). On the other hand, in neutral and alkaline soils, phosphate combines with calcium (Ca) to form calcium phosphates. In this form, phosphate often lacks solubility and its accessibility for plants is reduced. However, some forms of these calcium phosphates can interact with organic acids, which can increase their solubility in soil, and hence their bioavailability may increase to some extent (Mabagala et al., 2022).

The bioavailability of phosphate in soil solution also depends on the activities of soil microorganisms. In particular, microorganisms are able to mineralize organic phosphates into inorganic phosphate, leading to increased sources of phosphate accessible to plants. This mineralization process varies depending on the density and activity of soil microflora (Zhu et al., 2018).

5. Soil pH and Phosphate Availability

5.1. Availability of Phosphate in Acidic Soils

In acidic soils, the pH is usually below 5 and under these conditions the solubility of phosphate is greatly reduced. In acidic environments, phosphate ions often react with iron (Fe) and aluminum (Al) to form phosphate compounds with low solubility. These compounds become inaccessible to plants. Iron and aluminum phosphates, in particular, are forms of phosphate that are common in acidic soils and these compounds bind most of the phosphate, thus reducing its bioavailability. This binding process causes phosphate to remain in low concentration in the soil solution, which makes it difficult for plants to take up phosphate (Smith et al., 2003).

5.2. Phosphate Availability in Neutral and Alkaline Soils

When soil pH is neutral (pH 6-7) or alkaline (pH > 7), the solubility of phosphate changes again, but this time the phosphate binds with calcium (Ca) to form insoluble calcium phosphates. Calcium phosphates are particularly common in alkaline soils and in this form phosphate shows limited bioavailability to plants. However, in some cases, organic acids and other soil soluble compounds can increase the solubility of calcium phosphates and thus improve the bioavailability of phosphate to some extent (Hou et al., 2018). Therefore, strategies to lower pH can be applied to improve the bioavailability of phosphate in alkaline soils.

5.3. Interactions of Phosphate Availability and pH

The relationship between soil pH and phosphate bioavailability is not limited to the solubility of mineral compounds. The activities of microorganisms also play an important role in this process. In acidic soils, some microorganisms can mineralize organic phosphates into soluble inorganic phosphates, thus increasing the bioavailability of phosphate. Similarly, in alkaline soils, organic acid production by microorganisms can increase the solubility of calcium phosphates and improve the bioavailability of phosphate (Adnan et al., 2018). However, microorganism activities often work in interaction with soil pH, and extreme levels of pH can negatively affect the activity of microorganisms. The bioavailability of phosphate in soil can be optimized by pH management. Raising pH in acidic soils can increase the solubility of iron and aluminum phosphates, making phosphate more accessible to plants. On the other hand, lowering pH in alkaline soils can increase the solubility of calcium phosphates. Therefore, optimizing soil pH is an effective way to increase the bioavailability of phosphate (Wei et al., 2018).

6. Factors Affecting the Bioavailability of Phosphate in Soil

Phosphate bioavailability in soil is one of the most important factors determining how efficiently plants can uptake phosphate. Phosphate bioavailability is influenced by many factors, including soil pH, organic matter content, microorganism activity, soil mineral composition and fertilization efficiency. Each of these factors significantly affects the degree of solubility of phosphate in the soil solution and hence its availability to plants.

6.1. Soil pH and Phosphate Bioavailability

Soil pH is one of the most important factors directly affecting the bioavailability of phosphate. Acidic and alkaline soils affect phosphate solubility in different ways. In acidic soils, phosphate ions often bind with iron (Fe) and aluminum (Al) and lose their solubility, making phosphates in this form inaccessible to plants. In neutral and alkaline soils, phosphate usually combines with calcium (Ca) to form calcium phosphates, which have limited bioavailability. Soil pH directly affects the bioavailability of phosphate by affecting the solubility of these mineral bonds (Penn et al., 2019).

6.2. Soil Organic Matter Content and Bioavailability of Phosphate

Soil organic matter content is also an important factor affecting the bioavailability of phosphate. Organic matter leads to the presence of phosphate in organic form, which cannot be taken up directly by plants. However, organic phosphates are mineralized by microorganisms into inorganic phosphate and this conversion increases the bioavailability of phosphate. In soils with high organic matter content, the potential of microorganisms to mineralize phosphates is higher, which increases the bioavailability of phosphate (Mabagala et al., 2022). Furthermore, the presence of soil organic acids can increase the solubility of phosphate and thus facilitate its uptake by plants (Barrow and Hartemink, 2023).

6.3. Role of Microorganisms

Microorganisms play an important role in the phosphate cycle and are one of the most important factors that increase the bioavailability of phosphate. Soil microorganisms mineralize organic phosphates, converting them into the inorganic form of phosphate, thus increasing plant access to phosphate. In addition, some microorganisms produce organic acids that can increase the solubility of phosphate. These organic acids increase the solubility of phosphate in the soil solution, allowing plants to better take up this nutrient. In addition, microorganisms can alter the interactions of phosphate with the minerals to which it is bound in soil, which can positively affect the bioavailability of phosphate (Zhu et al., 2018).

6.4. Effect of Soil Structure and Minerals

Soil structure has an important influence on the bioavailability of phosphate. In particular, soil minerals play a major role in the solubility and bioavailability of phosphate. Soil minerals such as iron, aluminum and calcium interact with phosphate to form different phosphate compounds. These compounds often reduce the solubility of phosphate, making it difficult for plants to take up this nutrient. Aluminum and iron phosphates are common in acidic soils, while calcium phosphates are more common in alkaline soils. The binding of these minerals with phosphate is a factor limiting its bioavailability (Reynolds and Davies, 2001). Phosphate fertilization is a common way to increase the bioavailability of phosphate. However, the effectiveness of fertilizers depends on soil properties and fertilization strategies. The application of phosphate fertilizers can affect soil pH and microorganism activities. Phosphate fertilizers usually contain soluble phosphate ions, but these ions can lose their solubility over time by binding with minerals present in the soil. Therefore, the effect of phosphate fertilization varies according to factors such as soil pH and organic matter content. Sustainable phosphate management can improve the bioavailability of phosphate by optimizing soil pH, increasing organic matter and promoting phosphate mineralization by microorganisms (Raes et al., 2014).

6.5. Phosphate Fertilization and Management Strategies

Phosphate fertilization and management strategies are critical for increasing productivity in agricultural production and maintaining soil fertility. Phosphate is a vital nutrient for plant growth and is often considered a limiting factor for agricultural production. However, applying and managing phosphate to the soil not only improves productivity, but is also important for environmental sustainability. Strategies for phosphate fertilization include a variety of methods to increase the bioavailability of phosphate and ensure its efficient utilization in the soil. Phosphate fertilization is the addition of phosphate ions to the soil with the aim of enabling plants to take up this nutrient. However, since the solubility of phosphate in soil is limited, the effectiveness of this fertilization often depends on soil properties and environmental factors. The basic strategies for phosphate fertilization include timing the fertilizer correctly, applying the right amount and choosing the right form of phosphate. The timing of phosphate fertilizers should be regulated according to the growth period of the plants and their need for phosphate. In particular, phosphate fertilizers should be applied when plants need phosphate the most (de Sousa et al., 2015). In addition, the correct form of phosphate must be selected in order to utilize phosphate effectively in the soil. Phosphate fertilizers usually come in soluble phosphate forms, but under some soil conditions, the bioavailability of soluble phosphates may be limited. Therefore, the effectiveness of phosphate fertilization may vary with soil pH, organic matter content and microorganism activity (Bolland and Gilkes, 2017).

Soil pH is one of the most important factors influencing the bioavailability of phosphate. In acidic soils, the solubility of phosphate decreases due to its interactions with iron (Fe) and aluminum (Al). In alkaline soils, phosphate binds with calcium (Ca), forming insoluble calcium phosphates. Therefore, to enhance the effectiveness of phosphate fertilizers, soil pH should be optimized. In acidic soils, raising the pH can prevent phosphate from binding with iron and aluminum, thereby increasing its solubility. In alkaline soils, lowering the pH can increase the solubility of calcium phosphates (Gupta et al., 2014).

The organic matter content of the soil is another factor affecting the effectiveness of phosphate fertilization. Organic matter can mineralize phosphates through microorganisms, making them available to plants. Therefore, in soils with high organic matter content, the bioavailability of phosphate fertilizers may be higher (Hedley et al., 1982).

6.7. Sustainable Phosphorus Management and Environmental Impacts

Phosphate fertilization, if not properly managed, can lead to environmental problems. Excessive phosphate use can result in phosphate accumulation in surface waters, causing water pollution. Therefore, phosphate fertilization must be carried out sustainably. To ensure that phosphate remains in the soil for an extended period and to minimize losses, fertilizers must be applied correctly. For this, phosphate fertilizers should be applied in the right amounts and at the times when plants need phosphate the most (Roberts and Johnston, 2015). Additionally, to reduce phosphate losses, techniques that enhance the bioavailability of phosphate in the soil can be used. For example, increasing organic matter content can enhance phosphate solubility and promote microbial activity.

7. New Approaches for Phosphorus Management

New phosphorus management strategies aim to increase the efficiency of phosphate addition to the soil while reducing environmental impacts. These strategies include methods that enhance the availability of phosphate to plants through microorganisms and increased organic matter content, optimizing soil pH, and ensuring the correct timing of fertilization. Additionally, to improve the efficient use of phosphate, it is important to customize phosphate fertilizers according to local soil conditions and to develop better application methods. These strategies offer sustainable solutions for the efficient use of phosphate and the reduction of environmental impacts (Hermann et al., 2018).

8. Environmental Impacts of Phosphorus and Pollution

Although phosphorus is an essential nutrient in agricultural production, excessive and improper fertilization practices can lead to environmental pollution. The environmental impacts of phosphorus are particularly associated with phosphorus pollution in aquatic ecosystems. Phosphorus is a naturally limited element, and its overuse can result in water pollution and ecosystem degradation. This section will explore the environmental impacts of phosphorus, the causes and consequences of phosphorus-induced pollution, and management strategies in detail.

8.1. Environmental Impacts of Phosphorus and Water Pollution

One of the primary environmental impacts of phosphorus is water pollution. When phosphorus is used as a fertilizer in agriculture, it can be transported to water bodies after application to the soil. This can lead to water pollution, causing excessive nutrient loading (eutrophication) in ponds, lakes, and rivers. Since phosphorus is a soluble component, it can easily move with surface runoff and accumulate in water sources. Eutrophication leads to algal blooms in water bodies, reducing oxygen levels, deteriorating water quality, and decreasing biodiversity. Eutrophication is a significant environmental issue that threatens aquatic life, particularly in freshwater ecosystems (Chislock et al., 2013).

The main pathway for phosphorus to contribute to environmental pollution is its accumulation in the soil. Excessive phosphorus accumulation in soils can be transported to water bodies, especially during rainy periods. Rainwater can carry the soluble form of phosphorus from the soil solution to rivers, lakes, and seas. This transportation becomes more pronounced with over-fertilization, excessive application of phosphorus, or acidic conditions that increase phosphorus solubility in the soil (Islam et al., 2024). Additionally, the insolubility of phosphorus in the soil can prevent its release into the environment through microbial mineralization or binding with organic matter, but these processes are slow and time-consuming. Excessive phosphorus in water causes various negative effects on ecosystems.

Eutrophication leads to overgrowth of aquatic plants and algae, which lowers oxygen levels. This makes it difficult for fish and other aquatic organisms to survive. Algal blooms can lead to the proliferation of toxin-producing species and degrade water quality. This results in a loss of biodiversity in drinking water sources and aquatic ecosystems. Furthermore, eutrophication creates problems for agricultural water use, as the water requires further treatment to become safe for both animals and humans (Khan and Mohammad, 2014).

8.2. Phosphorus Environmental Pollution and Global Climate Change

Phosphorus pollution not only has negative effects on aquatic ecosystems but may also be linked to climate change. Oxygen depletion resulting from eutrophication can lead to the release of greenhouse gases such as methane in the seas. Additionally, the decay of organic matter during algal blooms can release methane and other greenhouse gases, potentially triggering global warming. Excessive use of phosphorus and its transport to water bodies can create environmental impacts related to climate change. The release of phosphorus into the environment accelerates biodiversity loss and increases greenhouse gas emissions (Fetahi, 2019).

A range of strategies and practices has been developed to reduce phosphorus pollution and manage environmental impacts. Phosphorus fertilization should only be applied in the correct amounts and at the right time to meet plant needs. This can help prevent the over-application of phosphorus to soil and its transport to water bodies. Moreover, various techniques can be used for applying phosphorus fertilizers; for instance, reducing the amounts applied locally can prevent phosphorus from being transported to water bodies (Vantaraki, 2021). Soil management techniques and methods to increase organic matter content can also reduce environmental pollution by controlling the bioavailability of phosphorus. Additionally, applications that enable phosphorus recycling can be effective in reducing environmental impacts (Pitois et al., 2001).

9. The Future of Phosphorus: New Research and Technologies

Phosphorus plays a critical role as an essential nutrient in global agriculture. However, the limited availability of phosphorus sources and environmental concerns have led to increased research aimed at ensuring efficient phosphorus use and minimizing its environmental impact. The future of phosphorus is being shaped by new research and technological advancements. This section will explore recent studies and technological developments regarding the future of phosphorus.

9.1. The Limitation of Phosphorus Resources and Search for Solutions

The depletion of global phosphorus resources is one of the biggest threats to the sustainability of phosphorus. Phosphate minerals are naturally occurring but limited in many parts of the world. These limited resources are facing increasing demand. In this context, the future of phosphorus is closely tied to developing new technologies to optimize the efficient use of phosphorus resources and enhance its recycling. Phosphorus recycling has emerged as a key strategy for the efficient management of phosphorus (Desmidt et al., 2015). New methods have been developed for recovering phosphorus from waste, wastewater, and even organic materials. Technologies that recover phosphorus from waste will allow for its more efficient use and extend the lifespan of phosphorus resources (Daneshgar et al., 2018).

9.2. New Technologies and Phosphorus Recovery

The future of phosphorus is directly linked to technological innovations. Several technologies have been developed to enhance phosphorus recovery. One example is biotechnology methods that combine biological and chemical processes. For instance, using microorganisms to extract phosphorus from wastewater can significantly improve phosphorus recovery efficiency. This process can be applied in wastewater treatment plants and has great potential for reducing phosphorus's environmental impact (Pradel and Aissani, 2019). Additionally, there is ongoing research to develop technologies that allow phosphorus to be used more efficiently and for a longer duration in the soil. For example, new methods have been developed to increase the bioavailability of phosphorus through biological and physical interactions during the application of phosphate fertilizers to the soil (Khan et al., 2023). These technologies enable more effective and reduced application of phosphorus, increasing agricultural productivity while also minimizing environmental impact. New-generation fertilization methods aim to apply phosphorus in a more targeted and efficient manner. The concept of "precision agriculture" allows for better phosphorus management using technology. These methods ensure that fertilizers are applied at the right time and in the right amounts based on soil analysis and plant nutrient needs. This reduces phosphorus losses and improves efficiency. Advanced agricultural technologies such as drone technology, remote sensing, and artificial intelligence (AI) enable the monitoring of soil and plant conditions to prevent unnecessary phosphorus use, thereby reducing environmental impact (Vellingiri et al., 2025). These technologies play a crucial role in ensuring efficient phosphorus use.

9.3. Phosphorus Zero-Waste Approach and Sustainability

Sustainability will remain a central theme for the future of phosphorus. The depletion of phosphorus resources and the need to reduce environmental impacts make the zero-waste approach and circular economy-based solutions crucial. Recovering phosphorus from waste and recycling processes enhances its reusability, contributing to the conservation of natural resources. Particularly, studies focusing on recovering phosphorus from agricultural waste, household waste, and wastewater have emerged as key steps toward reducing phosphorus's environmental damage and meeting future phosphorus demands. Additionally, sustainable agricultural practices such as organic fertilizers and local fertilization techniques can ensure efficient phosphorus recovery into the soil (Mrunalini et al., 2022). These innovative strategies are vital to ensuring the sustainable use of phosphorus. New research on increasing phosphorus bioavailability will significantly contribute to its efficient use. For instance, research into biotechnological methods that accelerate phosphorus solubilization by microorganisms may enable more efficient integration of phosphorus into the soil. Research in this field is focused on developing strategies that allow phosphorus to reach the soil and plants more quickly and effectively (Bindraban et al., 2020). Furthermore, new agricultural techniques used to minimize phosphorus's environmental impact are gaining importance. Adding organic matter to the soil can increase microorganisms' ability to solubilize phosphorus, enhancing its bioavailability. Such strategies can improve phosphorus integration into the soil, boosting agricultural productivity (Richardson et al., 2011).

10. Conclusion and Future Perspectives

The environmental impacts of phosphorus, particularly in aquatic ecosystems, pose significant threats and highlight the importance of sustainable agricultural practices. Phosphorus pollution not only threatens agricultural productivity but also the health of water resources. Therefore, more conscious, environmentally friendly, and sustainable approaches to phosphorus fertilization and management are needed. To reduce phosphorus's impact on the environment, it is crucial that fertilizers are applied at the right time, in the right amounts, and in the right way. Additionally, strategies for phosphorus recycling and increasing its bioavailability can help reduce phosphorus pollution and environmental impacts. The future of phosphorus will be shaped by innovative technologies and sustainable management strategies. The limited availability of phosphorus resources makes its efficient use and recycling necessary. New research and technologies have the potential to reduce phosphorus's environmental impact and increase agricultural productivity. Efficient and sustainable phosphorus management not only helps conserve limited phosphorus resources but also contributes significantly to environmental sustainability. In the future, the use of phosphorus will be shaped by more efficient fertilization methods, biotechnological solutions, and zero-waste approaches. This will ensure that phosphorus is used more sustainably worldwide (Guelfi et al., 2022).

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Asymmetric Price Transmission of Diesel Prices and Exchange Rates on Egg Prices

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ABSTRACT: Global economic and demographic growth has increased awareness of healthy and quality nutrition. This has led to a rise in the demand for animal-based proteins, raising concerns about food supply and causing raw material and energy prices to surge. Eggs, as a key animal-based food, hold economic and health importance due to the need for stable pricing. Price transmission in egg markets is primarily driven by fluctuations in exchange rates and diesel prices. This study examines the effects of positive and negative shocks in diesel prices and exchange rates on egg prices in Turkey between 1994 and 2023 using the NARDL model. The results reveal an asymmetric price transmission between exchange rates, diesel prices, and egg prices in both the short and long term. In the short term, positive shocks in exchange rates and negative shocks in diesel prices significantly impact egg prices. In the long term, both shocks contribute to rising egg prices. These findings highlight the importance of considering price transmission in policymaking for the egg market.

Keywords: Egg Prices, Asymmetric Price Transmission, NARDL Model

INTRODUCTION

The growth of the global population and the economic development of nations have significantly heightened awareness of healthy and high-quality nutrition. Among the fundamental animal-based proteins underpinning conscious eating, eggs stand out due to their rich nutritional profile and cost-effectiveness, making them one of the most widely preferred animal-based protein sources globally. Eggs have been a staple of daily life for centuries, valued not only for their palatability but also for their exceptional nutritional composition, which includes high-quality protein, fatty acids, various vitamins, iron, and phosphorus (Acıkgoz and Onenc, 2006). The affordability of eggs, their long shelf life, and their versatility across diverse culinary practices have established them as a globally essential food item (Obianwuna et al., 2022; Gunjan et al., 2024). According to FAO (2020) data, China leads global egg production with a 40% share of total output, maintaining its dominance in the sector. The United States, India, Mexico, and Brazil are also prominent egg-producing countries. Turkey ranks as the tenth-largest producer worldwide, contributing 16% to global egg exports. These rankings underscore the production capacities and the prominence of the agricultural sectors in these countries. Egg consumption, an integral aspect of culinary traditions worldwide, has shown a consistent upward trajectory. The global average annual per capita egg consumption is 153, compared to 288 in the United States, 210 in the European Union, and 196 in Turkey (FAO, 2020; TOB, 2023). Despite being one of the most widely traded animal protein sources, egg prices remain vulnerable to external factors, including pandemics, fluctuations in oil prices, and variations in the costs of essential energy and raw materials. Consequently, a detailed investigation into the factors influencing egg prices is imperative, given their critical role in human nutrition and international trade (Altıntaş, 2016; Gunjan et al., 2024).

Global food prices experienced a sharp increase in 2011 following the 2007-2008 food crisis. Post-2020, prices have risen again. This surge in food prices, combined with currency exchange rate fluctuations and rising oil prices, has led to an increase in agricultural food prices (FAO, 2024). The rising cost of imported raw materials for agricultural production and food manufacturing has been reflected in food prices. Price increases and market fluctuations have reached levels that threaten food security and economic stability, adversely affecting living conditions in developing countries (Altintas, 2016; Yavuz Dilek, 2019). In Turkey, while food price increases paralleled global trends until 2010, domestic food prices have continued to rise since the 2018 economic crisis, even as global food prices have declined. As of 2024, the global food price index is approximately 121.5, while Turkey’s index stands at 168.5, about 47.5% higher than the global average. This increase in food prices is a primary driver of inflation, significantly reducing the purchasing power of low-income households (FAO, 2024). The avian influenza outbreaks in 2006 and 2015 created additional crises in the egg sector, causing export disruptions and price volatility (Keskin and Kaplan, 2021). Moreover, since a significant portion of the raw materials used in egg production is still imported, fluctuations in exchange rates adversely affect egg prices. While Turkey accounts for 16% of global egg exports, its dependence on imported raw materials and reliance on trade with a single country for exports poses a significant risk to the sector. Price instability in the egg market forces producers to sell below cost, leading to market stagnation. The pricing of eggs based on production costs makes the sector vulnerable to price fluctuations (Cicek and Tandogan, 2007; Yildirim, 2013; Keskin and Kaplan, 2021). Despite having a natural protective shell, eggs are perishable with a short shelf life, making proper packaging, transportation, and storage conditions crucial for the sector. To minimize damage and ensure timely delivery to consumers, eggs are typically transported via roadways. In addition to production costs, transportation expenses, including rising diesel prices, significantly impact egg prices (Yildirim, 2018; Yuceer and Caner, 2021). Diyab and Karaki (2023), in their historical analysis, explicitly highlight the significant impact of diesel prices on food prices. Recent analyses of egg prices reveal that while consumer prices fell by

85% in 2005, between 2006 and 2018, producer prices increased by 3.26 times, and consumer prices rose by 3.79 times (Keskin and Kaplan, 2021).

Understanding how market fluctuations affect product prices helps determine the policies to be implemented in both domestic and international markets. Knowing the relationship between prices in different markets aids in price determination for exports and imports, assessing their response to changes, and ensuring supply-demand balance to establish suitable conditions for an efficient market (Cınar, 2017). The impact of price changes in one market on other markets is explained by price transmission. Price transmission is a critical issue for ensuring the effective functioning of markets, stabilizing product prices at national and international levels, and determining policies related to foreign trade products (Demirel et al., 2017). Grey and Manera (2007) stated in their study that the most commonly used variables in the literature for price transmission include the retail price of the product, exchange rates, and oil prices. Regarding egg prices, studies have been conducted on the short-term price transmission in the egg industry chain in China (Li ZheMin et al., 2010), price transmission in Iran's egg market (Daneshvar Khakhki and Heidari Kamalabadi, 2011), the analysis of price fluctuations in egg prices (Yuhuan and Fu, 2018), and U.S. egg prices affected by the food supply chain (Mitcheel et al., 2024). In Turkey, studies have been conducted on factors affecting egg prices (Cicek and Tandogan, 2007), long-term price transmission between eggs and feed wheat (Kucuk et al., 2022), and the impact of crises in the egg sector on the industry (Keskin and Kaplan, 2021).

Eggs, a product of critical importance both for consumption at national and international levels and for public health, have increasingly been the focus of studies examining the influence of other market prices on their market price fluctuations. This study aims to determine the price transmission effects of exchange rates and diesel prices on egg prices in Turkey. Sub-objectives of the study include examining asymmetric price transmission, estimating short- and long-term coefficients, and investigating the existence of cointegration among the variables.

Material and Method

The monthly data for egg and diesel prices between 1994 and 2023 were obtained from the Turkish Statistical Institute, while exchange rate data were sourced from the Central Bank of Turkey. Cointegration examines the equilibrium state of economic variables in the long term and explains the relationship between non-stationary time series (Cemrek, 2006). It is a method that identifies stationarity and reveals both short- and long-term relationships between variables (Umoh and Effiong, 2013). The model developed by Engle and Granger tests relationships in univariate systems in two stages. However, as the number of variables increases, this model is unable to test long-term relationships. To address this limitation, cointegration analysis permitting multiple cointegrations, such as the methods proposed by Johansen (1988) and Johansen and Juselius (1990), was employed, along with the maximum likelihood estimation approaches developed by Engle and Granger (1987) and Phillips and Hansen (1990). Cointegration arises when deviations from equilibrium either return to the equilibrium point or exhibit temporary divergence. Through cointegration, the stationarity of the linear combinations of non-stationary economic variables can be analyzed, or their long-term equilibrium relationships can be investigated (Guney, 2007; Yildirim, 2013). In cointegration analysis, the Autoregressive Distributed Lag (ARDL) bounds testing approach is frequently used to examine long-term relationships between variables without considering their order of integration. However, a key condition for the model is that the variables must not be integrated of the second order or higher (Ozata, 2020).

In this study, the Nonlinear Autoregressive Distributed Lag Model (NARDL), a form of the ARDL model suitable for nonlinear relationships in economic and financial time series, is utilized. NARDL has significant advantages over other modeling methods due to its ability to produce robust cointegration test results in small samples, its flexibility by relaxing error correction assumptions, and its capability to estimate both short- and long-term dynamics simultaneously. The asymmetric long-term cointegration model, which forms the basis of the NARDL model in its error correction form, is represented as follows (Gordon, 2017; Icen, 2018; Hu et al., 2018; Ozata, 2020):

$$\Delta y_t = \alpha + \rho y_{t-1} + \theta^{+\prime} x_{t-1}^{+} + \theta^{-\prime} x_{t-1}^{-} + \sum_{j=1}^{p-1} \gamma_j \, \Delta y_{t-j} + \sum_{j=1}^{q-1} (\varphi_j^{+\prime} \; \Delta x_{t-j}^{+} + \varphi_j^{-\prime} \Delta x_{t-j}^{-}) + \varepsilon_t =$$
$$p\xi_{t-1} + \sum_{j=1}^{p-1} \gamma_j \, \Delta x_{t-j} + \sum_{j=1}^{q-1} (\varphi_j^{+\prime} \, \Delta x_{t-j}^{+} + \varphi_j^{-\prime} \Delta x_{t-j}^{-}) + \; \varepsilon_t \qquad (1)$$

To investigate hidden cointegration between dependent and independent variables, it is necessary to decompose these variables into positive and negative sub-variables that explain their asymmetric effects in the short and long term (Schorderet, 2001). Accordingly, in the NARDL estimation, the positive and negative rate of change in exchange rates and diesel prices are incorporated into the model. The general representation of the NARDL model used for egg prices in this study is as follows. Since the most accurate results for the model were obtained in logarithmic form, the logarithms of the variables were taken and included in the analysis.

$$\Delta lnP_j = \alpha + \rho lnP_{j_{t-1}} + \; \theta_{ij}^{+} lnX_{ij_{t-1}}^{+} + \; \theta_{ij}^{-} lnX_{ij_{t-1}}^{-} + \; \sum_{i=1}^{p-1} \gamma_{ij} \; \Delta lnP_{ij_{t-i}} + \; \sum_{i=0}^{q} \pi_{ij}^{+} \Delta lnX_{ij_{t-i}}^{+} +$$
$$\sum_{i=0}^{q} \pi_{ij}^{-} \Delta lnX_{ij_{t-i}}^{-} + \epsilon_t \qquad (2)$$

Results and Discussion

For the NARDL model to be applicable to the examined time series, the assumptions outlined below must be satisfied. To avoid spurious regression in time series and identify meaningful relationships between variables, the stationarity of the series must first be tested. The stationarity and the degree of stationarity can be determined using tests such as the Augmented Dickey-Fuller (ADF) test and the Phillips-Perron (PP) test. It is essential to identify the number of differencing operations required to render each variable stationary (Ertek, 2019).

Table 1. ADF and Phillips-Perron (PP) Unit Root Test Statistics

	Level		**1. Difference**	
Variables	**ADF**	**PP**	**ADF**	**PP**
Egg price	-0.6028	-0.5519	-15.4927***	-15.1791***
Exchange rate	-1.7681*	--2.5321	-13.7146***	-12.3932***
Diesel prices	0.9011	- 0.9221	-18.1964***	-18.2053***

*: levels of significance: *:10%, **.5%, ***.1%

The results indicate that the exchange rate, diesel prices, and egg prices achieve stationarity at their first differences at the 1% significance level (Table 1). The stationarity of the variables at the first difference confirms their suitability for NARDL analysis.

Table 2. Cointegration Test

Tests	***f* value**	**Prob.**
Exchange rate (Wald Test)	0,372	0,542
Diesel prices(Wald Test)	0,437	0,509
Autocorrelation (Durbin Watson test)	2,009	-
Seri Correlation	0,812	0,445
Heteroscedasticity (White test)	1,223	0,106
Ramsey Reset test	0,198	0,657

When testing the model assumptions, the results are evaluated by rejecting the null hypothesis (H_0), which supports the negative case (Table 3). The Wald F-statistic test results, which reject the H_0 hypothesis (indicating no asymmetric relationship between the variables) at the 1% significance level, confirm the presence of an asymmetric relationship between egg prices, exchange rates, and diesel prices. Under the bounds testing approach, the Durbin-Watson statistic (2.009) for detecting autocorrelation in the error terms indicates no presence of autocorrelation. This finding was further supported by serial correlation values, which showed a p-value greater than 0.05. The model's heteroscedasticity was validated through the White test, while the absence of misspecification in the model structure was confirmed using the Ramsey RESET test. These diagnostic tests demonstrate that the NARDL model estimates are both reliable and stable (Table 3).

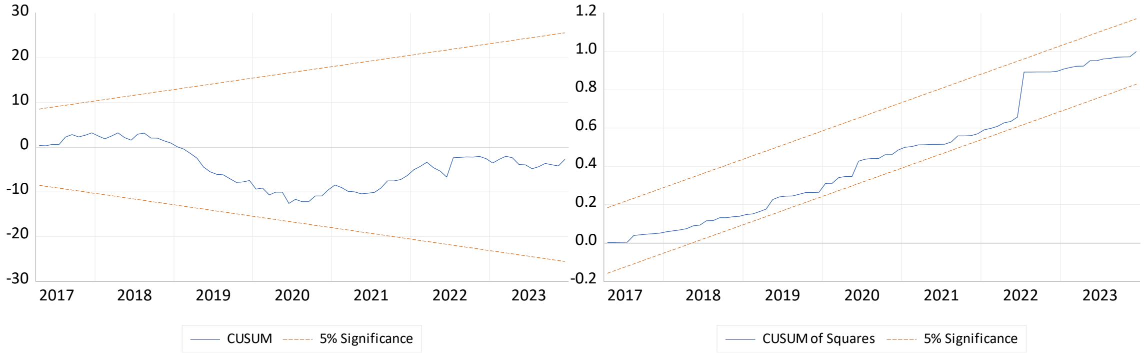

Figure 1. Egg Price CUSUM Tests

The CUSUM test results indicate the absence of structural breaks in egg prices and confirm that the model maintains a stable structure throughout the forecast period (Figure 1).

Table 4. Short-Term and Long-Term Forecast Results

Short Term	**Coefficient**	**Standard error**	***t* value**	***p* value**
C	0.165682***	0.025308	6.546658	0.0000
D(LEGG(-1))	0.202936***	0.050078	4.052365	0.0001
D(LEGG(-2))	0.073586	0.050940	1.444572	0.1495
D(LDSL_POS)	0.030942	0.107412	0.288065	0.7735
D(LDSL_POS(-1))	-0.196929**	0.078335	-2.513934	0.0124
D(LDSL_POS(-2))	-0.268080***	0.079388	-3.376837	0.0008
D(LEX_NEG)	0.097419	0.080714	1.206968	0.2283
D(LEX_NEG(-1))	-0.159455**	0.079485	-2.006094	0.0456
DUMMY	-0.037730***	0.008633	-4.370205	0.0000
CointEq(-1)	-0.122909***	0.018816	-6.532340	0.0000
Long Term	**Coefficient**	**Standard error**	***t* value**	***p* value**
LDSL_POS	0.174236	0.252177	0.690928	0.4901
LDSL_NEG	1.197178***	0.305052	3.924505	0.0001
LEX_POS	0.232515***	0.049430	4.703947	0.0000
LEX_NEG	0.084254	0.054740	1.539174	0.1247
R^2	0,955			
Adjusted R^2	0,953			
f value	560,667			
p value	0,000			

*: levels of significance: *:10%, **.5%, ***.1%

The short-term and long-term coefficients related to egg prices, along with information about the model, are presented (Table 4). The R^2 value indicates that the independent variables explain 95.5% of the variance in the dependent variable. The significance of the model is determined by the magnitude of the F-statistic. The differing coefficients of the variables in the short term are another indication of the presence of an asymmetric relationship (Meo et al., 2018). The inclusion of the dummy variable, which eliminates structural breaks in the model, is found to be significant. The error correction coefficient (CointEq (-1)) tested in the short-term analysis is significant, indicating that a long-term deviation converges by 12.3% in the subsequent period.

In the short term, shocks in egg prices from the previous period are statistically significant at the 1% level. Positive shocks in diesel prices from the preceding period significantly influence egg prices at the 5% level, while positive shocks from two periods earlier are significant at the 1% level. Diab and Karaki (2023) highlighted the significant impact of diesel prices on food prices in their study. Furthermore, short-term shocks in the exchange rate from two periods earlier are found to significantly affect egg prices at the 1% level. Cicek and Tandogan (2007) also noted that exchange rate increases during crises lead to higher egg prices.

In the long term, negative shocks in diesel prices and positive shocks in the exchange rate have been found to exert significant effects on egg prices. Specifically, a 1% change in diesel prices leads to a remarkable 119.7% increase in egg prices, highlighting the substantial influence of diesel price fluctuations. Additionally, a change in positive shocks in the exchange rate results in a 23.3% increase in egg prices, underscoring the sensitivity of egg prices to exchange rate variations over the long term.

Conclusion

This study aims to determine the effects of exchange rates and diesel prices on egg prices using the NARDL model. According to the results of the NARDL analysis, an asymmetric price transmission is observed between egg prices and the variables. This finding indicates that, in the long term, egg prices move in tandem with exchange rates and diesel prices. In the short term, the egg price from the previous month significantly affects the current price at the 1% significance level. Positive shocks in diesel prices from two months earlier influence the current price of eggs, while positive shocks in diesel prices from one month earlier and negative shocks in exchange rates from two months earlier affect the current price at the 5% significance level. In the long term, negative shocks in diesel prices emerge as a determining factor for egg prices. Positive shocks in exchange rates and negative shocks in diesel prices significantly impact egg prices over the long term, while the lagged values of these variables are influential in the short term. Based on the short- and long-term analysis results, it is evident that exchange rates and diesel prices, which substantially affect the prices of eggs—a product with significant production and trade activity in Turkey—should be carefully considered in market policy formulation. This is crucial for ensuring sustainability.

Acknowledgement

I would like to express my gratitude to the organizers and participants of ICOFAAS24 for providing the opportunity to present this work. I am also grateful to everyone who has inspired and supported me throughout the research process. This research has been conducted entirely independently, without any external financial or academic assistance.

Funding

No funding was received for this research.

Statement of Conflict of Interest

The authors declare no conflict of interest.

Authors' Contributions

The author designed and analyzed the research, arranged the studies, prepared the pictures and tables, contributed to the writing of the article, participated in the publication process, and approved the final version of the manuscript.

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Cornelian Cherry (*Cornus mas* L.) Native to Anatolia: History, Distribution, Research Trends, Human Health Promotion Aspect

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ABSTRACT: Anatolia, which is very important in terms of plant biodiversity in the world, is home to many cultivated fruits. In addition to cultivated fruits, there are also wild edible fruit species that are widely distributed in Anatolia and have been consumed with pleasure by the people of Anatolia for centuries. These fruit species are grown in a wide variety of forms depending on the region and are mostly consumed by processing due to their high dry matter content. In this sense, the most used fruit is cornelian cherry (Cornus mas L.). Anatolia, which is the homeland and natural distribution area of cornelian cherry, has been home to different cornellian cherry genotypes for centuries. In recent years, steps have been taken to create a variety by selecting productive cornelian cherry genotypes with superior fruit characteristics among the rich cornellian cherry populations grown from seeds. cornellian cherry is very rich in vitamin C, pectin, anthocyanins and phenolic compounds, which are very important for human health. Studies on cornelian cherry worldwide are increasing year by year.

Keywords: Cornellian Cherry, Biodiversity, Cultural Heritage, Composition, Human Health

INTRODUCTION

History and Distribution in the World

Cornelian cherry (*Cornus* spp.) has over 60 species distributed different parts of the World and it is believed to originated in central and southern Europe and parts of Asia including Anatolia (Asia minör). The ancient Greeks and Romans used it to produce lance shafts, and the bark has traditionally been used to make tool handles, spokes, and ladder rungs, while it is known primarily as an ornamental plant in the northern America. The plant has cherry-like fruits with high dry matter content. Thus, have been processeed into syrup, jelly, jams, wine, and baked goods for centruies (Brindza et al., 2007; Jacimovic et al., 2015; Skender et al., 2022; Liu et al., 2023; Skender et al., 2024). The distribution areas of *Cornus* species in the World (Figure 1) indicated that the most important species for fruit production is *C. mas* (cornelian cherry) is mainly distributed in Eastern Europe, Southern Europe and Asia Minor. *C. sanguinea* L. (European *Cornus*, blood twig *Cornus*, or common *Cornus*) is in general cultivated in Caucasus and found in the other parts of Europen countries (Tenuta et al., 2022). *C. officinalis* Torr. ex Dur is mainly distributed in East Asia including China, Japan and South Korea. The *C. sanguinea* L., *C. kousa*, *C. controversa*, are also found in Asia Minor and the Balkans, China, and Korea (Klymenko et al., 2021). *C. australis*, *C. hungarica*, *C. sericea*, *C. alba*, *C. florida*, etc. are known as ornamental plants (Forman et al., 2015).

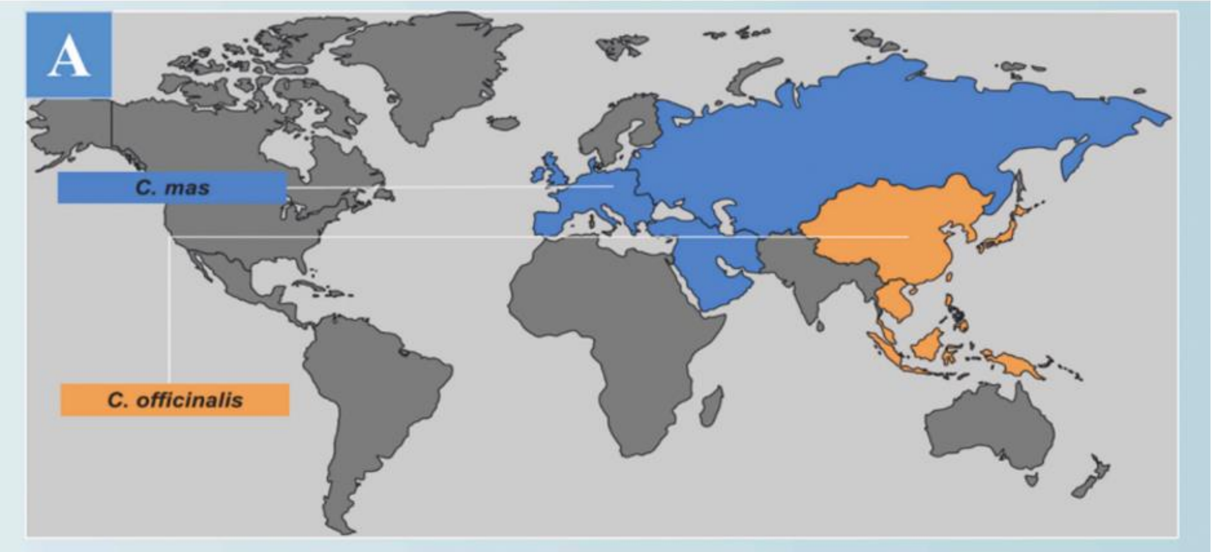

Figure 1. Distribution map of major *Cornus* species (Liu et al., 2023).

Among species, *Cornus mas* and *Cornus officinalis* have special emphazises because it has a long history of use as a food (Bijelic et al., 2011; Drkenda et al., 2014). Neolithic food remains from northern Greece include the plant's seeds of *Cornus mas*. In eastern Europe and western Asia, *Cornus mas* fruits is very popularly eaten fresh or processed into jams, pickles, syrups and alcoholic beverages. Consuming the fruit is often associated with health benefits. It is an important part of Anatolian's people life and they used cornelian cherry fruits not only nutrition but also in traditional medicine for centuries (Ercisli, 2004; Yilmaz et al., 2009; Sengul et al., 2014).

Cornelian cherry fruits have been used as food in the world for many years. In archaeological excavations, the seeds of the plant were found among the Neolithic food remains in Northern Greece. Cornelian cherries are an important part of the life of the Anatolian people, and they have used the cornelian cherry fruit not only in nutrition but also in traditional medicine for centuries (Ercisli et al., 2008; Ersoy et al., 2019) Cornelian cherry is a wild fruit known for its sour taste. The plant is in the form of a small tree, is one of the native fruits of Anatolia. It also constitutes an important fruit group in the Balkan and Eastern European countries. It has variable colored fruits (Figure 2). Harvested in September and November, this fruit is rarely consumed fresh. It is usually found in dried or juice form, and is also evaluated in the form of jam, marmalade, and fruit pulp. It provides health benefits thanks to its high nutritional value and antioxidant structure (Capanoglu et al., 2011; Ercisli et al., 2011).

Figure 2. Fruits of different cultivars of *Cornus mas* L. (1-Ekzotychnyi; 2-Koralovyi Marka; 3-Koralovyi; 4-Uholok; 5-Yantarnyi), *C. officinalis* Siebold & Zucc. (6) and *C. mas* × *C. officinalis* (7) of a selection of M.M. Gryshko National Botanical Garden (Kyiv, Ukraine) (Klymenko et al., 2021).

Research Trends

As indicated in Figure 3, there were an increased number of publications in SCI indexed journals on cornelian cherry in the world. In particular in 2019, 2020 and 2021 years enourmous number of publications were published in SCI indexed journals related to cornelian cherry.

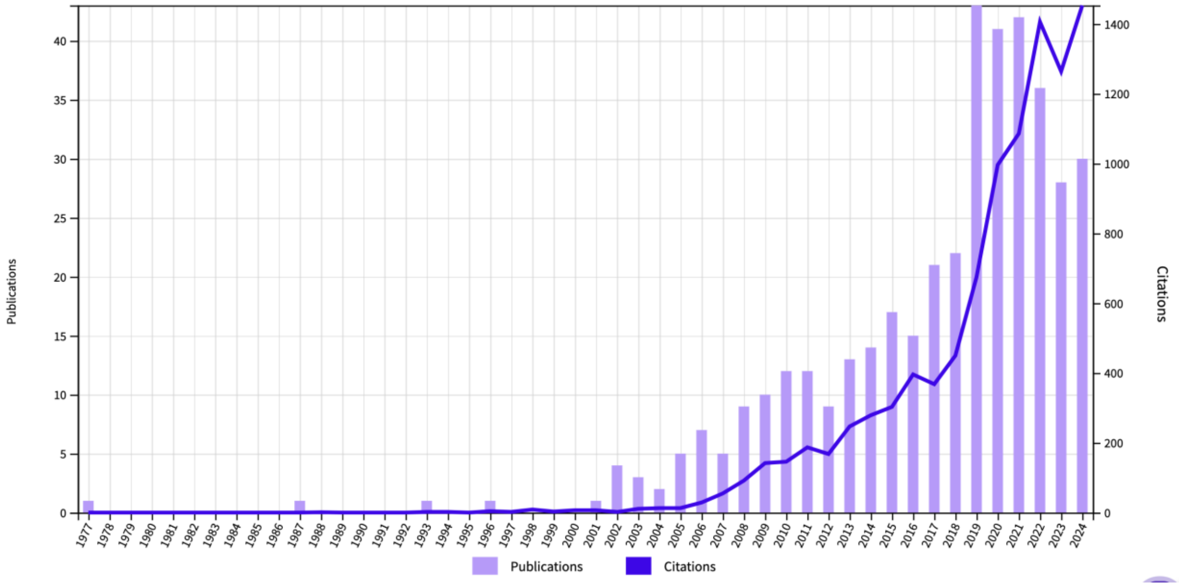

Figure 3. Research trends on cornelian cherry between 1977-2024 in the world

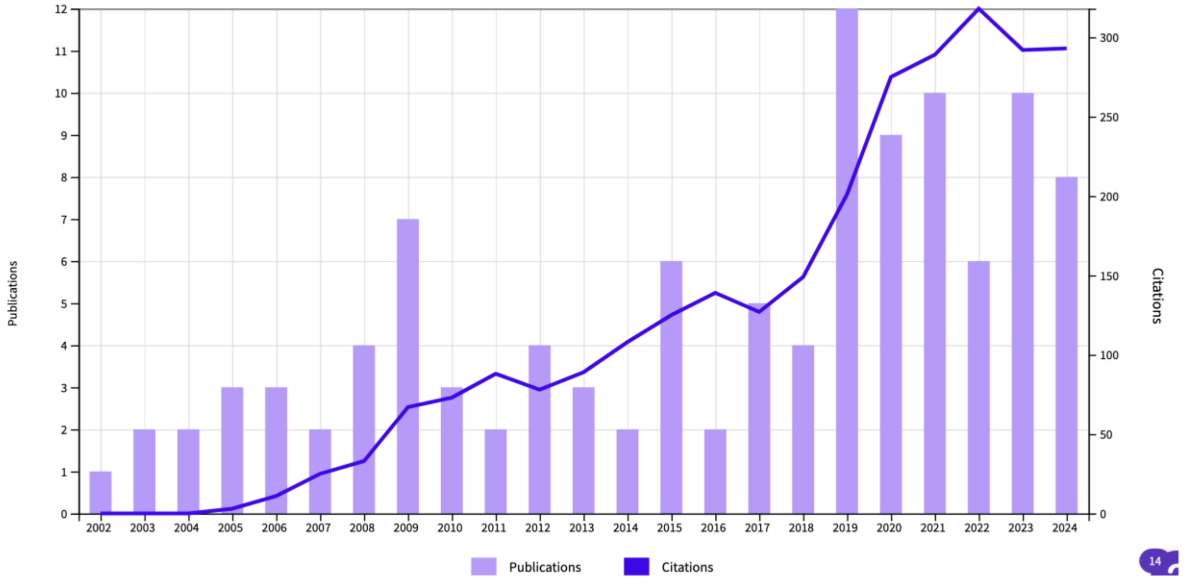

Figure 4. Research trends on cornelian cherry between 1977-2024 in Turkey

As indicated in Figure 4, similar trends with world has been occurred in Turkey on studies related to cornelian cherry. There were an increased number of publications in SCI indexed journals on cornelian cherry in the Turkey as well. In particular in 2019, 2021 and 2023 years an increased number of publications were published in SCI indexed journals related to cornelian cherry in Turkey.

Human Health Promotion of Cornelian Cherry Fruits

Tree, flower and leaf in the wild & Immature fruits, mature fruits, and seeds have human health promotion substances of cornelian cherry fruits (Figure 5). Previous studies revealed that as a wild grown fruit, cornelian cherries have attractive colorful red, yellow, dark red fruits. The attractive fruits same time have rich of bioactive contents including organic molecules, carbohydrates, fatty acids, vitamins and minerals. The most important organic molecules in cornelian cherry fruits are anthocyanins, iridoids, phenolic acids, flavonoids, and tannins (Szczepaniak et al., 2019). Studies are also revealed that the amount of those substances change genotype to genotype, growing conditions, and ripening degree of the genotypes (Dinda et al., 2016; Szczepaniak et al., 2019).

The fruits of cornelian cherry are widely used in folk medicine for the treatment of a wide range of diseases such as diabetes, digestive ailments, anemia, liver and renal diseases etc. in different culture, in particular eastern Europea and Western Asian countries.

The most distinguished properties of cornelian cherry fruits are high levels of anthocyanins and iridoids. The seeds, fruits, leaves even barks reported antioxidant, antimicrobial, antidiabetic, cytoprotective, neuroprotective properties. It also have anticancer and antiinflammatory effects due to its composition of phenolic compounds and ursolic acid (Dinda et al., 2016; Kaya and Koca, 2021).

Moreover, more recently superfood terminology widely used for some fruits that include high biological activity and among these fruits cornelian cherry have been reported rich in polyphenols, vitamin C and minerals (Bayram and Ozturkcan, 2020). In Türkiye, fruits is considered as a valuable nutritional supplement thanks to the richness in flavonoids, carotenoids, anthocyanins, iridoids, vitamins, phenolic acids, pectins, tannins, minerals and sugars (Kaya and Koca, 2021).

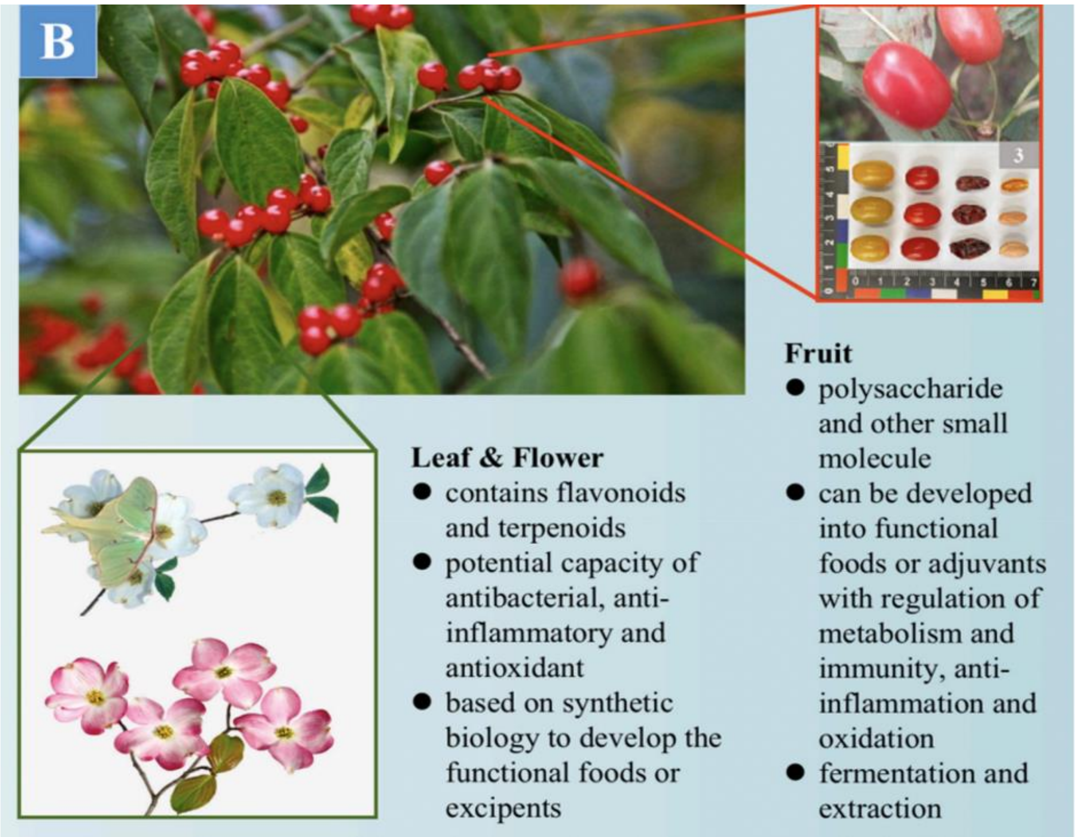

Figure 5. Cornus tree, flower and leaf in the wild & Immature fruits, mature fruits, anhydrous substance and seed (Liu et al., 2023).

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Indispensable Propagation Element for Wild Fruit Species: Propagation by Seeds

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ABSTRACT: Wild edible fruit species have become increasingly important in recent years in the face of global warming and climate change that the world has been facing. These species, which are more resistant to adverse conditions, also attract attention with the biologically active substances in their fruits, which can be considered quite high in terms of human health. In recent years, vegetative propagation studies on the propagation of wild edible fruit species have revealed the importance of their seed propagation. The difficulties in vegetative propagation have made seed propagation more important. Seed propagation of wild fruit species also makes very important contributions to biological diversity in the geography where they are found. In species that have difficulty in seed propagation, the fact that they produce a large number of seeds appears as an advantage. They try to turn their low propagation capacity into an advantage by scattering a lot of seeds around.

Keywords: Seeds, Propagation, Dispersion, Diversity

INTRODUCTION

Seeds are very important for plant life. The continuity of life in different plant species depends on seed propagation. Seeds of different plant species are indispensable food sources primarily for animals. Seeds of some species (peas, lentils, beans, chickpeas, corn, etc.) are also an important food source for humans. Seeds are transported from one place to another in various ways (especially animals and humans) and contribute significantly to the expansion of their growing areas. The seed is the main element in the survival of species and their transfer from generation to generation. Seeds protect themselves against heat, cold, and drought underground (Corlett, 2009; Fleming et al., 2011; Masaki et al., 2012).

In the animal kingdom, birds and mammals, especially those attracted by seeds, are the primary seed dispersers (Zhou et al., 2008; Tsunamoto et al., 2020). After eating fleshy and nutritious fruit containing seeds, birds and mammals ingest the seeds and eventually return them to nature (Wandrag et al., 2018). Seed mortality is reduced by dispersing seeds farther from the parent plant, and survival is increased if new microhabitats are colonized (Cousens et al., 2008). In addition, seed dispersal promotes gene flow within and between plant populations (Wandrag et al., 2018).

Indigenous or wild edible fruit species play an important role in rural areas in different parts of the world. There were over 400 wild edible fruit species around the world and are gained more popularity in recently. Wild edible fruit species has diverse genetic structure and they include high content of non-nutritive, nutritive, and bioactive compounds such as flavonoids, phenolics, anthocyanins, phenolic acids, and as well as nutritive compounds such as sugars, essential oils, carotenoids, vitamins, and minerals. Moreover, wild edible fruits have distinct flavor and taste, excellent medicinal value and health care functions as well (Ercisli, 2024).

It is well known that the most of the wild edible fruit species propagated by natural way, seed propagation themselves. However, information on how they propagate by seeds for these species is scantily available (Figures 1 and 2).

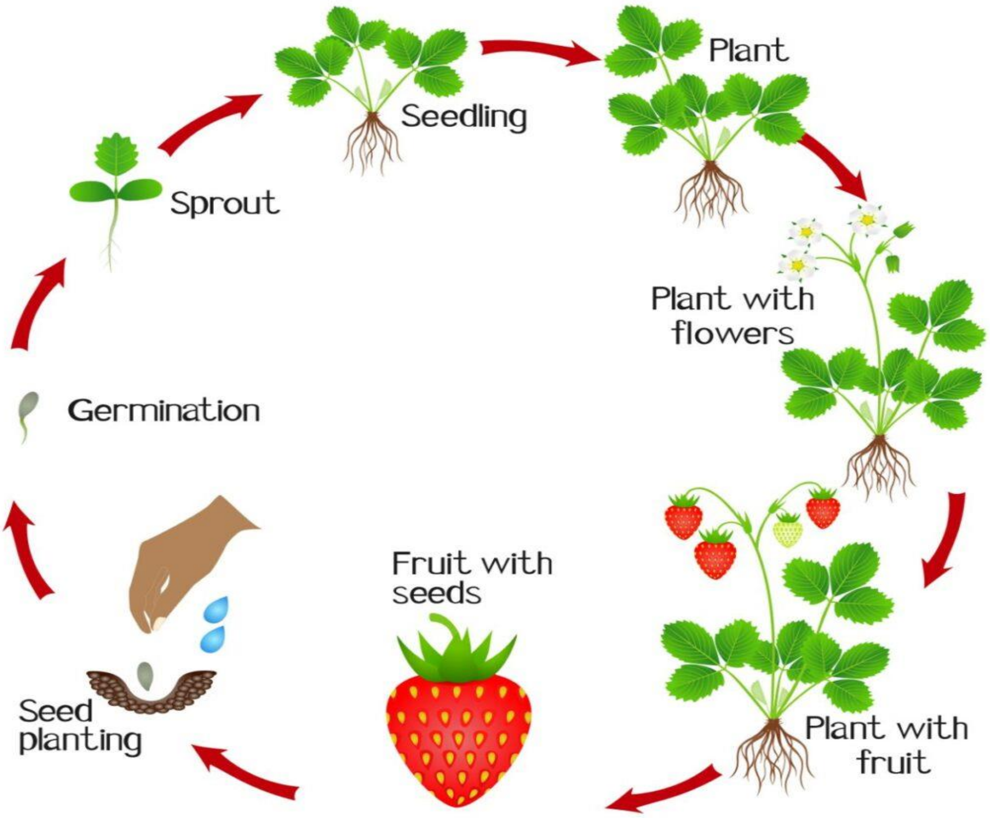

Figure 1. Seed propagation of wild *Fragaria vesca*

Seed germination is a physiological process that follows many metabolic changes and ultimately results in the emergence of a young plant. After the seeds are separated from the mature plant, they generally do not germinate and remain dormant. Although there are many factors that prevent germination, it may be due to the hard and impermeable seed coat, the presence of substances that prevent germination in the seed, or the improper development of the embryo. After harvest, many treatments are made to bring the seeds to germination maturity. In fact, not germinating the seeds after harvest is of great importance for the continuation of the generation of the relevant species (Fu et al., 2024). Seed dormancy was classified into three categories as follows: eco-dormancy, regulated by environmental factors; para-dormancy, regulated by physiological factors outside of the affected structure; and endo-dormancy, controlled by physiological factors inside of the affected structure (Gregory et al., 1987).

Figure 2. Seed propagation of wild apples

Bird dispersal is a process in which a frugivorous bird consumes the pulp and regurgitates or excretes all or some of the seeds unharmed (Figure 3).

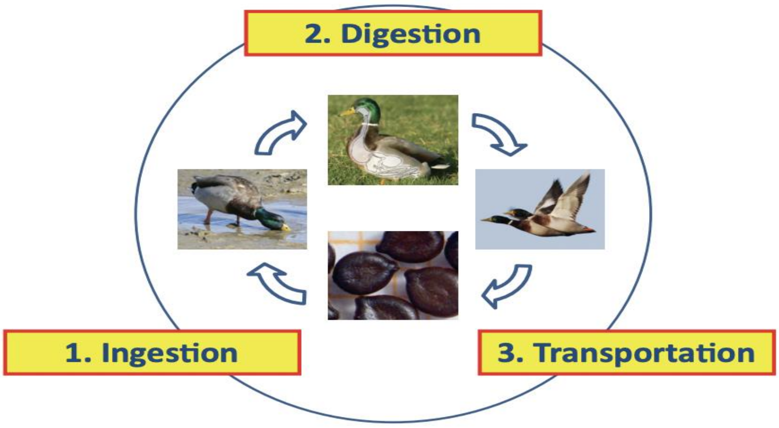

Figure 3. Schematic representation of the fundamental steps in the waterbird-mediated endozoochorous dispersal process, which represent the main focal points of this thesis (Kleyheeg, 2015).

It has been suggested that this process is advantageous as, among other effects, it enhances germination. Removal of the seed from the pulp which contains germination inhibitors, or the modification of the coat structure of the seeds are both considered as factors which may enhance germination (Jordano et al., 2014).

Despite the fact that wild edible fruit species producing fleshy fruits represent a very prominent fraction of the vegetation in the different agroclimatic region in the world, and most of the wild edible fruit crops is eaten by birds (Herrera et al., 2011; Jordano, 2014). It is known that germination response of seeds which had passed through avian digestive tracts is evident.

Seed Germination of Wild Edible Fruit Species

Most of the wild edible fruit species had hard seeds that germinate poorly and unevenly and require more time for seedling emergence. The dormancy in seeds of wild edible fruit species might be due to hard seed coat, impermeability to water and gases, physiological immaturity of embryo, deficiency of some endogenous growth promoters or excess of endogenous growth inhibitors.

Breaking Dormancy Methods of Wild Edible Fruit Seeds

Different methods like water soaking, mechanical scarification, acid scarification and chemical treatments are used for breaking dormancy in such seeds to improve germination.

Water Soaking

Soaking of seeds in water promotes germination by softening the hard seed coat of wild edible fruits, activating the enzymes and diluting the effects of inhibitors. Duration of soaking varies from over night to 3 or 4 days depending on the nature of seed coat.

Scarification

Scarification is a method used to wear away the hard seed structure in wild edible fruit species. It is examined under two groups as mechanical scarification and chemical scarification. Mechanical scarification is considered a more environmental friendly application. The basis of both processes is to eliminate germination barriers, ensure water absorption of the seed and improve gas exchange.

Mechanical and Acid Scarification

In mechanical scarification, the seeds are simply placed on a concrete floor and abraded by moving them left and right under pressure with a boot. In addition, scarification processes are carried out on the surface of the seed using sandpaper. The duration of scarification varies according to the structure of the seed. It is kept longer in species with pressed seed coats such as olive, cornelian cherry, Russian olives. In acid treatment, acid is used for a longer time or in higher concentrations depending on the hardness of the seed coat. Especially after acid application, the seeds must be rinsed with water. Seeds can be treated H_2SO_4 or some kind of plant growth regulators such as GA_3 for 12 to 48 hours.

Bird Dispersal of Seeds Belongs to Wild Edible Fruits

Birds, especially those that consume the fruits and disperse the seeds to germinate and develop, are of great importance in ensuring the continuity of wild fruit species in the world and their protection (Gasperin and Pizo, 2012). In fact, birds, in a sense, perform the scarification process. Indeed, endozoochory, which is the passage of edible seeds through the digestive tract of birds and their subsequent dispersal in a viable form (Fukui, 2003), is considered one of the most effective ways of transporting reproductive cells (Figure 4).

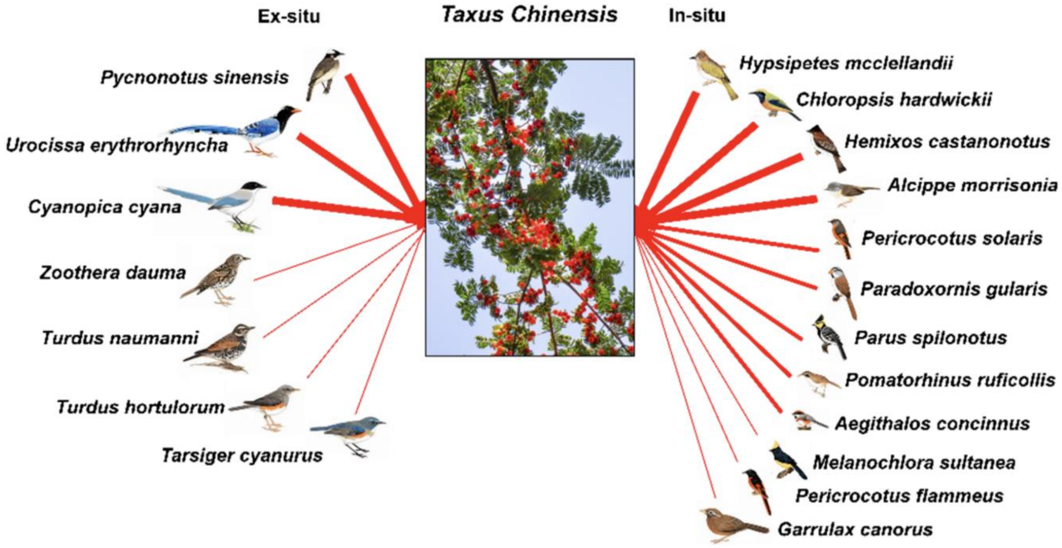

Figure 4. A network approach showing seed dispersal interaction between *Taxus chinensis* (Pilger) Rehd and frugivorous birds across in-situ and ex-situ sites, Southeast China. Line thickness represents interaction strength, based on the number of seeds removed. Bird pictures are cited from the A Field Guide to the Birds of China (MacKinnon et al., 2000)

In this process, birds that consume wild edible fruits effectively perform the scarification of the seed (i.e. the scarification and loss of the hard seed coat without affecting the embryo) and cause the seed to wear out in a shorter period of time (Samuels and Levey, 2005; Varela and Bucher, 2006). Birds, in particular can affect germination by scarification, removing the pulp and fertilizing the seed. An increment in germination results in an increase in the potential number of individuals that can establish in the ecosystem, and thus, the endozoochory is an important process in the life cycle of some plant species (Traveset, 1998). A variety of studies have described the positive effect of endozoochory by birds on both germination percent and rate (Lovas-Kiss et al., 2020), though this positive contribution is not fully generalizable (Traveset, 1998), as the ingestion and passage through the gut can reduce the viability of some seeds (Domínguez-Domínguez et al., 2006).

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Phytochemical Profiles, Enzyme Inhibitory and Antioxidant Activities of *Lycium barbarum* L.: The Effect of Solvent Polarity

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ABSTRACT: Since the discovery and identification of phytochemicals, plants have been considered a reservoir of active compounds that can be used in the development of plant-based medicines or functional foods. Herein, a comprehensive evaluation of *Lycium barbarum* L. was conducted by investigating its phenolic profiles, enzyme inhibitory activity, antioxidant capacity, and total polyphenol content, along with the effect of solvent polarity. The polar and nonpolar extracts were analyzed for the presence of 53 phenolics and 7 triterpenoids using LC-MS/MS and GC-MS, respectively. Quinic acid was the dominant phenolic among the 21 compounds detected. The enzyme inhibitory activities of the extracts were evaluated against seven enzymes that are considered to be major targets in the treatment of neurodegenerative diseases. The nonpolar extract exhibited the highest inhibitory activity against angiotensin converting enzyme (99.88%), exceeding the commercial standard (98.99%). The highest antioxidant activity was also observed in the nonpolar extract, with an IC_{50} value of 39.94 for DPPH scavenging activity and 85.98% for linoleic acid/β-carotene bleaching capacity. The total phenolic content of the polar and nonpolar extracts was also determined to be 22.80 mg GAE/g and 17.47 mg GAE/g, respectively. Correlation analysis was used to investigate the interaction between each specific phenolic and enzyme inhibitory activity.

Keywords: *Lycium barbarum* L., Phenolic Profile, Enzyme İnhibitory Activities, Antioxidant Capacity, Correlation Analysis

INTRODUCTION

Natural bioactive compounds, including several major groups such as phenolics, terpenoids, fatty acids, and polysaccharides, are associated with various therapeutic and functional properties, making them valuable sources for pharmaceutical and healthcare applications (Vo et al., 2024). These compounds play a critical role in improving human health through their antioxidant, antimicrobial, anticancer, antidiabetic, antihypocholesterolemic, and inhibitory activities (Julshahril et al., 2025). As a result, the demand for potent bioactive compounds is increasing, driving the need for efficient and sustainable extraction of these compounds from their natural sources. Extraction efficiency is affected by several factors, such as solvent polarity, concentration, time, and temperature. The most important factor in extracting different compounds according to their chemical properties is the solvent used. Since a single solvent is unlikely to extract all the phytochemicals in a plant material, the use of solvents with different polarities can facilitate access to possible active compounds (Gil-Martín et al., 2022).

Lycium barbarum L., also known as goji berry or wolfberry, is a deciduous shrub widely grown in the dry and semi-dry regions of northwestern China, southeastern Europe, and the Mediterranean region. The fruit of *L. barbarum* has been used in traditional medicine in east Asia for more than 2300 years, and with the discovery of its biological activities and pharmacological functions, it has recently been used as a super food and anti-aging drug around the world. Its known bioactivities include antipyretic, anti-inflammatory, anti-senile, antidiabetic, antihyperlipidemic, and antithrombotic activities. It also plays an important role in the prevention and treatment of various chronic diseases, including immunodeficiency, cancer, hepatitis, and infertility (He et al., 2024; Jin et al., 2013; Liu et al., 2024).

Goji berry is one of the most popular berries worldwide due to its functional properties and has been extensively studied to highlight its phytochemical content and bioactivities (Rodrigues et al., 2021; Wang et al., 2023). On the other hand, the individual compounds responsible for the bioactivities have not been clarified. To this end, in the present study a comprehensive phytochemical analysis of polar and nonpolar goji berry extracts was performed using 53 phenolic and 7 triterpenoid standards. In order to improve the health of people suffering from neurodegenerative diseases, the enzyme inhibitory activities of the extracts were evaluated against seven enzymes (tyrosinase, acetylcholinesterase (AChE), butyrylcholinesterase (BChE), urease, elastase, collagenase, and angiotensin-converting enzyme (ACE)) that are the key factors in the treatment of these diseases. Correlation analyses were conducted to establish the interaction between phenolic compounds and bioactivity in accordance with the results.

Material and Methods

1. Plant Collection

Fresh fruits of *Lycium barbarum* L. sold in a market in Mersin, Türkiye were brought to the laboratory and cleaned with sterile distilled water and then dried by lyophilization.

2. Preparation of Polar and Apolar Extracts from Fruits of *Lycium barbarum* L.

Three grams of crushed dried fruits were mixed with 20 mL of deionized water or an 80:20 (v:v) ethanol-water mixture containing 1M HCl and then the mixtures were subjected to sonication (SK06GT Kudos, Korea) at 30–40 °C for 30 minutes. To collect the supernatant, the extract was centrifuged for 15 minutes at 8,000xg (Hanil Science Industrial Combi 514R, Korea). The process was repeated three times by combining the three supernatants, which were then stored at -80°C until analysis (Ciniviz & Yildiz, 2020).

3. LC-MS/MS-based Qualitative and Quantitative Determination of Phenolic Compounds

The phenolic profile of the polar and nonpolar extracts was investigated by the method reported by (Findik et al., 2024). For the qualitative and quantitative analysis of the extracts, 53 of the standards listed in Figure 1 were used.

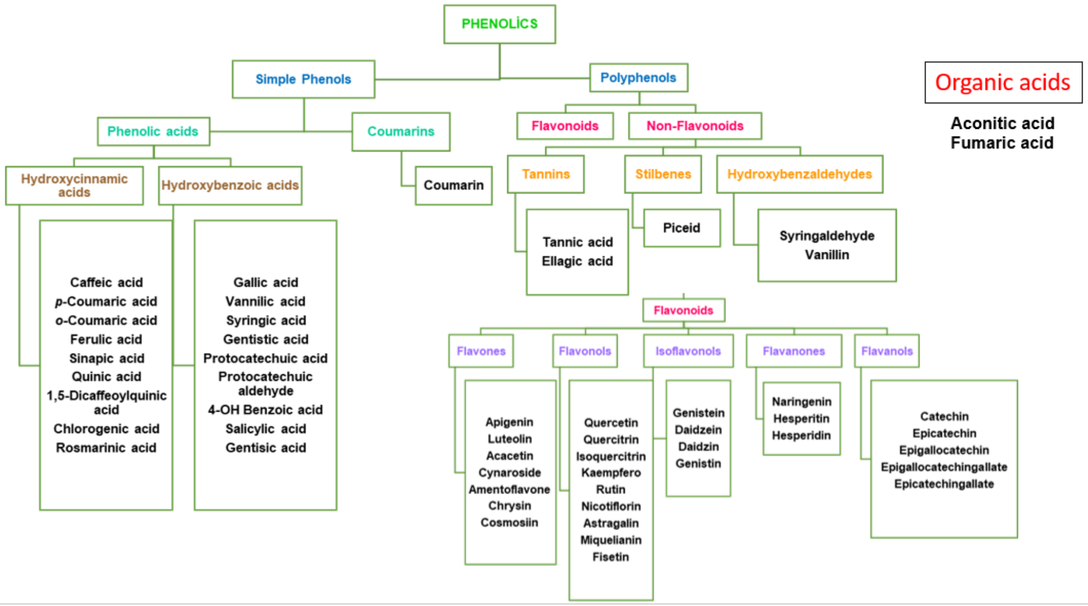

Figure 1. Phenolic standards used in phytochemical characterization by LC-MS/MS

4. Screening of Triterpenoid Content by GC-MS

The triterpenoid content of the extracts was analyzed for 7 standard triterpenoids (moronic acid, ursolic acid, ursonic acid, α-amyrin, betulinic acid, oleanolic acid, and oleanonic acid) according to the method reported by (Findik et al., 2024).

5. Determination of the Enzyme İnhibition Activity of the Polar and Nonpolar Extracts

The inhibitory activities of the polar and nonpolar extracts against AChE, BChE, tyrosinase, urease, elastase, collagenase, and ACE were determined by the method described by (Findik et al., 2024).

6. ANTİOXİDANT CAPACİTY OF THE POLAR AND NONPOLAR EXTRACTS

Both DPPH free radical scavenging and β-carotene bleaching capacities of the extracts were evaluated according to the method described by (Ciniviz & Yildiz, 2020). As standard reference, butylated hydroxyanisole (BHA) was used. Experiments were carried out in three replications.

7. Total Polyphenols Content (TPC) of the Polar and Nonpolar Extracts

The TPC of each extract was determined using the Folin-Ciocalteu method (Ciniviz & Yildiz, 2020). The TPC content of the extracts was expressed as the equivalent of gallic acid (mg GAE/g), which was used as a standard.

8. Statistical Analysis

ANOVA was used to evaluate the statistical differences between the extracts. Duncan's multiple comparison test was used to compare means, and $P < 0.05$ was considered significant. SPSS statistical software, version 22.00 (IBM SPSS Statistics for Windows, version 28.0. Armonk, NY: IBM Corp.), was used for statistical analysis. For correlation analysis, the Pearson correlation coefficient was computed, and $P < 0.05$ was used as the significance level. Significance was assessed at a 95% confidence level ($P < 0.05$). To facilitate data visualization and comprehension, principal component analysis (PCA) was used to distill the relationships among many variables into a more manageable collection of basic dimensions. Data from phenolic profiles and ACE inhibition were correlated using PCA.

Results and Discussion

In this study, a thorough evaluation of the phytochemical composition and bioactivity of *L. barbarum* L. was conducted. The findings offer valuable insights into the fruit's potential for pharmaceutical applications and highlight how the polarity of the extraction solvent affects both the phytochemical composition and bioactivity.

1. Phenolic Profile of the Polar and Nonpolar Extracts of the *L. barbarum* L

In at least one extract, 21 of the 53 phenolic compounds that were utilized as standards were detected at varying concentrations. Table 1 and Figure 2 list the phenolic components of the extracts.

Table 1. Identification and quantification of phenolic compounds in the extracts of the fruit of *L. barbarum L* by LC-MS/MS

Reference Phenolics	**M.I. (m/z)^1**	**F.I. (m/z)^2**	**U^3**	**Quantification (mg/100 g DW)**	
Simple Phenols				**Polar**	**Non-polar**
Phenolic acids					
Hydroxycinnamic acids					
Caffeic acid	179.0	134.0	0.0354	ND	0.408
Chlorogenic acid	353.0	85.0	0.0213	ND	0.934
p-Coumaric acid	163.0	93.0	0.0516	2.262	1.576
Ferulic acid	192.8	149.0	0.0181	ND	0.852
Quinic acid	190.8	93.0	0.0082	73.228	43.946
Hydroxybenzoic acids					
4-OH Benzoic acid	137,2	65.0	0.0237	0.57	ND
Protocatechuic acid	152.8	108.0	0.0411	ND	1.11
Salicylic acid	137.2	65.0	0.0158	0.038	0.046
Coumarins					
Coumarin	146.9	103.1	0.0383	ND	0.538
Polyphenols					
Flavonoids					
Flavonols					
Kaempferol	285.0	239.0	0.0209	ND	0.120
Nicotiflorin	592.9	255.0/284.0	0.0276	1.064	0.482
Rutin	608.9	301.0	0.0159	0.014	2.266
Quercetin	301.0	272.9	0.0543	ND	1.542
Isoquercitrin	463.0	271.0	0.0220	ND	0.022
Flavanones					
Hesperidin	611.2	449.0	0.0262	ND	1.972
Hesperetin	301.0	136.0/286.0	0.0562	ND	0.100
Naringenin	270.9	119.0	0.0521	0.002	0.010
Non-Flavonoids					
Tannins					
Tannic acid	182.8	78.0	0.019	ND	0.048
Hydroxybenzaldehydes					
Protocatechuic aldehyde	137.2	92.0	0.0396	ND	0.034
Organic acids					
Aconitic acid	172.8	129.0	0.0247	0.044	0.076
Fumaric acid	115.2	40.9	0.0124	ND	2.852
Rutin-D3-IS^d	612.2	304.1	ND	IS	IS
Ferulic acid-D3-IS^d	196.2	152.1	ND	IS	IS
Quercetin-D3-IS^d	304.0	275.9	ND	IS	IS

a: Parent ion (m/z): Molecular ions of the standard compounds (mass to charge ratio),b: MS2(CE): MRM fragments for the related molecular ions (CE refers to related collision energies of the fragment ions), IS: Internal standard, N.D: not detected

Using solvents with varying polarity had an impact on the content of the individual phenolic compounds. It was discovered that the nonpolar extract's phenolic component diversity was greater than that of the polar extract. While 20 of the 21 detected phenolics were found in nonpolar extract, only 8 compounds were detected in polar extract. On the other hand, although quinic acid was found to be the most dominant species in both extracts, it was 1.7 times higher in the polar extract. Therefore, the polar extract was found to be a very rich reservoir for quinic acid. The order of the predominant phenolics was quinic acid, fumaric acid, rutin, hesperidin, and *p*-coumaric acid. To the best of our knowledge, 4-OH benzoic acid, hesperetin, protocatechuic aldehyde, and aconitic acid were also identified in goji berry for the first time in the present study.

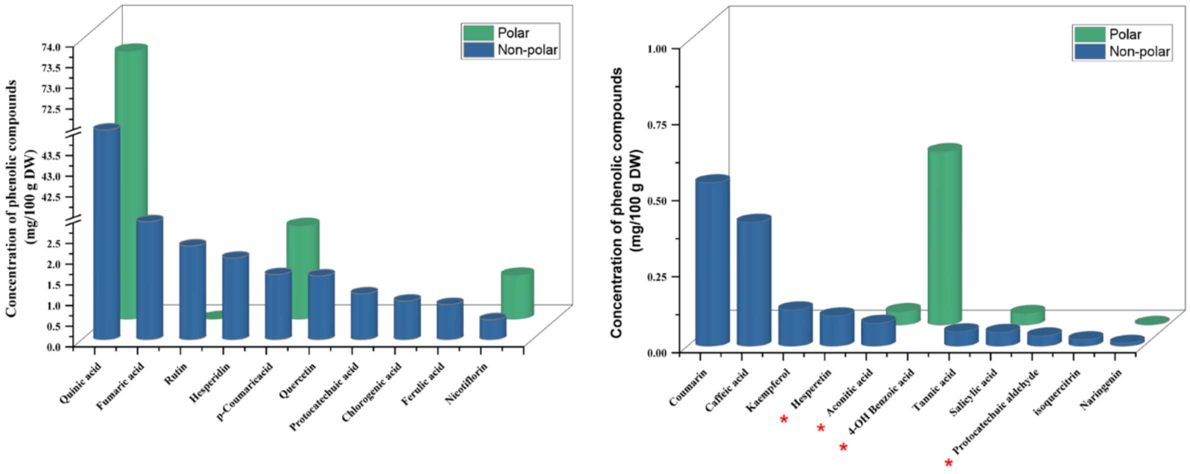

Figure 2. Order of phenolic compounds detected in polar (green) and nonpolar (blue) extracts from most to least abundant.

2. Contents of Triterpeneoids in the Polar and Nonpolar Extracts of the *L. barbarum* L.

None of the 7 triterpenoids used as standards were determined in either of the extracts.

3. Enzyme Inhibition Activities of the Polar and Nonpolar Extracts of the *L. barbarum* L.

The enzyme inhibitory activity of the *L. barbarum* L. extracts was examined against seven enzymes. While the extracts showed inhibitory activity against ACE, urease, elastase, and collagenase, neither nonpolar nor polar extracts showed any inhibitory activity against AChE, BChE, or tyrosinase (Figure 3). The highest enzyme inhibitory activity was detected against ACE in nonpolar extract (99.88%), which exceeded the commercial standard, lisinopril (98.99%). The polar extracts also expressed moderate activity with an inhibitory value of 66.15%. ACE, a zinc-dependent peptidase, controls blood pressure by changing inert angiotensin I into angiotensin II, a molecule which narrows blood vessels and results in hypertension. Therefore, ACE inhibition is a key treatment approach for hypertension, a frequent condition that can lead to many other health issues (Wu et al., 2022). The results indicate that the nonpolar extract of *L. barbarum* L. holds potential as a valuable source for use as a pharmaceutical and functional reagent in the treatment of hypertension.

The nonpolar extract had a strong urease inhibitory action (84.65%), which was comparable to the commercial standard of thiourea (97.74%). With an inhibitory value of 12.02%, the polar extract exhibited extremely poor action. One type of hydrolase that quickens the rate at which urea is hydrolyzed into ammonia and carbamic acid is urease, an enzyme that is dependent on Ni^{2+}. Urea is detrimental to agriculture and human health because it plays a role in pathohenesis. Additionally, it has been linked to peptic ulcers, pyelonephritis, and kidney stones. Owing to all of these urease-related impacts, urease inhibitors with low toxicity and good stability may offer a useful therapeutic strategy for urease-induced illnesses (Valentová et al., 2023).

The main components of connective tissue are collagen and elastin, and when these proteins are excessively reduced in tissues by elastase and collagenase, aging processes in the skin and joints are accelerated. (Figueiredo et al., 2023). Therefore, the benefits of inhibiting these enzymes in the prevention of connective tissue diseases have garnered attention recently. The nonpolar extract showed very low elastase and collegenase inhibitor activities.

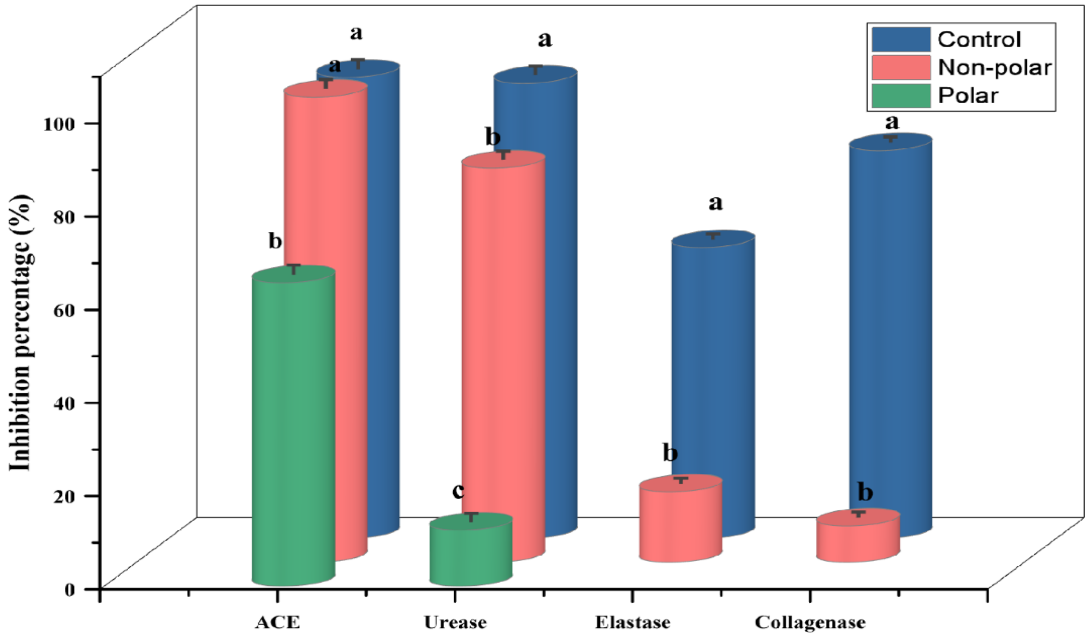

Figure 3. The enzyme inhibition activity of the extracts of *L. barbarum* L.

4. Antioxidant Activity of the Polar and Nonpolar Extracts of the *L. barbarum* L.

The antioxidant activity of the polar and nonpolar extracts was investigated using DPPH free radical scavenging and β-carotene bleaching assays, and the results are represented in Figure 4. The standard was BHA. Nonpolar extracts had significantly more antioxidant activity than polar extracts in both assays. The TPC of the polar extract (22.80 ± 2.14 mg GAE/g) was higher than that of the nonpolar extract (17.47 ± 1.35 mg GAE/g) ($P < 0.05$). Quinic acid is the most dominant species, especially in polar extracts, but it is a phenolic with very low antioxidant activity (Ercan & Doğru, 2022). This may explain the variation of the antioxidant activities among extracts.

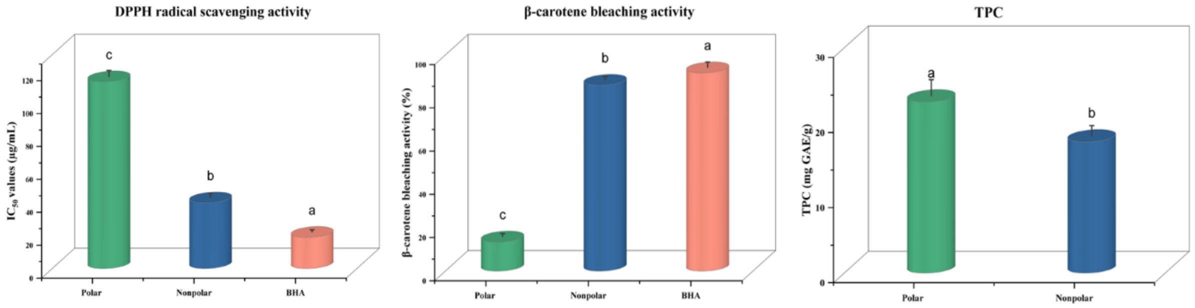

Figure 4. Antioxidant capacities and TPC of polar and nonpolar extracts. Results are expressed as mean ± standard error. Different letters indicate a significant difference between each extract ($P < .001$).

5. Correlation Analysis

Pearson correlation is a statistical method that measures the similarity or correlation between two variables by comparing their attributes and calculating a score ranging from -1 to +1. A high score means a positive relationship, while a score close to -1 means a negative relationship. Using Pearson correlation analysis, the correlation between phenolics and the ACE and urease inhibitory activities of the extracts was highlighted (Figure 5A). Of the 21phenolics, 17 exhibited a positive correlation, whereas four exhibited a negative correlation with the inhibition of enzymes (ACE and urease) (Figure 6). Caffeic acid, ferulic acid, chlorogenic acid, protocatechuic acid, salicylic acid, coumarin, quercetin, isoquercitrin, kaempferol, rutin, naringenin, hesperetin, hesperidin, tannic acid, protocatechuic aldehyde, aconitic acid and fumaric acid showed a high positive correlation with ACE and urease inhibitory activity. *p*-Coumaric acid, quinic acid, 4-OH-benzoic acid, and nicotiflorin showed a negative linear relationship with ACE and urease inhibition.

To evaluate the connection between the phenolic compounds and the enzyme inhibitory activities, PCA was utilized to plot the contributions of the variables to the PCs (Figure 5B). Of the entire variance, 99.7% was explained by the first principal component (Dim 1), and 0.2% by the second principal component (Dim 2). Therefore, all of the variation was explained by the PCs. The degree of correlation between these variables is estimated by the angle between the vectors reflecting the original variables. Positive correlations are indicated by small angles, while negative correlations are indicated by angles that are close to 180 degrees. Seventeen of the phenolics are grouped on the right side of the PCA plot, as can be seen in the plot, suggesting that they have positive relationships with ACE and urease inhibition. However, the phenolics that have negative correlation are represented by four of the phenolics that are grouped on the left side of the PCA plot: *p*-coumaric acid, quinic acid, 4-OH-benzoic acid, and nicotiflorin.

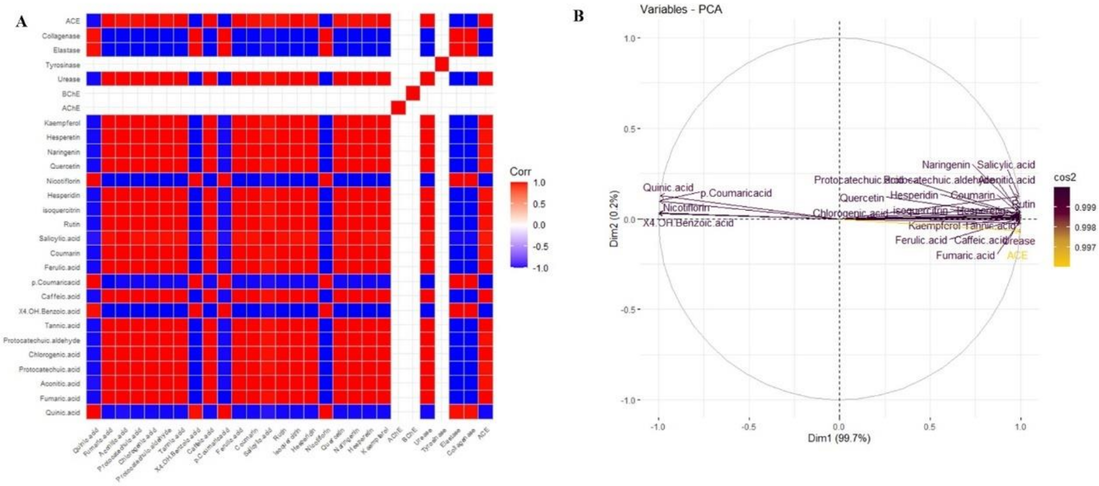

Figure 5. (A) Pearson correlation: The intensity of red and blue colors indicates higher to lower correlation levels. (B) Principal component analysis.

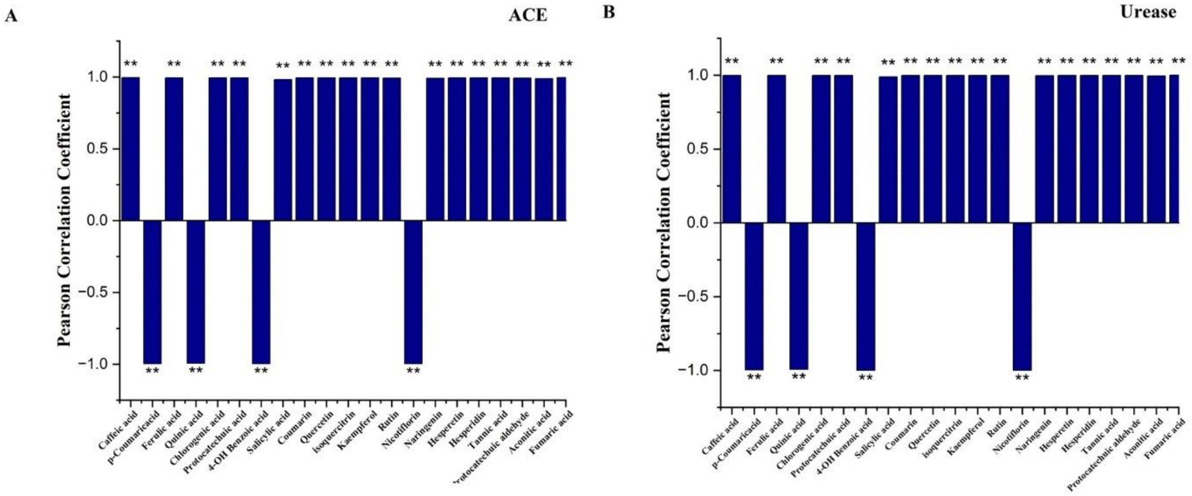

Figure 6. Bar chart that displays the correlation between each phenolic compound and enzyme inhibition. (**) indicates *P* values less than 0.001.

Conclusion

In this study, the phytochemical composition and bioactivities of polar and nonpolar extracts of *L. barbarum* L. were investigated, and the possible components responsible for the activity were elucidated using statistical methods. The results showed that the polarity of the solvent used in the extraction was an important factor in terms of both phytochemical composition and bioactivity. The findings indicated that *L. barbarum* L. is an excellent source for quinic acid, fumaric acid, rutin, hesperidin, and *p*- coumaric acid. The *L. barbarum* L. could be a promising supplement for pharmaceutical and nutritional applications due to its ACE and urease inhibitory activities.

Statement of Conflict of Interest

The authors declare that they are no conflict of interest.

Authors' Contributions

Bahar Tuba Findik, Hilal Yildiz and Esma Birisci designed and analyzed the research. All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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Overview of Milk Consumption in Türkiye

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ABSTRACT: The aim of this study is to calculate per capita milk consumption and protein intake from milk consumption of buffalo, cattle, sheep and goat milk in Turkey for 10-year periods. The calculations are based on FAOSTAT milk production, export and import data and population data for the period 1961-2022. The results show that the annual per capita consumption of buffalo milk decreased from 9.06 litres in 1961-1970 to 0.63 litres in 2021-2022, cattle milk consumption increased from 173.65 litres to 242.70 litres in the same period, sheep milk consumption decreased from 25.35 litres to 13 litres and goat milk consumption decreased from 16.26 litres to 6.84 litres. In the 1960s, 5.4 percent of the protein obtained from the milk of these animals came from buffalo, 80.40 percent from cattle, 7.1 percent from sheep and 7.1 percent from goats. In 2021-2022, 0.4% of the protein came from buffalo milk, 94% from cattle, 2.5% from sheep and 3.10% from goat milk. The per capita protein intake from these milks increased from 15.5-20.5 g in 1961-2000 to 24.17 g in 2021-2022, and this increase is thought to be related to increased health awareness, increased demand for milk and dairy products, development of modern production technologies and population growth.

Keywords: Nutrition, Protein Requirement, Health, Milk Consumption, Consumer Awareness

INTRODUCTION

The rapid growth of the world's population has created serious global challenges for nutrition and food security (FAO, 2021). Rapid population growth in developing countries is leading to an oversupply of labor in the agricultural sector, negatively affecting agricultural productivity and exacerbating the problem of malnutrition (Özşahin and Güven, 2023). This has made the role of proteins of animal origin even more important in ensuring a balanced diet for societies. In particular, the protein-rich nature of milk plays an important role in meeting this need (Yıldız and Demir, 2021).

The role of milk and dairy products in the diet is to provide proteins with high biological value. Milk proteins have a positive effect on human health because they contain all the essential amino acids needed by the body in the right proportions (Korhonen and Pihlanto, 2006). Milk is also an important source of micronutrients such as calcium, phosphorus, vitamin D, and riboflavin, which support muscle and bone health (Heaney, 2000). Increasing milk consumption in developing countries not only fills protein deficiency but also prevents problems such as growth retardation in children (Smith and Jones, 2021). In addition, by providing essential nutrients for growth and development, dairy products support the healthy development of children (Brown et al., 2022).

Although cow's milk accounts for the majority of global milk production, alternative milk sources such as goat, sheep, and buffalo milk play an important economic and cultural role in certain regions. Especially in developing countries, low-income families use goat and sheep milk as a source of income and as a staple food. Buffalo milk is a key ingredient in the production of traditional dairy products in countries such as India and Pakistan (Haenlein, 2020).

Türkiye predominantly produces cow's milk. It accounts for about 90 percent of total production. In addition, sheep, goat, and buffalo milk production accounts for 10% of total production (TÜİK, 2023). While sheep's milk is widely used in the production of traditional cheeses such as feta and tulum, goat's milk has become increasingly popular in recent years due to its compatibility with healthy eating trends and its high digestibility (Yalçın and Akyüz, 2020; Park et al., 2021). While buffalo milk attracts attention for its dense cream and high fat content, it is used as an important raw material, especially in the production of buffalo cream, yogurt, and ice cream in regions such as Afyon, Istanbul, and Samsun (Doğan et al., 2020; Kırmızı and Çelik, 2021).

Although buffalo milk production in Türkiye is more limited than other types of milk, its high fat content and dense cream play an important role in the production of high value-added products (such as buffalo cream, yogurt, and ice cream) (Akın et al., 2022). In Türkiye, buffalo milk production accounts for a limited share of only 0.3% of total milk production; however, it holds significant importance due to its use in the production of high value-added products. Although buffalo milk production in Türkiye is more limited than other types of milk, it is important for its use in the production of high value-added products (Yılmaz and Kara, 2019).

Small farms in Türkiye mostly produce buffalo milk and process it using traditional methods. However, modernizing and incentivizing this production can increase the economic potential of the sector. Small-scale family enterprises in Türkiye typically produce buffalo milk using traditional methods. However, modernizing these production processes and encouraging them with government support can play an important role in increasing the economic potential of the sector. This situation, together with increasing production capacity, also makes it possible to achieve rural development goals and environmental sustainability (Saner et al., 2022).

There are significant differences between animal milks in terms of protein content, nutritional value, and industrial use. Although the world's milk production is largely based on cow's milk, buffalo, goat, and sheep milk also make important contributions, both economically and nutritionally. Particularly, infants prefer goat's milk for its nutritional and digestibility properties (Tüfekci, 2023). The protein content and composition of milk have a direct effect on its processability and the quality of the final products (Tuncel, 2005; Uzundumlu et al., 2018). On average, cow's milk contains 3.2% protein, goat's milk 3.6%, sheep's milk 5.6%, and buffalo milk 4.5% (OECD, 2023).

Milk protein is a highly valuable ingredient for the food industry. Generally, we divide the protein fractions of milk into two main groups: casein (80%) and whey (whey protein, 20%). While casein is the basic protein structure of milk used in cheese making, whey protein is widely used in sports nutrition as a highly bioavailable and rapidly digestible source of protein. These two groups of proteins play an important role in determining the textural properties, processability, and nutritional value of foods (Walstra et al., 2021). Proteins from buffalo, sheep, and goat milk have a denser and richer composition than cow's milk proteins. Hard cheeses particularly favor sheep's milk due to its high casein content. Similarly, buffalo milk is of particular nutritional and technological importance, improving the quality of traditional products such as cream and yogurt with its high protein and fat content (Okur, 2014).

Milk protein is critical not only to the food industry but also to sustainable agricultural practices and economic value creation. Milk protein is critical not only to the food industry. It is also critical to sustainable agriculture and economic value creation. Efforts to diversify milk production in Türkiye offer an important opportunity both to expand the industrial use of milk proteins and to increase the added value of local products. In particular, the unique protein composition of buffalo, goat, and sheep's milk enables their wider use in traditional and modern foods (Saner et al., 2022).

Therefore, this study aimed to compare the daily amounts of animal protein obtained from per capita consumption of buffalo, sheep, cow, and goat milk over the ten-year period from 1961 to 2022.

Material and Method

Material

The Food and Agriculture Organization Statistics (FAOSTAT) provided the data for the study. The study also utilized national and international articles, papers, books, internet resources, and master's and doctoral theses.

Method

This study used Excel to calculate annual milk consumption per capita and animal protein values for buffalo, sheep, goat, and cow milk consumption per capita in Türkiye for the years 1961-2022, taking into account milk production, the conversion of dairy products to milk, export and import data, and population data for Türkiye. In the study, the values for buffalo (4.38%), sheep (5.73%), goat (3.26%), and cow (3.42%) were used to calculate the animal protein value of milk (Süt Dünyası, 2014). Dairy products are not included.

Research Findings and Discussion

Milk Production, Export and Import in Türkiye

In 1961, Türkiye's total milk production was around 6 million tonnes, 90% of which was cow's milk (Süt Dünyası, 2014). In the same year, total world milk production was about 200 million tonnes, and Türkiye's bovine milk production in 1961 was about 2.7% of world production (Çatalbaş, 2022). In 2022, Türkiye's total raw milk production decreased by 7.1% to 21,563,492 tonnes compared to the previous year. 92.3% of this production is cow's milk (TÜİK, 2024). Total world milk production in 2022 is estimated to be around 935.9 million tonnes. In this context, Türkiye's cow's milk production represents about 2.1 percent of the world's total milk production (FAO, 2024).

Türkiye's exports of milk and milk products increased by 2.5% in 2022 compared to the previous year, reaching 46,900 tonnes. Most of these exports are products such as milk powder, cheese, and yogurt. Germany, Iraq, Italy, and the United Kingdom are among the leading exporters. On the import side, Türkiye's imports of milk and milk products increased by 5.8% year-over-year to reach 1 million tonnes in 2022. Most of these imports are based on cow's milk and products. Germany, the Netherlands, and France are the main importers (SİTSO, 2023). In the 1960s, Türkiye's foreign trade in milk and dairy products was quite limited. During this period, the production of milk and milk products primarily focused on domestic consumption, resulting in a low volume of external trade. Therefore, in 1961, the import and export of buffalo milk and related products were negligible. Türkiye's industrialization policy, based on import substitution, reflects an economic structure that supports this limited volume of foreign trade (Çatalbaş, 2022). According to the data of the Turkish Statistical Institute for 2022, the total raw milk production in Türkiye was 21,563,492 tonnes. Approximately 0.2% of this production, i.e., 43,127 tonnes, is buffalo milk (TÜİK Türkiye recorded around 248,000 tonnes of buffalo milk production in 1961. In the same year, total buffalo milk production worldwide was around 17.8 million tonnes. Based on these data, Türkiye's buffalo milk production accounts for approximately 1.39% of world production (Kılıç Topuz and Yavuz, 2022).

Türkiye played a significant role in the world's sheep milk production in 1961, with an estimated 750 thousand tonnes produced. This represents around 13.5 percent of the world's total sheep's milk production (Süt Dünyası, 2019). Türkiye produced sheep's milk and related products to meet domestic consumption in the 1960s, when its foreign trade in milk and dairy products was very limited. In 1961, local needs largely dominated foreign trade, with negligible imports and exports of sheep's milk. Türkiye's industrialization policy, based on import substitution, reflects this limited volume of foreign trade (Çatalbaş, 2022). In 2022, sheep's milk accounted for 4.9% of Türkiye's total raw milk production. This corresponds to approximately 1,056,612 tonnes of sheep's milk (TÜİK, 2024).

In 1961, the production of goat's milk in Türkiye was about 523,395 tonnes. This production represents approximately 2.46% of the world's total goat milk production (FAO, 2024). Türkiye has a concentrated structure of goat milk production, especially in regions with a Mediterranean climate. Türkiye's foreign trade in milk and dairy products was quite limited in the 1960s, with goat milk production primarily catering to domestic consumption and not holding a significant share in foreign trade. In 1961, imports and exports of goat's milk were negligible, and Türkiye's trade in this area was focused on local needs (Çatalbaş, 2022). In 2022, goat's milk accounts for 2.5% of Türkiye's total raw milk production, i.e., around 539,087 tonnes (TÜİK, 2022). Despite the limited data on global goat milk production, Yüksel and Yüksel (2022) reported that Türkiye accounted for 2.69% of global goat milk production in 2016. This ratio shows that Türkiye has a significant share in the world production of goat milk.

Milk Consumption per Capita

The table below, which assumes no waste or spoilage and only human consumption, calculates the per capita consumption of milk by adding the values of total milk production, imported milk and milk products converted into milk, and exported milk and milk products converted into milk.

Table 1. 10-year average annual per capita milk consumption in Türkiye (l) *(Calculations from FAOSTAT)*

Races	**1961-1970**	**1971-1980**	**1981-1990**	**1991-2000**	**2001-2010**	**2011-2020**	**2021-2022**
Buffalo	9.06	6.94	4.56	1.93	0.59	0.76	0.63
Cattle	173.65	166.14	157.63	150.14	147.80	223.12	242.70
Sheep	25.35	25.02	22.80	15.74	10.98	14.83	13.00
Goat	16.26	11.94	7.82	4.66	3.46	5.96	6.84
Total	224.33	210.04	192.80	172.46	162.83	244.68	263.17

According to the 1961–1970 average, annual per capita consumption of buffalo milk decreased from 9.06 l in the 1970s to 6.94 l in the 1970s, 4.54 l in the 1980s, 1.93 l in the 1990s, 0.59 l in the 2000s, 0.76 l in the 2010s, and 0.63 l in 2021–2022. In parallel with the decline in the number of water buffaloes in Turkey during the period 1970–2010, Özdemir and Uzundumlu (2024) reported that while the number of water buffaloes in the world increased by 80.9% during this period, the number of water buffaloes in Turkey decreased from 1,178,000 to 87,207. This situation caused Türkiye's share of the world buffalo population to fall from 1.1% to 0.05%. However, between 2008 and 2020, the number of water buffaloes in intensive production farms established with government incentives increased by 127.3%, moving Türkiye to 10th place in world water buffalo milk production. According to the 1961–1970 average, annual per capita consumption of cow's milk increased from 173.65 l in the 1970s to 166.14 l in the 1970s, 157.63 l in the 1980s, 150.14 l in the 1990s, 147.80 l in the 2000s, and 223.12 l in the 2010s with the implementation of the School Milk Program in schools. The school milk program's introduction aimed to enhance children's milk consumption habits and promote a balanced diet. This program has led to a significant increase in milk consumption, in particular (Yalçın et al., 2015). The average for 2021–2022 will be 242.70 liters. Engindeniz et al. (2021) determined the annual per capita milk consumption as 37.43 l, yogurt consumption as 32.84 kg, and cheese consumption as 18.48 kg in İzmir province in 2020, while Karakaya and İnci (2020) determined the annual per capita milk consumption as 38.31 l in Bingöl province in 2018. Ağır et al. (2024). They determined the consumption of open and packaged milk per capita in Kahramanmaraş province as approximately 288 l. However, since Akbay and Tiryaki (2007) determined the annual per capita milk consumption as 32.5 l in 2006 for the same province, Ağır et al. (2024) may have used this value as the equivalent of milk and its products.

According to the 1961–1970 average, annual sheep milk consumption per capita decreased from 25.35 l in the 1970s to 25.02 l in the 1970s, 22.80 l in the 1980s, 15.74 l in the 1990s, 10.98 l in the 2000s, 14.83 l in the 2010s, and 13 l in 2021–2022. Sheep's milk, known for its distinctive taste and smell, is not suitable for drinking due to its strong flavor. However, because of its high fat content, cheese, yogurt, casein, and butter production prefer it (Yerlikaya and Karagözlü, 2008).

According to the 1961–1970 average, annual per capita goat milk consumption decreased from 16.26 l in the 1970s to 11.94 l in the 1970s, 7.82 l in the 1980s, 4.66 l in the 1990s, and 3.46 l in the 2000s, while it increased to 5.96 l in the 2010s and 6.84 l in 2021–2022. According to Şirin et al. (2020), goat rearing in Türkiye is an animal production activity generally carried out in mountainous regions that cannot be used for other activities and the success of goat rearing in the Mediterranean and Southeast Anatolia regions in converting feed into milk compared to other animal production branches, the abundance of feed varieties they can consume, the ability to establish goat farms with little capital, high fertility, resistance to disease factors and adverse conditions, body and hoof structures suitable for grazing and mountain life, and superior utilisation of feed raw materials with high cellulose content compared to other species make it advantageous.

Protein from Milk Consumption per Capita

The table below shows the calculation of per capita milk consumption and the corresponding daily milk proteins, assuming no losses, the exclusion of spoilage and losses, and the inclusion of animal consumption.

Table 2. Milk protein consumption per capita per day in Türkiye (g) *(Calculations from FAOSTAT)*

Races	**1961-1970**	**1971-1980**	**1981-1990**	**1991-2000**	**2001-2010**	**2011-2020**	**2021-2022**
Buffalo	1.09	0.83	0.55	0.23	0.07	0.09	0.08
Cattle	16.27	15.57	14.77	14.07	13.85	20.91	22.74
Sheep	1.45	1.07	0.70	0.42	0.31	0.53	0.61
Goat	1.45	1.43	1.31	0.90	0.63	0.85	0.74
Total	20.26	18.90	17.32	15.62	14.86	22.38	24.17
81 percent of the total	16.41	15.31	14.03	12.65	12.03	18.13	19.58

At the end of six periods of 10 years each, starting in 1961–1970, milk consumption in Turkey increased by about 1.2 times, and correspondingly, the per capita protein from milk increased by about 1.2 times. According to the FAOSTAT statistics for Türkiye, humans consume about 81% of the protein from milk without wasting it.

According to the average of the years 1961-1970, when there was no waste and consumption was considered to be only by humans, 20.26 g of protein were provided by total milk consumption per capita, 18.90 g of protein in the 1970s, 17.32 g of protein in the 1980s, but in parallel with the decrease in milk consumption in the 1990s, 15.62 g of protein were provided as a decrease in the protein provided by milk, and after this period it increased to 14.86 g in the 2000s, 22.38 g in the 2010s and 24.17 g in 2021-2022. Milk provides 19.58 g of protein, with a ratio of 81%. In the 1960s, buffalo accounted for 5.4% of milk's protein, cattle contributed 80.4%, sheep contributed 7.1%, and goats contributed 7.1%. In the 2010s, buffalo milk accounted for 0.4%, cow milk for 93.42%, sheep milk for 2.36%, and goat milk for 3.79% of the protein obtained from milk. In 2021-2022, 0.4% of milk protein will come from buffalo, 94% from cattle, 2.5% from sheep and 3.10% from goats.

Conclusions and Recommendations

Milk has an important place in the human diet as a high-quality source of protein. Therefore, the aim of this study was to calculate the per capita consumption of buffalo, cattle, sheep, and goat milk and protein intake in Türkiye for 10-year periods. We used milk production, exports, and imports in Türkiye for the years 1961-2022 from FAOSTAT and year-by-year population data to achieve this goal.

Therefore, the annual per capita consumption of buffalo milk will decrease from 9.06 liters in the 1961-1970 average to 0.63 liters in 2021-2022, while the consumption of cow's milk will increase from 173.65 liters to 242.70 liters during the same period. Sheep milk fell from 25.35 liters to 13 liters, and goat milk from 16.26 liters to 6.84 liters over the same period. In the 1960s, 5.4 percent of the protein from milk came from buffalo milk, 80.4 percent from cow's milk, 7.1 percent from sheep's milk, and 7.1 percent from goat's milk.

In the 2010s, buffalo milk accounted for 0.4%, cow milk for 93.42%, sheep milk for 2.36%, and goat milk for 3.79% of the protein obtained from milk. In 2021-2022, 0.4% of milk protein will come from buffalo, 94% from cattle, 2.5% from sheep, and 3.10% from goats. Per capita milk consumption peaked at 20.26 grams of protein in the 1960s. During this period, milk consumption was an important source of nutrition due to the large rural population and widespread local production. By the 1970s, it had fallen to 18.90 grams. The decrease in milk consumption due to economic crises and urbanization may have contributed to this decline. In the 1980s, the amount of protein per capita fell to 17.32 grams. During this period, changes in the global economy, reforms in agricultural policies, and increases in import-based consumption may be among the factors influencing milk consumption. In the 1990s, the amount of protein from milk consumption fell to 15.62 grams. Increasing urbanization, a shift away from rural production, and changing consumer preferences can explain this. In the 2000s, the amount of protein per capita fell to its lowest level of 14.86 grams. This is due to a general decline in milk consumption and increased consumption of processed foods. The consumption of milk increased to 22.38 grams in the 2010s. Initiatives such as the 'School Milk Programme,' aimed at promoting milk consumption, raising health awareness, and launching campaigns, have effectively contributed to this increase. In the 2020s, the amount of protein per capita reached its highest level in recent years at 24.17 grams. The rise of healthy eating trends, increased consumption of dairy products, and supportive agricultural policies are the main reasons for this increase. Agricultural policies, economic conditions, and societal dietary habits closely influence the fluctuations in per capita milk consumption's protein content. Increased awareness of milk consumption and the development of better production and distribution systems can explain the recent increase in protein. However, in order to make the increase in these figures sustainable, it is important to continue policies that encourage milk production and consumption.

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Investigation of the Possibilities of Using Some Essential Oils in Controlling Plant Pathogens That Cause Storage Diseases

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ABSTRACT: In this study, the usability of essential oils obtained from some wild and cultivated medicinal and aromatic plants (lavender, thyme, mint, thyme etc.) in the control against fungal and bacterial pathogens that cause significant losses in storages was investigated. Plants growing naturally and/or wild in Erzurum province and its districts were collected and brought to the laboratory under appropriate conditions. After the plants were dried in the shade, they were ground and their essential oils were obtained using a clavenger device. In order to obtain pathogenic organisms to be used in the study, diseased fruits and vegetables were collected from markets, greengrocers and storages and brought to the laboratory under appropriate conditions. As a result of the isolations made from these diseased samples, 77 fungal isolates and 48 bacterial strains were obtained. As a result of pathogenicity tests performed on fungal isolates in their own hosts, it was observed that 42 isolates gave positive results, and as a result of pathogenicity tests performed on bacterial strains in their own hosts, 10 strains gave positive results. The essential oils obtained from the collected plants were tested against pathogenic bacterial strains in in vitro conditions. According to the results obtained, the highest inhibition zone of Satureja hortensis essential oil against EEB-40 bacterial strain was 59 mm and the lowest inhibition zone was 0 mm, meaning that different essential oil applications were ineffective against different pathogen strains. When compared with the control, it was determined that the antimicrobial effects of *Satureja hortensis*, *Satureja montana* and *Thymus sipyleus* essential oils were significant. In the study, after antimicrobial tests against fungal isolates were also performed, in vivo trials of effective essential oils will be conducted. The phytotoxic effects of highly effective essential oils will be determined and the potential of using essential oils without any toxic effects as an alternative to the chemical drugs used will be investigated.

Keywords: Essential Oil, Antimicrobial Activity, *Satureja spp*.

INTRODUCTION

In the world and in our country, essential oils obtained from various medicinal and aromatic plants have been used against fungal and bacterial disease agents seen after harvest. These studies have investigated the antifungal and antibacterial properties of essential oils against plant pathogens.

In the study conducted by Camele et al. (2012), essential oils obtained from *Verbena officinalis*, *Thymus vulgaris* and *Origanum vulgare* plants were tested in vitro against plant pathogens *Botrytis cinerea*, *Penicillium italicum*, *P. expansum*, *Phytophthora citrophthora* and

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* This study was prepared from a part of the project titled 'The Possibilities of Using Essential Oils in Biological Control Against Pathogens in Some Vegetables and Fruits in Warehouses' by Emre ERDEN, a graduate student.

* This study is supported by the project numbered FDK-2023-12771 by Atatürk University Scientific Research Projects Coordination Office (BAP).

Rhizopus stolonifer. As a result of the studies, very strong results were obtained depending on the metabolites contained in the essential oils.

In another study, the antifungal effects of 21 essential oils against some fungal pathogens were examined. In this study, the most effective results against *Botrytis cinerea*, *Aspergillus niger* and *Rhizopus stolonifer* were obtained from blue mountain sage oil and lemon grass oil (Surapuram, 2014).

In a study conducted by Dadaşoglu, the antibacterial effect of *Ferula communis* essential oil and extracts against 18 bacterial isolates was examined. As a result of the study, the highest inhibition zone was determined as 14 mm and the lowest inhibition zone as 10 mm (Dadaşoğlu, 2016).

In another study, essential oils obtained from *Satureja* species were applied against bacterial pathogens that cause diseases in beans and their antibacterial effect was determined. As a result of the studies, it was determined that the antimicrobial properties of essential oils obtained from Satureja species differed among different species of the same genus. It was determined that the most effective result against *Pseudomonas syringae* pv. *syringae* was obtained from *Saturaje spicigera* essential oil with an inhibition zone of 18.05 mm (Dönmez, 2020). In a study the antifungal effect of rosemary essential oil against *Alternaria brassicicola* was investigated. As a result of the experiments, a strong antifungal effect was obtained at concentrations of 80 µl/20ml PDA and above in in vitro conditions (Aydın and Altın 2022).

Material and Method

Collection of Diseased Plants and Bringing to the Laboratory

For the research, samples showing disease symptoms from different vegetables and fruits (tomato, carrot, radish, banana, melon, onion) will be collected, each will be labeled separately and brought to the laboratory in polyethylene bags.

Isolation and Stocking of Bacterial and Fungal Pathogens

Fungal and bacterial pathogens will be isolated from the plant samples brought to the laboratory and then purified and stored in stock media (Klement et. al. 1967; Lelliot et al. 1987).

Pathogenicity Test

Pathogenicity tests will be performed on the bacterial and fungal agents obtained as a result of the isolations and pathogens will be determined. Re-isolation will be performed from the parts where disease symptoms are seen to determine whether the pathogen used is present (Schaad et al. 2001).

Method of Obtaining Essential Oils

The essential oils of plant samples dried in the shade are isolated by hydrodistillation using a clevenger apparatus. The obtained essential oils are extracted with chloroform and purified from water with anhydrous sodium sulfate.

Determination of Antimicrobial Activities of Plant Essential Oils

The most reported properties of essential oils are their antimicrobial properties, and the tests that reveal these properties are not subject to a certain standardization and can be performed in appropriate laboratories. Generally used techniques; Agar diffusion, Broth-dilution method and Disk diffusion method in this study, the disk diffusion method was used.

Results and Discussion

As a result of the isolations made from these diseased samples, 77 fungal isolates and 48 bacterial strains were obtained. As a result of pathogenicity tests performed on fungal isolates in their own hosts, it was observed that 42 isolates gave positive results, and as a result of pathogenicity tests performed on bacterial strains in their own hosts, 10 strains gave positive results.

Table1. Antimicrobial test results of some essential oils against pathogens

Strain No	Control	***Mentha longifolia***	***Ferula orientalis***	***Prangos ferulacea***	***Lavandula* sp.**	***Thymus sipyleus***	***Saturaje hostensis***	***Saturaje montana***
EEB-12	0 mm	19 mm	23 mm	14 mm	13 mm	44 mm	34 mm	37 mm
EEB-20	0 mm	0 mm	0 mm	0 mm	11 mm	23 mm	21 mm	19 mm
EEB-22	0 mm	0 mm	0 mm	0 mm	12 mm	58 mm	46 mm	38 mm
EEB-23	12 mm	11 mm	11 mm	11 mm	10 mm	34 mm	31 mm	28 mm
EEB-27	0 mm	0 mm	0 mm	0 mm	0 mm	15 mm	14 mm	12 mm
EEB-28	0 mm	0 mm	0 mm	0 mm	0 mm	15 mm	13 mm	12 mm
EEB-38	0 mm	0 mm	0 mm	0 mm	0 mm	11 mm	0 mm	0 mm
EEB-39	0 mm	0 mm	0 mm	0 mm	12 mm	16 mm	21 mm	23 mm
EEB-40	0 mm	0 mm	0 mm	0 mm	0 mm	18 mm	59 mm	21 mm

The results obtained from the antimicrobial tests are given in Table 1. According to the results obtained, the highest inhibition zone of *Satureja hortensis* essential oil against bacterial isolate EEB-40 was 59 mm and the lowest inhibition zone was 0 mm, meaning that different essential oil applications were ineffective against different pathogenic isolates. When compared with the control, it is seen that the antimicrobial effects of *Satureja hortensis*, *Satureja montana* and *Thymus sipyleus* essential oils are especially significant. According to literature research, it is known that the essential oils obtained from the above 3 plants have antimicrobial properties against many pathogens that cause plant diseases both in the world and in Turkey (Ballester-Costa et.al. 2013; Dönmez et al. 2022; Bozkurt et.al. 2020).

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International Conference on
Food, Agriculture and Animal Sciences
19-22 December 2024, Erzurum, TÜRKİYE

Econometric Analysis of Dynamic Relationships Between Agricultural Inputs, Producer and Consumer Prices and Policy Projections in Türkiye

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ABSTRACT: There is a strong relationship between agricultural input prices, producer and consumer price indices of agricultural products, and these interactions are of critical importance in terms of economic stability and price policies. In this study, the dynamic relationships between Agricultural Input Price Index (NPI), Consumer Price Index (CPI) and Producer Price Index of Agricultural Products (CPI) in Turkey were analyzed using monthly data for the period 2015-2024. Within the scope of the analysis, the stationarity of the variables was evaluated with the Augmented Dickey-Fuller (ADF) test, and then the Vector Autoregression (VAR) model was established. Causality relationships between variables were examined with the Granger Causality Test, and Impulse Response Function (IRF) was applied to analyze the effects of shocks over time. In addition, Variance Decomposition analysis was performed to evaluate the factors caused by the variances of the variables.

The results show that TGFE has a strong long-term effect on both CPI and CPI. While the effect of CPI on TGFE is positive and increases over time, the effect of CPI on TGFE is fluctuating in the short term and positive in the long term. However, it has been observed that the effect of CPI on CPI is limited and consumer prices do not directly determine producer costs. It has been established that TGFE is the main determinant of agricultural costs and drives both producer and consumer prices. These findings reveal that the management of agricultural costs is critical in achieving both producer and consumer price stability. The study offers suggestions for the development of cost control and support policies for agricultural inputs.

Keywords: Agricultural Input Prices, CPI, Econometric Analysis, Granger Causality, Impulse Response Function

INTRODUCTION

The food and agriculture sector is strategically important for economic growth and social welfare. The sustainability of agricultural production can be ensured not only by the conservation of natural resources, but also by balanced relations between producers, consumers and input markets. In developing countries such as Turkey, price movements in these markets and the interactions between these prices play a critical role in increasing the effectiveness of agricultural policies and in the management of economic fluctuations (Schnepf, 2008; Timmer, 2009).

Agricultural input prices (e.g., fertilizer, energy and seed prices) are one of the most important determinants of production costs, while producer prices are among the main factors affecting the income level of farmers and consumer prices are among the main factors affecting household food security and welfare. The dynamic relationships and interaction mechanisms between these three price groups have a direct impact on the overall performance of the agricultural sector and the success of policy decisions (Gardebroek and Hernandez, 2013). In particular, price pass-through mechanisms are frequently emphasized in the literature in terms of agricultural production and market equilibrium (Mundlak and Larson, 1992; Azzam and Schroeter, 1995).

In this study, the short and long-term relationships between agricultural input, producer and consumer prices in Turkey were examined using Granger causality test and VAR (Vector Autoregression) models. Although there are many studies in the literature that deal with the transitivity and causality relationships between agricultural prices, there are very few studies that analyze the dynamics between these three price groups with a holistic perspective in Turkey (Yavuz and Aksoy, 2009; Özer and Yıldız, 2021). For example, Yavuz and Aksoy (2009) discussed the transitivity between agricultural producer and consumer prices in Turkey, but did not examine the relationship with input prices in detail. Özer and Yıldız (2021), on the other hand, analyzed the producer-consumer price relationship from the perspective of causality, but the scope and method used in the study necessitate a broader framework for agricultural markets in Turkey.

The Granger causality test has been used as a powerful tool to identify directional interactions between prices and to reveal which price group influences others. This method offers effective results especially in the analysis of short-term causal relationships. The VAR model, on the other hand, modeled the dynamic structure of multivariate time series data and the simultaneous interactions between these variables, providing a basis for prospective simulations for the development of policy recommendations (Enders, 2014). Studies such as Götz, Qiu and Glauben (2013) and Erdoğan and Soytaş (2019) reveal how effective such methods are in understanding price dynamics in agricultural markets. However, the fact that these methods have been applied extensively in the context of Turkey points to a missing point in the literature.

The originality of this study stems from the fact that it deals with the effects of the interactions of agricultural prices in Turkey on both producer and consumer welfare in a single framework and empirically determines the direction of price pass-through. While existing studies in the literature generally focus only on producer or consumer prices, this research aims to contribute to the academic literature and produce applicable results in the context of agricultural policies by presenting a holistic analysis of the interactions between these three price groups.

In conclusion, this study takes an important step towards understanding the relationships between agricultural inputs, producer and consumer prices in Turkey and develops strategic recommendations that can guide agricultural sector policies. In this context, the findings are expected to serve as a guide for decision-makers on key issues such as food price stability, producer income security and consumer welfare.

Material and Method

Material

This study was conducted to analyze the relationships between Agricultural Input Price Index (NPI), Consumer Price Index (CPI) and Producer Price Index of Agricultural Products (CPI) in Turkey. The data cover the period of January 2015 - September 2024 and were obtained from the Turkish Statistical Institute (TurkStat) on a monthly basis. The variables used in the study were defined as follows:

- **TGFE:** It reflects the price movements of agricultural inputs.
- **CPI:** It refers to changes in the general consumer price level.
- **CPI:** It reflects the prices applied to the products of agricultural producers.

Methods

In this study, time series econometrics methods were used to examine the relationships between agricultural inputs, producer and consumer prices in Turkey. The methods used in the research were structured on the basis of approaches that are accepted in the literature and frequently used in similar analyzes.

Unit Root Test

In time series analysis, the stationarity of the variables is critical for the validity of the results obtained (Enders, 2014). Therefore, the stationary status of each variable was analyzed by the Augmented Dickey-Fuller (ADF) test. The ADF test is based on the following hypotheses:

H_0 (Null Hypothesis): The time series is not stationary (there is a unit root).

H_1 (Alternative Hypothesis): The time series is stationary (there is no unit root).

According to the results of the ADF test, the first difference operation (Δ\Delta) was applied to the non-stationary series and the series were made stationary. In the literature, similar studies emphasize the importance of unit root tests in the stationarity analysis of agricultural price series (Maddala and Kim, 1998; Gujarati, 2003).

VAR Model

The Vector Autoregression (VAR) model was used to analyze the dynamic relationships between the stationary series. The VAR model is recognized as an effective method for studying the concurrent relationships between variables in multivariate time series (Sims, 1980). The appropriate latency length of the model was determined using information criteria such as Akaike Information Criterion (AIC) and Schwarz Criterion (SC). The VAR model served as a basis for the Granger Causality Test, Impulse Response Function (IRF) and Variance Decomposition analyses. In the literature, it is seen that the VAR model is used effectively especially in determining price relations between agricultural markets (Götz, Qiu and Glauben, 2013; Erdoğan and Soytaş, 2019).

Granger Causality Test

Causality relationships between variables based on the VAR model were analyzed with the Granger Causality Test. The Granger Causality Test is a statistical method for determining whether one variable has a causal effect on another variable (Granger, 1969). The test is based on the following hypotheses:

H_0: The independent variable does not have Granger causality over the dependent variable.

H_1: The independent variable has Granger causality over the dependent variable.

The obtained p-values ($p<0.05p < 0.05$) showed whether there was a significant causality relationship between the variables. In the literature, the Granger Causality Test is widely used, especially in the analysis of agricultural prices and market integration (Yavuz and Aksoy, 2009; Özer and Yıldız, 2021).

Impulse Response Function (IRF)

IRF analysis has been used to examine the effects of a standard shock to one variable on other variables over time. The IRF is an important tool for visualizing the size and duration of the impact of shocks (Lütkepohl, 2005). In this study, the effect of shocks applied to each variable was analyzed over a 10-period horizon. In the literature, it is seen that IRF analysis is often preferred to understand the effects of price movements over time in agricultural markets (Gardebroek and Hernandez, 2013).

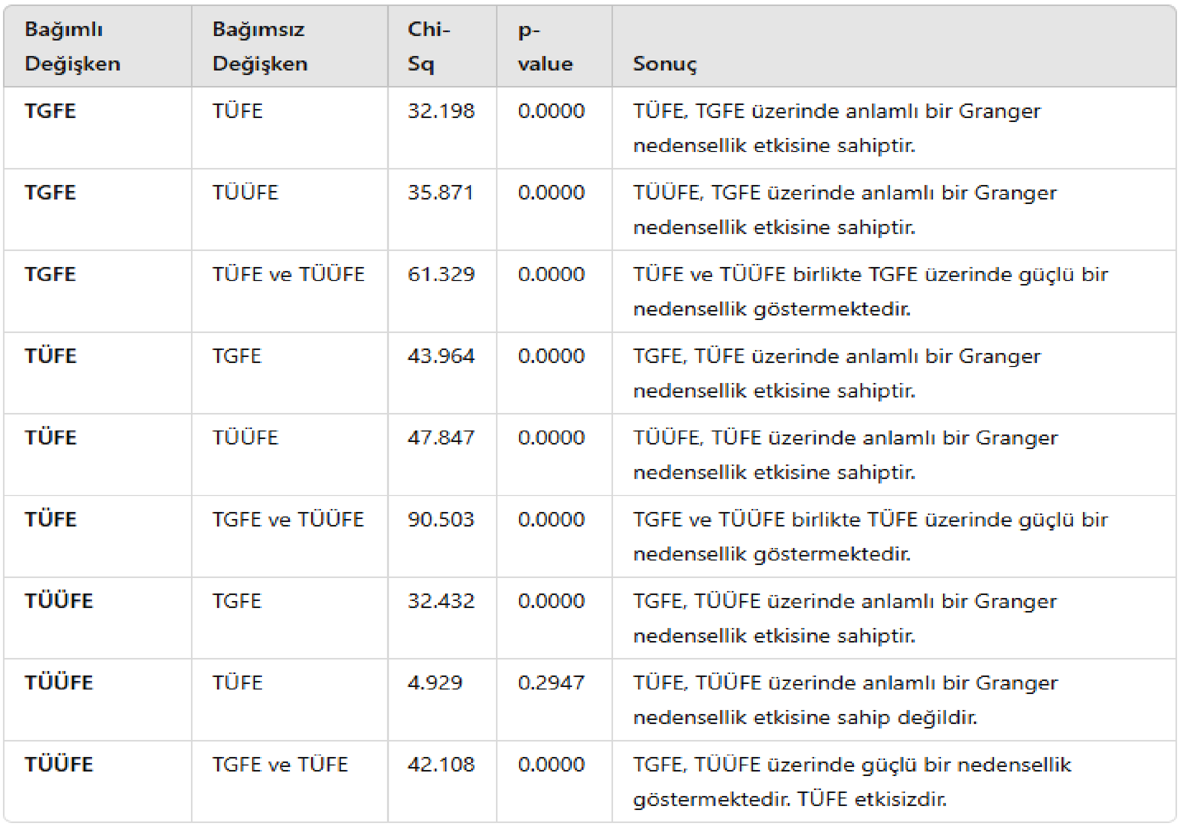
Variance Decomposition

Variance Decomposition analysis was performed to determine how much of the variances of the variables are due to their own dynamics and other variables. This analysis provides valuable information in terms of assessing the relative importance of the relationship and interactions between variables (Enders, 2014). The analysis evaluated the interactions between variables over a 10-period period. It has been stated in the literature that the Variance Decomposition method is an effective tool for understanding the complex structure of agricultural markets (Mundlak and Larson, 1992; Götz, Qiu, & Glauben, 2013).

Results

Table 1 examines the dynamic relationships between the agricultural input price index (NPI), the consumer price index (CPI) and the producer price index of agricultural products (CPI). The results show that TGFE has a strong causality effect on both CPI and CPI. This situation reveals that cost increases in agricultural inputs play a critical role in determining producer and consumer prices.

Table 1. Granger Causality Test Results



Bağımlı Değişken	Bağımsız Değişken	Chi-Sq	p-value	Sonuç
TGFE	TÜFE	32.198	0.0000	TÜFE, TGFE üzerinde anlamlı bir Granger nedensellik etkisine sahiptir.
TGFE	TÜÜFE	35.871	0.0000	TÜÜFE, TGFE üzerinde anlamlı bir Granger nedensellik etkisine sahiptir.
TGFE	TÜFE ve TÜÜFE	61.329	0.0000	TÜFE ve TÜÜFE birlikte TGFE üzerinde güçlü bir nedensellik göstermektedir.
TÜFE	TGFE	43.964	0.0000	TGFE, TÜFE üzerinde anlamlı bir Granger nedensellik etkisine sahiptir.
TÜFE	TÜÜFE	47.847	0.0000	TÜÜFE, TÜFE üzerinde anlamlı bir Granger nedensellik etkisine sahiptir.
TÜFE	TGFE ve TÜÜFE	90.503	0.0000	TGFE ve TÜÜFE birlikte TÜFE üzerinde güçlü bir nedensellik göstermektedir.
TÜÜFE	TGFE	32.432	0.0000	TGFE, TÜÜFE üzerinde anlamlı bir Granger nedensellik etkisine sahiptir.
TÜÜFE	TÜFE	4.929	0.2947	TÜFE, TÜÜFE üzerinde anlamlı bir Granger nedensellik etkisine sahip değildir.
TÜÜFE	TGFE ve TÜFE	42.108	0.0000	TGFE, TÜÜFE üzerinde güçlü bir nedensellik göstermektedir. TÜFE etkisizdir.

The increase in NPI is affected by both consumer prices (CPI) and producer prices (CPI). This shows that agricultural inputs directly increase production costs, reflecting on both the producer and the consumer. NPI stands out as one of the most important determinants of consumer prices (CPI) and creates a strong causality effect on the CPI.

The effect of CPI on TGFE and CPI is limited. Consumer prices cannot directly affect producer prices, but they can play an indirect role. The fact that the effect of CPI on CPI is not statistically significant shows that producer prices are more sensitive to agricultural inputs. On the other hand, CPI plays a role in shaping production costs with a significant effect on GDP.

In general, NPI (agricultural input prices) is the main determinant influencing both consumer and producer prices. Increases in agricultural input costs lead to higher consumer prices and increased costs of production processes. The management of agricultural inputs and keeping their costs under control can be an important policy tool in ensuring price stability.

These findings highlight the need to develop strategic policies for the agricultural sector to better understand the effects of agricultural costs and achieve price stability. The implementation of support mechanisms to make agricultural producer prices more predictable will be beneficial for both producers and consumers.

Figure 1. According to the Impulse Response Function (IRF) analysis, the dynamic relationships between the agricultural input price index (NPI), the consumer price index (CPI) and the producer price index of agricultural products (CPI) reveal the mechanisms that strongly affect each other in the economic system. While shocks in the CPI have a positive and strong effect on the CPI, it is seen that this effect increases over time and becomes evident in the long term. On the other hand, the effect of FDFE on CPI fluctuates in the short term and shows a positive trend in the long term. This suggests that increases in agricultural input costs directly affect both consumer prices and producer prices. Shocks in the CPI, on the other hand, have a positive effect on the CPI, while their effect on the CPI is limited; This shows that consumer prices indirectly affect agricultural production costs. While shocks to the CPI had a negative effect on the CPI in the short term, it was observed that this effect turned positive in the long term and the effect on the CPI was quite limited. Overall, the strong influence of CPI on CPI and CPI reveals that agricultural inputs are a critical factor driving consumer and producer prices, while the effects of CPI are more limited and time-bound. These results highlight the role of agricultural cost management on price stability.

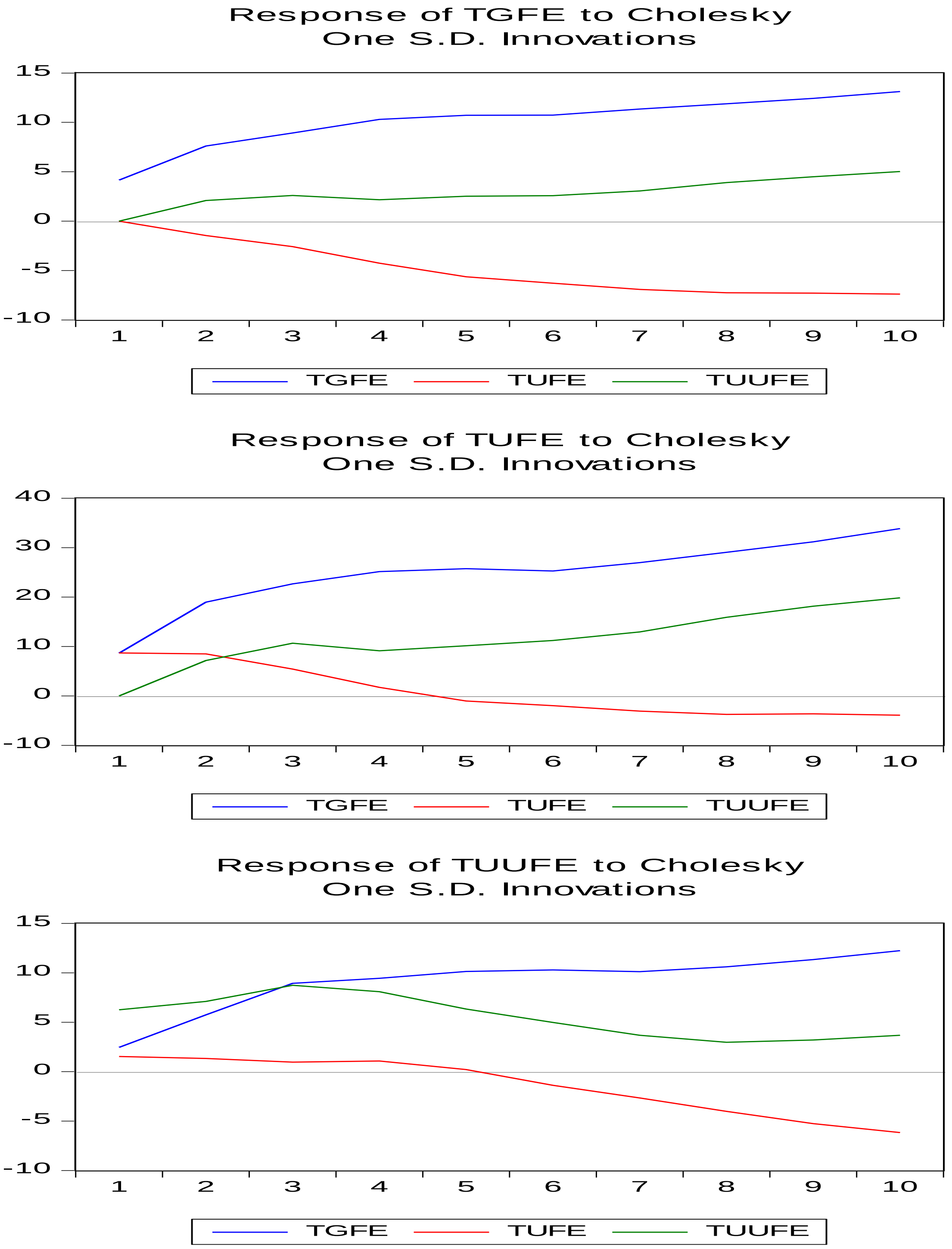


Figure 1. Dynamic Relationships of Short and Long Term Shocks Between NPI (Agricultural Input Price Index), CPI (Consumer Price Index) and CPI (Producer Price Index of Agricultural Products)

Variance Decomposition analysis shows how much the variances of FDI (Agricultural Input Price Index), CPI (Consumer Price Index) and CPI (Producer Price Index of Agricultural Products) variables are affected by their internal dynamics and other variables. Although the variance of the CPI is largely affected by its own historical values, the effect of the CPI increases over time and becomes an important explanatory. However, the effect of the CPI on the TGFE has been quite weak.

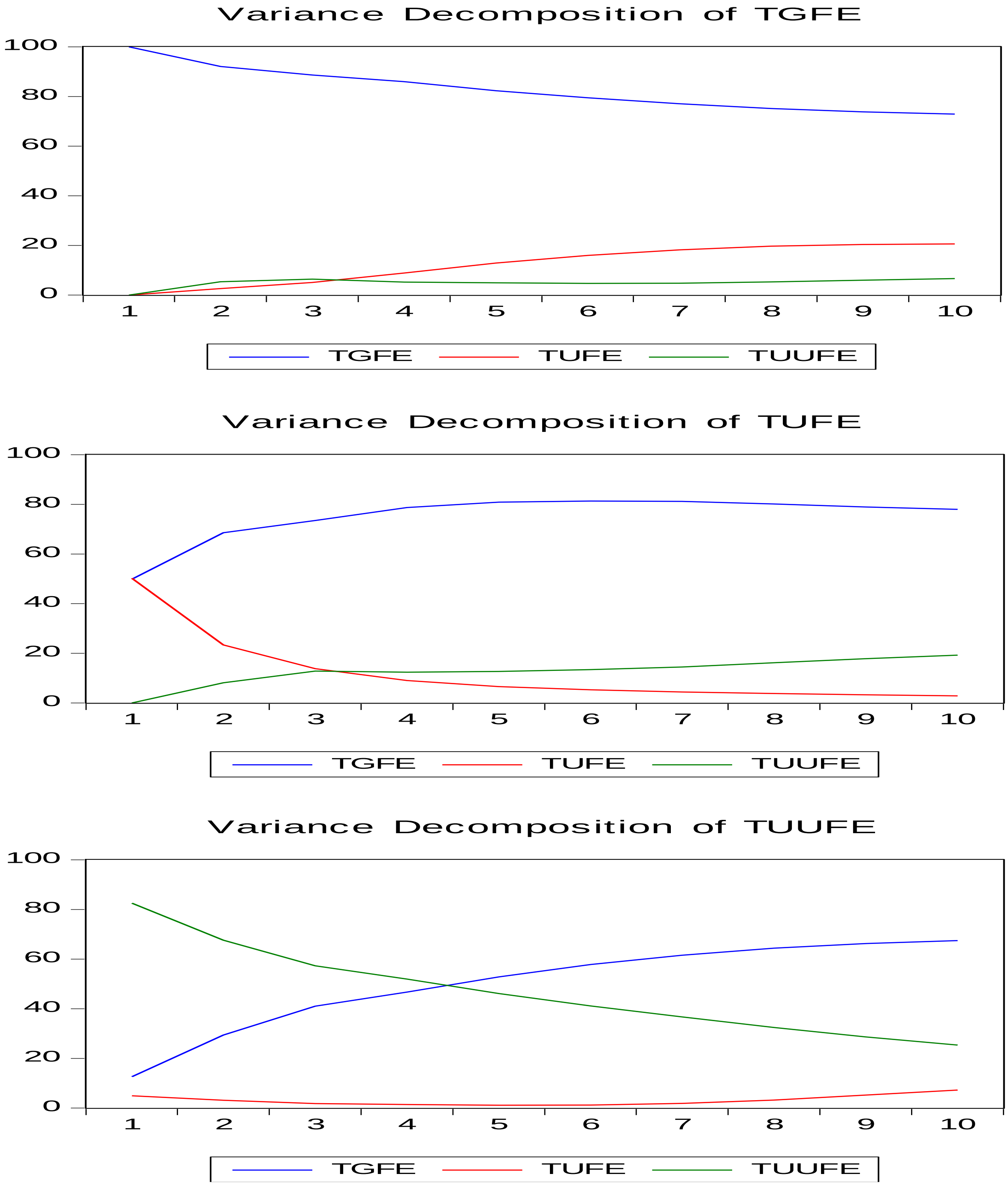


Figure 2. "Variance Decomposition of TGFE, CPI, and CPI: Analyzing the Contribution of Internal Dynamics and Cross-Variable Effects

In the CPI variance, NPI stands out as the strongest explanatory variable, and although the effect of CPI is strong at the beginning, it decreases over time. The historical values of the CPI itself, on the other hand, are becoming less and less effective in explaining the variance. While the effect of TGFE on CPI variance increases over time and becomes the strongest explanatory, although the internal dynamics of CPI are dominant at the beginning, its effect decreases over time. The effect of CPI on CPI is very limited and negligible. Overall, TGFE is an important explanatory on both CPI and CPI in the long run, and agricultural inputs are understood to have a strong impact on consumer prices. Although CPI has an impact on CPI, its effect on CPI remains limited; This situation shows that the cost and price dynamics of agricultural producers operate differently. The limited effect of CPI on NPI and CPI reveals that consumer prices are not a direct determinant of agricultural costs and producer prices.

Discussion

This study comprehensively examines the effects of agricultural input prices (CPI) on consumer prices (CPI) and producer prices of agricultural products (CPI) in Turkey. The findings show that agricultural input prices play a decisive role on producer and consumer prices, and this effect is significant both in the short term and in the long term. In the literature, various dimensions of this relationship have been discussed with different approaches and the findings of this study have been evaluated in accordance with the previous literature. According to the results of the Granger Causality Test, there is a statistically significant causality relationship of TGFE on CPI and CPI. This situation shows that agricultural input prices directly affect producer and consumer prices. Similar results were highlighted in a study by Ertürk and Kara (2021). In this study, it was stated that cost changes in the agricultural sector have long-term effects on the general inflation rate. In addition, Kara and Özkan (2020) revealed that increases in agricultural costs lead to price imbalances for both producers and consumers, and this effect is especially felt in food prices. In this context, the finding that the effect of CPI on FDI is more limited and that CPI has negative effects on FDI in the short term and positive effects on GDP in the long term coincides with the studies by Aydın and Demir (2019) on the external dependence of the agricultural sector and the effects of cost increases on its internal dynamics. This finding reveals that agricultural production processes have a dynamic structure and pricing mechanisms can change depending on time.

Impulse Response Function (IRF) Analysis results are similar to the literature. It shows that a shock in the CPI has positive and increasing effects on the CPI and CPI. This situation was also expressed in the study conducted by Topaloğlu and Şahin (2020), and it was stated that increases in input costs created an inflationary pressure on consumer prices. The finding that increases in NPI have significant effects on CPI in the medium and long term shows that inputs in the agricultural production process are a cost item that is directly reflected to the consumer. In addition, the finding that shocks in CPI have negative effects on NPI in the short term and positive effects in the long term is consistent with the study conducted by Yılmaz and

Gürkan (2023), showing that the effect of changes in producer prices on agricultural input costs generally occurs with a certain lag. Variance Decomposition analyses show that the FDI variance is largely due to its internal dynamics, but the effect of the CPI increases over time. Similarly, Çelik and Arslan (2022) stated that internal dynamics are strong in the agricultural sector, but external factors (e.g., exchange rate fluctuations and international prices of agricultural products) increase their impact over time, especially in the price formation of agricultural products. This study emphasizes that the FDI variance is largely due to its internal dynamics, but changes in producer prices over time may affect these dynamics. In this context, the results of the study coincide with the results of similar studies in the literature.

Conclusion and Recommendations

This study analyzes the dynamic relationships between Agricultural Input Price Index (CPI), Consumer Price Index (CPI) and Producer Price Index of Agricultural Products (CPI) in Turkey and reveals the importance of these variables on the economy. The analysis results show that TGFE has a strong and long-term effect on both CPI and CPI. The direct reflection of the changes in the NPI on consumer and producer prices emphasizes the importance of agricultural costs in terms of overall economic stability.

While the CPI expresses the general level of consumer expenditures, it is a basic indicator in terms of measuring and managing inflation. CPI, on the other hand, plays a critical role in terms of sustainability of agricultural production and price policies by reflecting producer costs in the agricultural sector. TGFE stands out as a key factor driving these two variables and affects the entire economic cycle, from agricultural production processes to consumer prices.

Based on the results of this analysis, the following policy recommendations have been developed to control agricultural costs, support producer incomes and manage consumer prices:

Reducing Agricultural Input Costs

- Reducing VAT and SCT rates on agricultural inputs can alleviate the costs of producers.
- Reducing dependence on imports by encouraging local production can alleviate cost pressure on inputs.
- Infrastructure investments should be made to reduce the logistics costs of basic inputs such as fertilizers, seeds and pesticides.

Producer Support Programs

- Floor price practices and comprehensive agricultural insurance systems should be expanded to secure producers' incomes.
- Production efficiency can be supported by disseminating precision agriculture technologies and increasing R&D investments.

Managing Consumer Prices

- Effective subsidy mechanisms can be implemented to offset the reflection of food price increases on consumers.
- Market controls should be increased to prevent speculative price increases.

Policies for Climate and Environmental Factors

- It is important to modernize irrigation infrastructure and encourage the use of renewable energy against the effects of drought and climate change.
- By encouraging green agricultural practices, both costs can be reduced and environmental sustainability can be achieved.

Long-Term Planning and Data Management

- More stable monetary policies should be implemented to reduce the impact of exchange rate fluctuations on agricultural costs.
- Regional agricultural policies should be developed and strategies suitable for local dynamics should be adopted.
- Agricultural data monitoring and early warning systems should be established to predict price fluctuations in advance.

Opportunities for Future Studies

Although this study has enabled the relationships between TGFE, CPI and CPI to be analyzed from a broad perspective, it offers important opportunities for future studies. For example:

- The relationship between FDFE and exchange rate, energy prices and global agricultural commodity prices can be examined in more detail.
- The effectiveness of local agricultural policies can be increased by analyzing production and price movements at the regional level.

- At the micro level, the production costs and market adaptation capacities of agricultural enterprises can be evaluated.

The fact that TGFE, CPI and CPI are related to each other once again reveals the critical position of the agricultural sector in the general economic structure. The management of costs for agricultural inputs is an important tool that affects not only producer prices, but also consumer prices and overall economic stability. In this context, policies that improve cost management, increase production efficiency and ensure price stability will be the main strategies to both maintain current economic balances and seize future opportunities. The fact that the agricultural sector plays such an important role in Turkey necessitates more investment and policy development in terms of economic sustainability and social welfare.

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Statement of Conflict of Interest

The authors declare that they have no conflict of interest.

Authors' Contributions

Ferda Nur ÖZDEMIR designed and analyzed the research. Ferda Nur ÖZDEMIR and Adem AKSOY arranged the studies. Ferda Nur ÖZDEMIR worked on the preparation of pictures and tables. All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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The Future of Türkiye's Olive Oil Exports: Strategic Forecasts with The ARIMAModel for the Period 2023-2030

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ABSTRACT: This study examines olive oil export forecasts for 2023-2030 using the ARMA model. The analysis is based on data from 1961 to 2022, with estimations performed in EViews. The Augmented Dickey-Fuller (ADF) test confirmed stationarity, and model parameters were estimated using the maximum likelihood method. The results predict a gradual decline in exports, with quantities decreasing from 89,246.91 units in 2023 to 79,290.00 units in 2030, representing an 11.2% drop. The ARMA model demonstrated strong explanatory power, with an R^2 value of 0.893, and all parameters statistically significant. Diagnostic tests, including inverse roots of AR/MA polynomials and correlogram analysis, validated the model's reliability.

The findings underscore the need for strategic interventions to mitigate the projected decline. Key recommendations include enhancing quality standards, investing in branding and technology to improve productivity, and accessing new markets. These measures aim to increase competitiveness and sustainability in the olive oil sector. The study offers valuable insights for policymakers and highlights the importance of further research to incorporate additional factors influencing export performance and to test predictions with alternative econometric methods. This work provides a roadmap for strengthening Turkey's position in the global olive oil market.

Keywords: Olive Oil, Export, Forecast, ARIMAModel, Period 2023-2030

INTRODUCTION

Olive oil is a key component of Mediterranean cuisine and is of global importance for healthy lifestyles and sustainable agricultural practices. Olive oil production worldwide is particularly intensive in the Mediterranean basin countries and Turkey is a major player in this field. Turkey ranks third worldwide in olive oil production and has great potential both in terms of production and exports. Especially the favorable climatic conditions of the Aegean and Mediterranean regions have made Turkey a favorable country for olive oil production (Republic of Turkey Ministry of Agriculture and Forestry, 2023; Başar, 2021). However, many international studies on increasing Turkey's production capacity emphasize the need for Turkey to become a competitive player in the evolving global market of the olive oil sector (Gambella et al., 2017; Koutsou et al., 2020).

Olive oil production has an important place in Turkey's agricultural sector and the Aegean Region is the center of this production. Provinces such as Aydın, Muğla, İzmir and Balıkesir meet the majority of Turkey's olive oil production (Özdemir & Yıldız, 2019). The increase in olive oil production in Turkey is the result of olive groves becoming more productive and the use of modern production techniques. However, there are also some challenges in the sector. Climate change, environmental factors and increasing production costs are among the major obstacles faced by olive oil producers (Başar, 2021). In the international literature, there are several studies indicating that environmental threats related to olive oil production are increasing, especially in Mediterranean countries. For example, studies on how olive groves are affected by climate change factors such as extreme heat and drought show that these threats reduce production efficiency (Trujillo et al., 2020; Gounari et al., 2023).

Olive oil is an important product not only in the domestic market but also in world markets. Turkey's olive oil exports have increased in recent years and Turkish olive oil is particularly popular in countries such as Germany, the US, Italy and France (International Olive Council, 2023; Yılmaz, 2022). The quality standard of Turkish olive oil and its impact on consumer preferences are emphasized in many studies on international trade. It has been observed that olive oil consumers, especially in the European market, have an increasing demand for organic and quality products (Benassi et al., 2021). However, some challenges need to be overcome for Turkish olive oil to become more competitive in the global market. Branding deficiencies, quality-oriented production inadequacies and the need to modernize traditional production methods are among the factors limiting the growth of the sector (Kara & Arslan, 2022). Furthermore, research at the international level emphasizes that in order to increase the potential of Turkish olive oil for importing markets, local producers should turn to more efficient, sustainable and organic production methods (Baccouri et al., 2020).

Looking ahead, Turkey's olive oil sector is projected to have a greater growth potential. Demand in the world olive oil market is on the rise, particularly driven by increasing health awareness and trends such as the Mediterranean diet (Benassi et al., 2021). Turkey's olive oil exports are projected to increase significantly by 2030. According to the International Olive Council (IOC), Turkey's production capacity is expected to reach 500,000 tons by 2025 (International Olive Council, 2023). Turkey's olive oil exports are expected to increase in parallel with this growth, as demand for Turkish olive oil increases, especially in European and North American markets (Koutsou et al., 2020). In addition, organic and sustainable olive oil production methods coming to the forefront in line with the increasing demand creates an important opportunity for Turkey (Gambella et al., 2017).

Studies conducted at the international level reveal that Turkish olive oil needs to invest more in branding and quality in order to be more competitive in the global market. By 2030, it is estimated that the share of Turkish olive oil in the world olive oil market could be as high as 15% (Trujillo et al., 2020). This potential can be supported by increasing sustainability in olive oil production, improving production quality and developing branding strategies.

This study aims to examine the current status and future projections of Turkey's olive oil production and exports. The research will address Turkey's potential in the olive oil sector, the challenges it faces and strategic recommendations for the future of the sector. The first part of the study will present information on the geographical distribution of olive oil production and production techniques in Turkey, while the second part will discuss the current situation and future trends in olive oil exports. Furthermore, the role of sustainable agricultural practices in the sector and recommendations on improving export strategies will be made.

In conclusion, Turkey's great potential in olive oil production can be further developed with the right strategies and investments. This study aims to put forward the necessary steps for the olive oil sector to increase its competitiveness in the global market.

Material and Method

The econometric analysis in this study was conducted on olive oil export quantities between 1961 and 2022. The data were obtained from the Food and Agriculture Organization (FAO) database.

In the econometric analysis process, unit root tests were applied to evaluate the stationarity of the data series. The Box-Jenkins model assumes that time series are stationary. If a series is stationary, it has a constant mean, constant variance and constant autocorrelation. For this purpose, ADF (Augmented Dickey-Fuller) and PP (Phillips-Perron) unit root tests were used to test whether the data were stationary. The series were made stationary by applying the difference process for non-stationary series.

The ARIMA (AutoRegressive Integrated Moving Average) model was used for forecasting modeling for stationary data series. Future sheep meat production quantities were estimated using past values and error terms with the ARIMA model. While determining the model parameters, appropriate autoregressive (AR) and moving average (MA) lag lengths were selected with the help of information criteria such as Akaike Information Criterion (AIC) and Schwarz Information Criterion (BIC). The ARIMA (p, d, q) Box-Jenkins Model proposed by

Box and Jenkins is a widely used method for creating a univariate time series forecasting model (Mensah 2015).

Box-Jenkins modeling involves determining an appropriate ARIMA process, fitting it to the data, and then using the appropriate model for forecasting. An attractive feature of the Box-Jenkins forecasting approach is that ARIMA processes cover a rich class of models and generally provide sufficient explanations for the data (Hyndman 2001). According to Box and Jenkins (1976), a non-seasonal ARIMA model is represented by ARIMA (p, d, q) where d represents the difference, p represents the autoregressive coefficients and q represents the moving average coefficients (Dasyam et al. 2015). These values are determined using autocorrelation functions (ACF) and partial autocorrelation functions (PACF) and the Dickey Fuller (ADF) test (Awal and Siddique, 2011). The ACF and PACF shapes are used as tools to determine the stationarity of the variables and the lag length of the ARIMA model when estimating ARIMA models. The Dickey Fuller (ADF) test is applied to the non-stationarity case during the stationarity test. The PACF or partial correlogram is used to determine the appropriate number of lags for the AR model. The number of non-zero relationships in the PACF determines where the AR lags should be included. The ACF correlogram is used to determine the number of lags for the MA model; Here too, non-zero relationships indicate where lags should be included.

An AR model function is as follows:

$$Yt = c + \phi\ 1\ Yt\text{-}1 + \phi\ 2\ Yt\text{-}2 + \ldots + \phi\ p\ Yt\text{-}p + \varepsilon_t$$

Here, Yt is the value of the time series at time t, c is a constant, $\phi1$, $\phi2$,...,ϕp are autoregressive parameters, and εt is the white noise error term.

Integrated (I) Component:

The integrated component involves differencing the time series to achieve stationarity. The order of differencing is denoted by d, and the integrated component is represented by:

$$Yt' = Yt - Yt - 1$$

The MA model function is:

The moving average component involves modeling the relationship between the current value of the time series and past forecast errors. The MA(q) component is represented by:

$$Yt = \mu + \theta 1 \varepsilon t - 1 + \theta 2 \varepsilon t - 2 + \ldots + \theta q \varepsilon t - q + \varepsilon t$$

Here, μ is the mean of the time series, $\theta 1$, $\theta 2$,...,θq are moving average parameters, and εt is the current error term.

Generally, the ARIMA model is as follows:

$$\Delta d\ Zt = c + (\O 1\ \Delta d\ Zt-1 + \ldots + \O p\ \Delta d\ Zt-p) - (\theta 1\ \varepsilon_t -1 + \ldots + \theta q\ \varepsilon_t -q) + \varepsilon_t$$

Here, Δ denotes the difference as shown below: Zt-1, Zt-p, are the values of the past series with delays of 1, p, respectively.

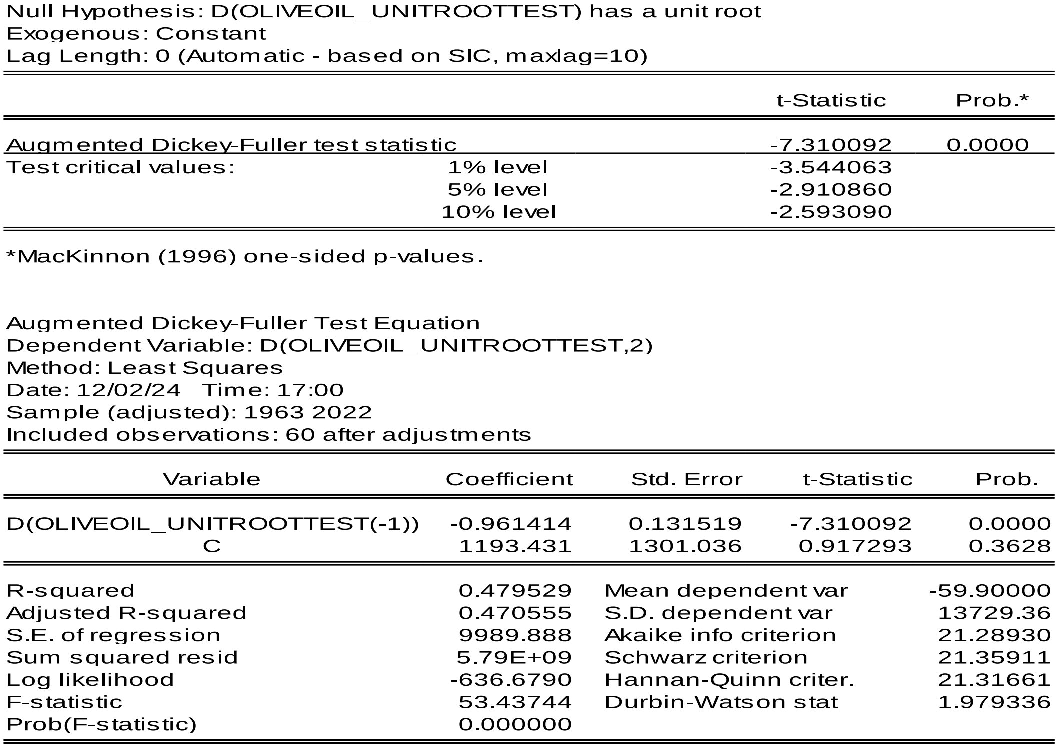
$$\Delta\ Zt = Zt - Zt-1$$

$$\Delta 2\ Zt-1 = \Delta Zt - \Delta Zt-1$$

Results and Discussion

The results of the Extended Dickey-Fuller (ADF) test applied to test the stationarity of the olive oil price series reveal that the series does not contain a unit root. The test statistic value is -7.310092, which is greater in absolute value than the critical value (-3.544063) at the 1% significance level. The calculated probability value of 0.0000 indicates that the null hypothesis is rejected at 1% significance level.

Table 1. Unit Root Test Results.



```
Null Hypothesis: D(OLIVEOIL_UNITROOTTEST) has a unit root
Exogenous: Constant
Lag Length: 0 (Automatic - based on SIC, maxlag=10)

                                                      t-Statistic    Prob.*

Augmented Dickey-Fuller test statistic                -7.310092      0.0000
Test critical values:          1% level               -3.544063
                               5% level               -2.910860
                              10% level               -2.593090

*MacKinnon (1996) one-sided p-values.


Augmented Dickey-Fuller Test Equation
Dependent Variable: D(OLIVEOIL_UNITROOTTEST,2)
Method: Least Squares
Date: 12/02/24   Time: 17:00
Sample (adjusted): 1963 2022
Included observations: 60 after adjustments

          Variable             Coefficient    Std. Error    t-Statistic    Prob.

D(OLIVEOIL_UNITROOTTEST(-1))   -0.961414      0.131519      -7.310092      0.0000
             C                  1193.431      1301.036       0.917293      0.3628

R-squared                       0.479529   Mean dependent var      -59.90000
Adjusted R-squared              0.470555   S.D. dependent var       13729.36
S.E. of regression              9989.888   Akaike info criterion    21.28930
Sum squared resid               5.79E+09   Schwarz criterion        21.35911
Log likelihood                 -636.6790   Hannan-Quinn criter.     21.31661
F-statistic                     53.43744   Durbin-Watson stat       1.979336
Prob(F-statistic)               0.000000
```

When the model results are analyzed, the coefficient of the lagged variable is estimated as -0.961414 and this coefficient is statistically significant (p=0.0000). The R^2 value indicating the explanatory power of the model was calculated as 0.479529. This value indicates that the model explains approximately 48% of the change in the dependent variable.

The Durbin-Watson statistic is calculated as 1.979336, which is very close to 2. This result indicates that there is no autocorrelation problem in the model. Akaike (21.28930) and Schwarz (21.35911) information criteria support that the model specification is appropriate.

In conclusion, the findings of the ADF unit root test statistically reveal that the olive oil price series is stationary, that is, it does not contain a unit root. This indicates that the series can be directly used in time series analysis.

The estimation results of the ARMA model reveal the dynamic structure of the olive oil price series. The model was estimated using the maximum likelihood method and converged after 22 iterations. AR(2) and MA(1) specifications were preferred in the model. All estimated parameters are statistically significant. The constant term (C) is estimated as 54939.33 and is significant at the 5% level (p=0.0101). The AR(2) coefficient is estimated as 0.912626 and the MA(1) coefficient is estimated as 0.942711 and both coefficients are statistically significant at the 1% level (p=0.0000). These coefficients indicate that the past values and error terms of the series have a strong impact on the current period values.

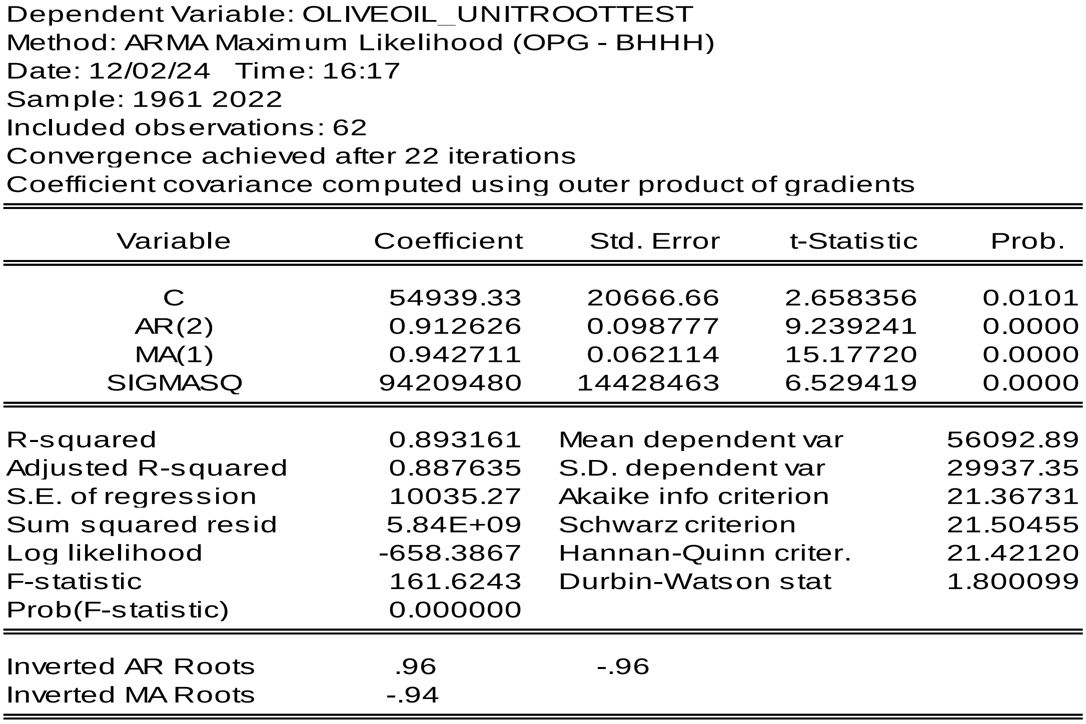
The explanatory power of the model is quite high. The R^2 value is calculated as 0.893161, which indicates that the model explains approximately 89% of the change in the dependent variable. The adjusted R^2 value (0.887635) also indicates a similar explanatory power.

When the diagnostic statistics of the model are analyzed, it is seen that the Durbin-Watson statistic is calculated as 1.800099. This value is close to 2, indicating that there is no significant autocorrelation problem in the model. Akaike (21.36731), Schwarz (21.50455) and Hannan-Quinn (21.42120) information criteria support the appropriateness of the model specification.

The fact that the AR and MA roots lie within the unit circle ($|0.96| < 1$ and $|-0.94| < 1$) indicates that the model satisfies the stationarity and transitivity conditions. The F statistic (161.6243) and the probability value (0.0000) indicate that the model as a whole is significant.

These results indicate that the estimated ARMA model successfully models the dynamic structure of the olive oil price series and can be used for forecasting purposes.

Table 2. ARIMA Model Analysis Results



```
Dependent Variable: OLIVEOIL_UNITROOTTEST
Method: ARMA Maximum Likelihood (OPG - BHHH)
Date: 12/02/24   Time: 16:17
Sample: 1961 2022
Included observations: 62
Convergence achieved after 22 iterations
Coefficient covariance computed using outer product of gradients
=========================================================================
        Variable          Coefficient    Std. Error    t-Statistic    Prob.
=========================================================================
            C              54939.33      20666.66      2.658356     0.0101
          AR(2)            0.912626      0.098777      9.239241     0.0000
          MA(1)            0.942711      0.062114      15.17720     0.0000
        SIGMASQ            94209480      14428463      6.529419     0.0000
=========================================================================
R-squared                  0.893161    Mean dependent var         56092.89
Adjusted R-squared         0.887635    S.D. dependent var         29937.35
S.E. of regression         10035.27    Akaike info criterion      21.36731
Sum squared resid          5.84E+09    Schwarz criterion          21.50455
Log likelihood            -658.3867    Hannan-Quinn criter.       21.42120
F-statistic                161.6243    Durbin-Watson stat         1.800099
Prob(F-statistic)          0.000000
=========================================================================
Inverted AR Roots           .96            -.96
Inverted MA Roots          -.94
=========================================================================
```

When the olive oil export quantity forecast results are analyzed, a general downward trend is observed between 2023 and 2030. Estimated at 89,246.91 units in 2023, the export quantity is projected to gradually decrease to 79,290.00 units by 2030. This decline corresponds to a decrease of approximately 11.2% over the eight-year period. When the rates of change by years are analyzed, the most significant decreases are expected to be 2.5% in 2023-2024, 2.4% in 2025-2026 and 2.3% in 2027-2028. In other years, a more moderate downward trend is projected. The forecasts indicate an average annual decline of 1.6% in olive oil exports. This suggests that structural changes may be needed in the sector and export-enhancing policies may need to be developed. In particular, international market conditions, production capacity and the development of strategies to increase competitiveness are important in preventing this downward trend.

Table 3. Türkiye's Export Forecast Results for 2023-2030

TARİH	TAHMİNİ İHRACAT MİKTARI
2023	89246.91
2024	86974.93
2025	86249.31
2026	84175.84
2027	83513.62
2028	81621.97
2029	81016.97
2030	79290.00

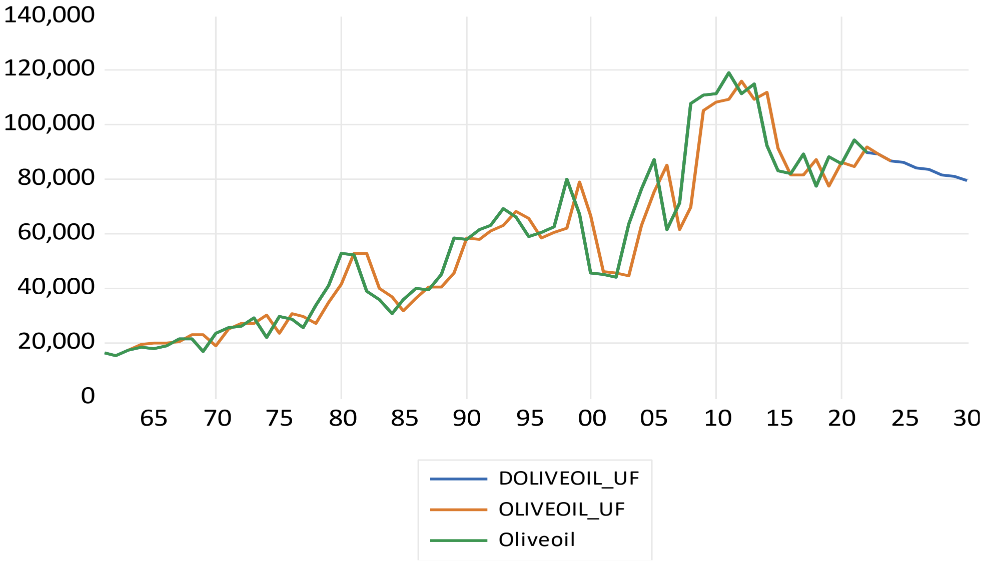


Figure 1. Türkiye’s Export Forecast Chart for 2023-2030

The graph showing the historical course of olive oil prices includes realized and predicted values between 1965 and 2030. Analyzing this long-term series, the 1965-1980 period was relatively stable, with prices moving in the 15,000-25,000 band. In the 1980s, a significant upward trend started and prices rose to around 50,000. The upward trend continued in the 1990s, but with more volatility. There was a sharp decline in the early 2000s, followed by a peak of around 120,000 between 2005 and 2015. After 2015, a significant downward trend in prices started and continued until 2020. Between 2020 and 2023, prices fluctuated around 80,000-90,000. In the forecast period of 2023-2030, a gradual decline is foreseen and prices are expected to fall below 80,000. The three different series shown in the graph (DOLIVEOIL_UF, OLIVEOIL_UF and Oliveoil) are quite close to each other, indicating the consistency of the forecast model. Overall, the chart reveals that olive oil prices follow an increasing trend in the long run, but have been on a downward trend in future projections.

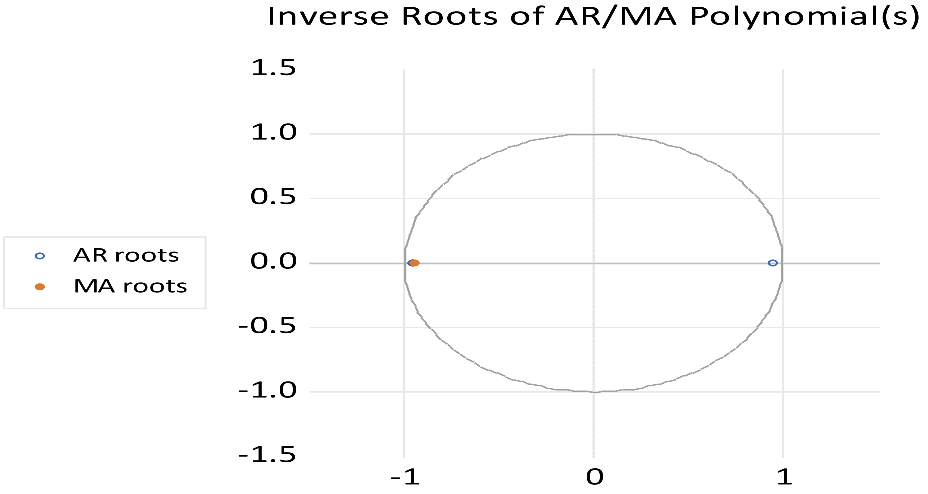
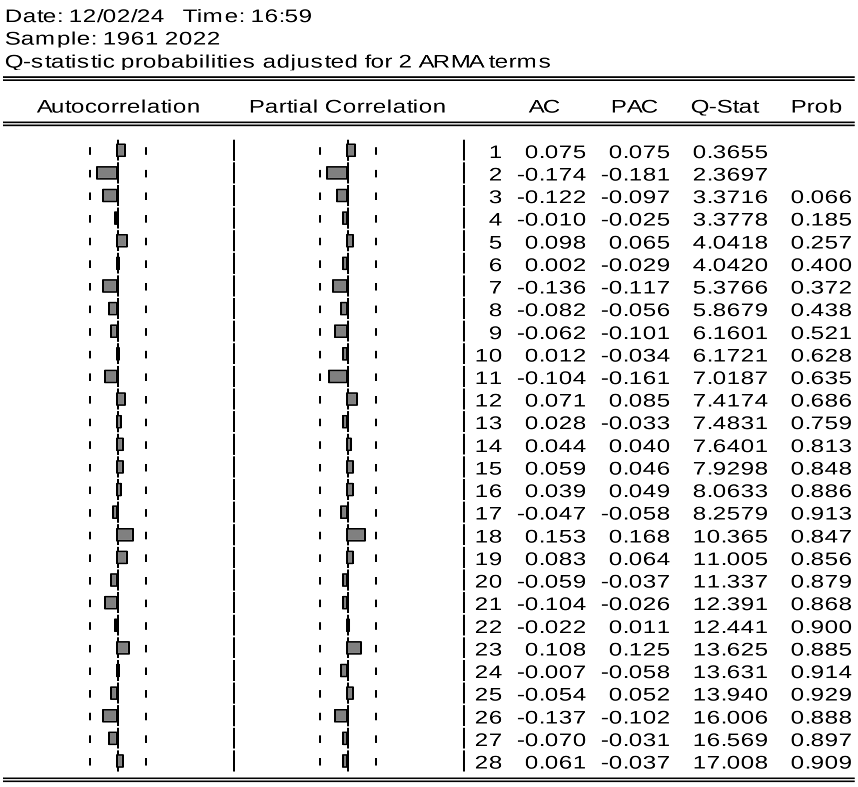


Figure 2. Arima Model Structure

This graph showing the inverse roots of the AR/MA model provides important information to assess the stationarity and transitivity conditions of the model. As can be seen in the graph, both AR (Autoregressive) and MA (Moving Average) roots are all located within the unit circle. The AR roots are located on the right side of the circle, while the MA root is located on the left side.

These roots located in the (-1, 1) interval of the unit circle indicate that the estimated ARMA model satisfies the stationarity and transitivity conditions. This suggests that the model is stable and can produce reliable forecasts. The roots are located far from the unit circle, indicating that the model has a robust structure. In conclusion, the inverse root analysis confirms that the estimated ARMA model is statistically appropriate and reliable.



```
Date: 12/02/24   Time: 16:59
Sample: 1961 2022
Q-statistic probabilities adjusted for 2 ARMA terms

 Autocorrelation   Partial Correlation        AC     PAC    Q-Stat   Prob

                                          1  0.075   0.075  0.3655
                                          2 -0.174  -0.181  2.3697
                                          3 -0.122  -0.097  3.3716   0.066
                                          4 -0.010  -0.025  3.3778   0.185
                                          5  0.098   0.065  4.0418   0.257
                                          6  0.002  -0.029  4.0420   0.400
                                          7 -0.136  -0.117  5.3766   0.372
                                          8 -0.082  -0.056  5.8679   0.438
                                          9 -0.062  -0.101  6.1601   0.521
                                         10  0.012  -0.034  6.1721   0.628
                                         11 -0.104  -0.161  7.0187   0.635
                                         12  0.071   0.085  7.4174   0.686
                                         13  0.028  -0.033  7.4831   0.759
                                         14  0.044   0.040  7.6401   0.813
                                         15  0.059   0.046  7.9298   0.848
                                         16  0.039   0.049  8.0633   0.886
                                         17 -0.047  -0.058  8.2579   0.913
                                         18  0.153   0.168  10.365   0.847
                                         19  0.083   0.064  11.005   0.856
                                         20 -0.059  -0.037  11.337   0.879
                                         21 -0.104  -0.026  12.391   0.868
                                         22 -0.022   0.011  12.441   0.900
                                         23  0.108   0.125  13.625   0.885
                                         24 -0.007  -0.058  13.631   0.914
                                         25 -0.054   0.052  13.940   0.929
                                         26 -0.137  -0.102  16.006   0.888
                                         27 -0.070  -0.031  16.569   0.897
                                         28  0.061  -0.037  17.008   0.909
```

Figure 3. Kalıntıların Korelogram Model Sonuçları

The autocorrelation and partial autocorrelation coefficients indicate that there is no systematic dependence structure in the series. In the correlogram output, autocorrelation and partial autocorrelation coefficients up to 28 lags are generally within confidence limits. Q-statistics and probability values indicate that there is no autocorrelation in the error terms of the model. The probability values (Prob) of the Q-statistics starting from the first lags up to lag 28 are greater than 0.05. This indicates that the null hypothesis “there is no autocorrelation among the error terms” cannot be rejected. In particular, the Q-statistic is 3.3716 (p=0.066) at lag 3, 7.4174 (p=0.686) at lag 12 and 17.008 (p=0.909) at lag 28, indicating that the residual terms of the model have a white noise process. These results confirm that the specification of the estimated ARMA model is appropriate and successfully captures the dynamic structure of the series.

Conclusion

In this study, olive oil export estimates for the period 2023-2030 were analyzed using the ARMA model. As a result of the analyzes, a gradual decline in olive oil exports is predicted in the coming years. The export amount, estimated to be 89,246.91 units in 2023, is estimated to decrease by approximately 11.2% to 79,290.00 units by 2030. This downward trend offers important political and strategic implications for the sector. Various diagnostic tests supporting the reliability of the model were performed. The ADF unit root test results showed that the series was stationary, which increased the reliability of the estimates. The estimation results of the ARMA model had a high explanatory power (R^2=0.893), and the parameters of the model were found to be statistically significant. The fact that the AR and MA roots were located within the unit circle confirmed that the model met the conditions of stationarity and translatability. The correlogram analysis results also showed that the residual terms of the model had a white noise process, confirming the suitability of the model specification.

Comprehensive policy measures need to be developed to prevent the projected downward trend in exports. First of all, it is important to raise quality standards and develop branding strategies to increase competitiveness in international markets. Supporting technological investments that will reduce production costs and increase efficiency is also critical for the sustainability of the sector. In addition, strategies need to be developed to develop new export markets and increase market share in existing markets.

The results of this study constitute an important reference source for decision-makers and policy-makers in the olive oil sector. However, in future studies, including other factors affecting export performance (climate change, international competition, consumer preferences, etc.) in the model may provide more comprehensive predictions. Encouraging sustainable production practices and disseminating environmentally friendly production methods should also be considered as important strategic goals for the future of the sector. In addition, testing the reliability of estimates using different econometric methods stands out as an important area of study for future research.

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Statement of Conflict of Interest

The authors declare that they have no conflict of interest.

Authors' Contributions

Ferda Nur ÖZDEMİR designed and analyzed the research. Ferda Nur ÖZDEMİR and Vahit Cem Tüzemen organized the studies. Ferda Nur ÖZDEMİR worked on the preparation of the pictures and tables. All authors contributed to the writing of the article and took part in the publication process, and read and approved the article.

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Effect of Biostimulants on Germination and Early Growth Properties of Radish*

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ABSTRACT: Some biostimulants can be employed to increase metabolic efficiency and thus improve germination. The effect of the biostimulants usually depends on the type of biostimulant, its concentration and the plant species. The aim of this study was to investigate the effects of different biostimulants at varying doses on radish germination and early growth properties. In study factorial treatments of four biostimulants [fulvic acid (FA), amino acid (AA), chitosan oligosaccharide (CO) and seaweed extract (SWE)] and four levels of biostimulants (FA: 2.5-40 mg/100 ml; AA: 0.5-8 mg/L; CO: 2.5-40 mg/100 ml; SWE: 2.5-40 mg/100 ml) were evaluated. In the control group, seeds were treated with distilled water and the effect of biostumulnat doses was compared with control group. The experiment was conducted in a factorial experiment based on completely randomized design (CRD) with three replicates consisted of two petri dishes containing 100 seeds each. Germination percentage (GP), germination index (GI), mean germination time (MGT), time to 50% germination (T50), mean germination rate (MGR), coefficient of variation of germination time (CVt), vigor index (VI), peak value (PV), hypocotyl length, sprout length, stem diameter and sprout fresh weight were recorded.

Keywords: *Raphanus sativus*, Germination, Fulvic Acid, Chitosan Oligosaccharide, Seaweed Extract, Amino Acid

INTRODUCTION

Radish (*Raphanus sativus* L.), belonging to the Brassicaceae family, is a popular root vegetable in both tropical and temperate regions. On the other hand, a wide variety of flavors and colors, high concentrations of bioactive compounds beneficial for human health, rapid germination and short growing time are the main reasons why many species of the Brassicaceae family are popular in microgreens production (Kamal et al., 2019).

Seed germination and the formation of healthy seedlings are the most important stages affecting crop production and ensuring the sustainability of plant generations. Seed germination is a complex process involving imbibition, activation of enzymes, hydrolysis of stored nutrients, cracking of the seed coat and emergence of the radicle and shoot (Copeland and McDonald, 1999). Seed germination and seedling growth characters are extremely important factors in determining yield (Rauf et al., 2007). This process can be controlled by many exogenous practices, including the application of biostimulants. Over the last years, suggestions for the use of biostimulants for sustainable crop production have increased (Gupta et al., 2022).

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*This study is a part of the Huriye ÖZDEMİR'in master thesis accepted by Ataturk University, Institute of Science

Biostimulants are derived from natural sources and can be used to improve plant growth and crop quality (Rouphael and Colla, 2018). The impact of biostimulants can often vary depending on the type of biostimulant, its concentration and the plant species (Makhaye et al., 2021). Kauffman et al. (2007) have defined biostimulants as “Biostimulants are substances other than fertilizers that promote plant growth when applied in low amounts”. However, biocitimulants can be used in replace chemical fertilizers to stimulate plant growth and improve the efficiency of nutrient utilization, and can increase crop yield and quality without adverse effects (Bulgari et al., 2015). Calvo et al. (2014) recognized all substances and microorganisms that are beneficial to the plant as biostimulants. Approaches to the definition and composition of plant biostimulants are still under development and it has been attributed to the wide of input diversity that have the potential to be utilized as biostimulants. Du Jardin (2015) has classified biostimulants into seven distinct categories: humic/fulvic acids, seaweed/herbal extracts, protein hydrolysates, biopolymers, beneficial minerals, beneficial bacteria and beneficial fungi. It is suggested that the efficacy of biostimulants is not driven by a single molecule/compound, but is the outcome of the synergistic effect of multiple bioactive molecules/compounds (Bulgari et al., 2019). Biostimulant seed treatments can lead to changes in gene expression and regulate metabolic processes, thus can promote better seed germination and seedling growth (Kisvarga et al., 2022; Gupta et al., 2022). In addition, biostimulants or their active compounds applied to seed have been reported to increase metabolic activity during seed germination and seedling formation, accelerate mobilization of seed reserve and promote nutrient uptake and assimilation, resulting in stronger, homogeneous and high-yielding plants (Gupta et al., 2022). Furthermore, some studies have reported the presence of hormone-imitating compounds in biostimulants (Ertani et al.2018; Kulkarni et al., 2019).

The aim of this study was to determine the effect of varying doses of fulvic acid, amino acid, chitosan oligosaccharide and seaweed extract biostimulants on radish germination.

Material and Method

Certified ecological seeds of radish variety (*Raphanus sativus* L. cv. Alçin) were purchased commercially from a local supplier. All biostimulants used in the study; fulvic acid (FA), amino acid (AA), chitosan oligosaccharide (CO) and seaweed extract (SWE) were obtained from a company with commercial manufacturers (HUMICO BIOTECHNOLOGY CO.,LTD, Huang, China).

The doses applied for each biostimulant were as follows:

- Fulvic Acid (FA): 2.5, 5, 10, 20, and 40 mg/100 ml
- Amino Acid (AA): 0.5, 1, 2, 4, and 8 mg/100 ml
- Chitosan Oligosaccharide (CO): 2.5, 5, 10, 20, and 40 mg/100 ml
- Seaweed Extract (SWE): 2.5, 5, 10, 20, and 40 mg/100 ml

Seeds were kept in 1% sodium hypochlorite solution (bleach) for 5 min for surface sterilization and then washed with sterilized water. Subsequently, seeds were dried on sterile filter paper under relatively aseptic conditions and placed in 90 mm diameter plastic Petri dishes (100 seeds per dish) covered with two layers of filter paper, between the paper. The experiment was conducted in three replicates according to a completely randomized factorial experimental design, and each replicate consisted of two Petri dishes. A total of 126 Petri dishes were used in the experiment and calculated as follows: 4 biostimulants × 5 doses × 3 replicates × 2 petri dishes + control group (3 replicates × 2 petri dishes). Petri dishes were soaked with 7 mL of solution (distilled water for control) and incubated in a growth chamber (temperature 23 ± 2 °C, 60% humidity) in dark (Kanjevac et al., 2022). For each treatment, germination was counted until the final count until further germination occurred. Seeds with radicals longer than 1 mm were considered to have germinated (Flórez et al., 2007).

$$Germination\ Percentage\ (GP) = \frac{Seed\ germinated}{Total\ seeds\ tests} \times 100 \qquad (Eq.1)$$

$$Germination\ index\ (GI) = \sum_{i=1}^{K} \frac{No\ of\ germinated\ seed}{the\ count\ day} \qquad (Eq.2)$$

Where: i =1 day one, k the last day of observation

$$Mean\ Germination\ Time\ (MGT) = \frac{\sum_{i=1}^{k} n_i t_i}{\sum_{i=1}^{k} n_i} \qquad (Eq.3)$$

Where: ti is the time from day one to the last day of observation, ni is an observed number of germinated seeds every day, and k is the last germination time.

$$Time\ to\ 50\%\ Germination\ (T50) = \frac{ti + [(\frac{N}{2} - ni)\ (ti - tj\ )]}{ni - nj} \qquad (Eq.4)$$

Where: N is the final number of emergence and ni, nj cumulative number of seeds germinated by adjacent counts at times ti and tj, respectively when ni < N / 2 < nj.

$$Mean\ Germination\ Rate\ (MGR) = \frac{\sum_{i=1}^{k} n_i}{\sum_{i=1}^{k} n_i t_i} \qquad (Eq.5)$$

Where: ti is the time from day one to the last day of observation, ni is an observed number of germinated seeds every day, and k is the last germination time.

$$Coefficient\ of\ Variation\ of\ the\ Time\ (CVt) = \frac{S_t}{MGT} \times 100 \qquad (Eq.6)$$

St is a standard deviation of the germination time, and MGT is the mean germination time.

$$Vigor\ Index\ (VI) = \frac{Mean\ seedling\ length\ (cm) x\ GP}{100} \qquad (Eq.7)$$

$$\text{Peak Value (PV)} = \frac{Highest\ seed\ germinated}{the\ number\ of\ days} \qquad (Eq.8)$$

Germination percentage (GP) was determined by dividing the number of seeds germinated on day seven by the total number of seeds tested (Eq. 1). Germination index (GI) is the summation of the germinated seeds number that counted every day divided by the count day from day one (i =1) to the last day of observation (k) (Eq. 2). Mean germination time (MGT) is defined as the time (in days) taken for the seed to germinate or emerge, and MGT can be calculated with Eq. 3. The time required for 50% germination was calculated according to Eq.4. The mean germination rate (MGR) indicates the speed of seed germination per unit time and is calculated as the inverse of the mean germination time (Eq. 5). The variation coefficient of germination time (CVt) was used to measure the germination time homogeneity (Eq. 6). Vigour index (VI) is denoted in Eq. 7 was used to measure the damage accumulations as viability declines. The peak value (PV) was obtained by dividing the cumulative percent germination for each measurement day by the number of days since the start of the germination test using Eq.8. Growth characteristics (hypocotyl length (mm), sprout length (mm), stem diameter (mm) and sprout fresh weights (g)) were evaluated 7 days after seed germination. Hypocotyl length and sprout length were measured using a digital caliper.

Experiments were performed in laboratory conditions with 3 replications according to the requirements of the relevant methods. The results were processed using ANOVA analysis of variance in the statistical software package SPSS 27.0 and the differences between the means were evaluated with Duncan's multiple range test at $p \leq 0.05$ significance level.

Results and Discussion

Figures 1, 2 and 3 show that five different doses of biostimulants had a statistically significant ($p < 0.05$) effect on the germination and early growth characteristics of radish seeds, with the exception of the stem diameter for FA. Radish sprouts germinated at varying doses of biostimulants are illustrated in Figure 2. For all biostimulant treatments, doses had a statistically significant effect on germination percentage. Some biostimulant concentrations reduced the germination percentage. The control group had the highest germination percentage of 99%. The highest germination percentage was obtained in the control with FA treatments II (98.83%) and IV (99%); CO treatments I (98.67%), II (97.33%), III (98.50%) and IV (97.17%). The highest AA dose (V) gave the lowest germination percentage (Figure 1). The germination index (GI) is defined as the weighted sum of the number of seeds that germinate on each day (Benech Arnold et al., 1991). The maximum weight is given to seeds germinating on the first day, less weight to seeds germinating on later days and the lowest weight to seeds germinating on the last day. The GI is therefore an indication of both the percentage and the rate of germination. A higher GI value means a higher percentage and a higher germination rate. The effect of the biostimulant doses on the germination index was significant for all the treatments. The highest results for the germination index were obtained in the FA-II and SWE-II treatments with 49.32 and 50.03, respectively. The germination index was lower than the control (43.63) for all doses of AA and CO biostimulants (Figure1).

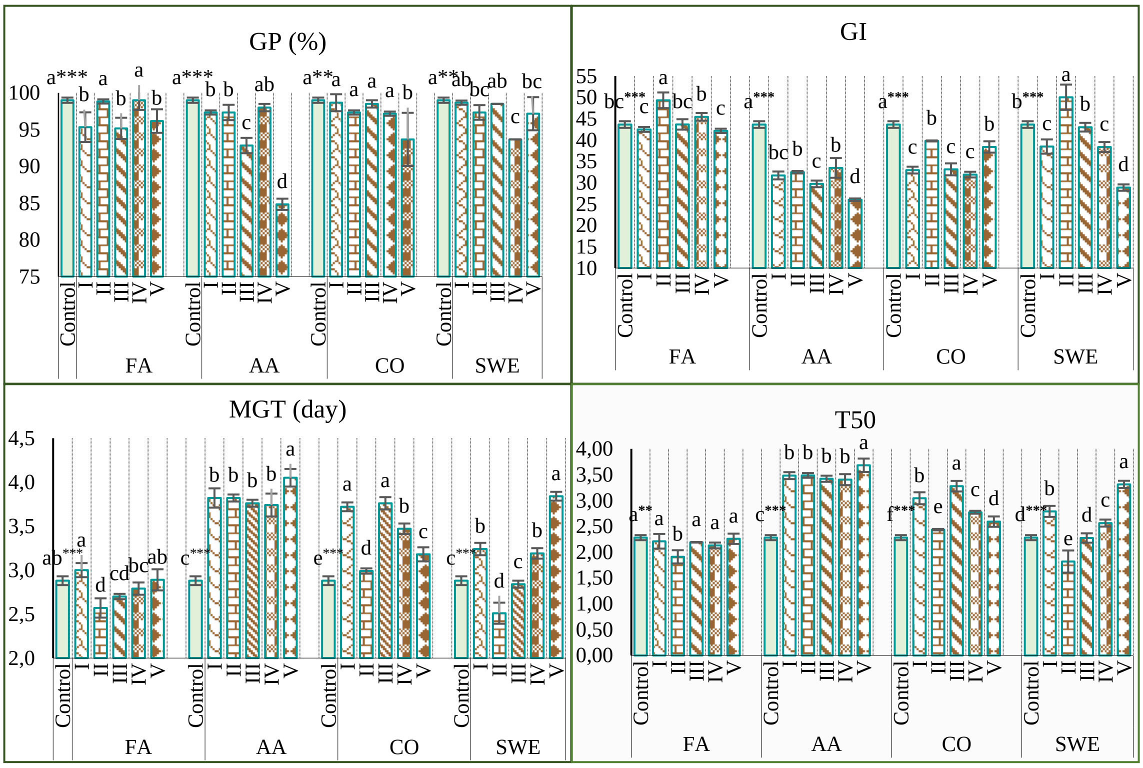

Figure 1. Effect of biostimulant applications on germination percentage (GP), germination index (GI), mean germination time (MGT), time to 50% germination (T50).

Fulvic acid at a dose of 80 mg L^{-1} has been shown to improve tomato seed germination rate and vigour index (Zhang et al., 2021). Soluble humates produced from vermicompost in soil substrate improved tomato seed germination by 31.6% (Olivares et al., 2015). Humic substances increased the germination rate and vigour index of cucumber seeds (Awad and

Ahmed, 2020). Mean germination time (MGT) calculates the average germination day; the lower the MGT, the faster a seed population germinates (Orchard, 1977). All biostimulant doses had a statistically significant effect on mean germination time. The fastest mean germination time, 2.57 and 2.51 days respectively, was obtained with FA-II and SWE-II treatments. All doses of AA and CO treatments showed higher mean germination time than the control (2.88 days) (Figure1). The time achieving 50% germination was significant for different doses of all biostimulants. The time required to germinate 50% of the total number of germinated radish seeds (T50) from the day the first germinated seeds appeared was the shortest for radish seeds treated with FA-II (1.91 days) and SWE-II (1.82 days). It took longer than the control (2.28 days) for the AA and CO biostimulant doses to reach 50% germination (Figure 1). In lettuce seeds primed with two seaweed suspensions (SWS) derived from the whole brown alga *Ascophyllum nodosum* or the lamina of *Laminaria hyperborea*, a reduction in mean germination time has been reported (Möller and Smith, 1998).

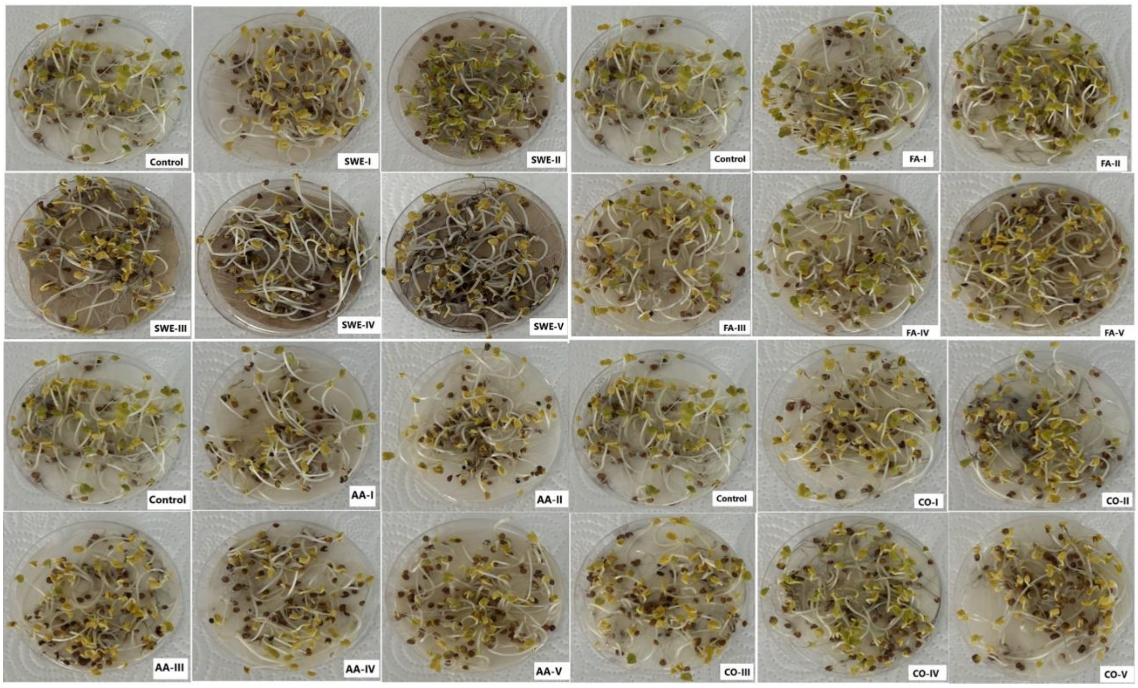

Figure 2. Radish sprouts germinated with five different doses of biostimulants

Mean germination rate (MGR) indicates the rate of seed germination per unit time and is calculated as the inverse of mean germination time (Abou Elezz and Ahmed, 2021). The MGR was significantly influenced by the doses of all biostimulant treatments. FA-II and SWE-II treatments resulted in the highest mean germination rate of 0.39 and 0.40 day^{-1}, respectively. All doses of AA and CO treatments had a lower mean germination rate than the control (0.35 day^{-1}) (Figure 3). Tamindži et al. (2024) found that biostimulants affected parsnip seed germination and early growth, with a mean germination rate ranging from 0.07 to 0.081. Braziene et al. (20-21) found that treating sugar beet seeds with fulvic acid increased GP by 4.2%, GI by 22.0%, CVG by 11% and reduced MGT by 9.8%. The coefficient of variation of germination time (CVt) evaluates the uniformity or variability of germination with respect to the average germination time (Ranal and Santana, 2006). The CVt was significantly affected by the change in the dose of the biostimulant. The highest CVt was obtained in the FA-I treatment (51.06%) and in the SWE-II treatment (49.55%). All doses of AA and CO biostimulants showed a lower coefficient of variation of germination time than the control (45.8%) (Figure 3). Fast seed germination has been considered an important trait, indicating rapid transition to the developing stage of the plant lifecycle (De Ron et al., 2016). Many studies have shown that seaweed can act as a biofertiliser or bio-stimulant to increase seed germination, growth and development, containing minerals, nutrients, amino acids, vitamins, pigments and polysaccharides (Calvo et al, 2014; Arioli et al., 2015; Du Jardin 2015). However, calcite base biostimulants applied to pepper seeds did not have a statistically significant effect on the CVt of germination (Vidak et al., 2024). In the study, the seed vigour index was calculated as the product of germination percentage (%) and seedling length. The seed lot with the higher seed vigour index is considered to be more vigorous (Abdul-Baki and Anderson, 1973). Among the application doses of all biostimulants, significant differences in vigour index were observed.

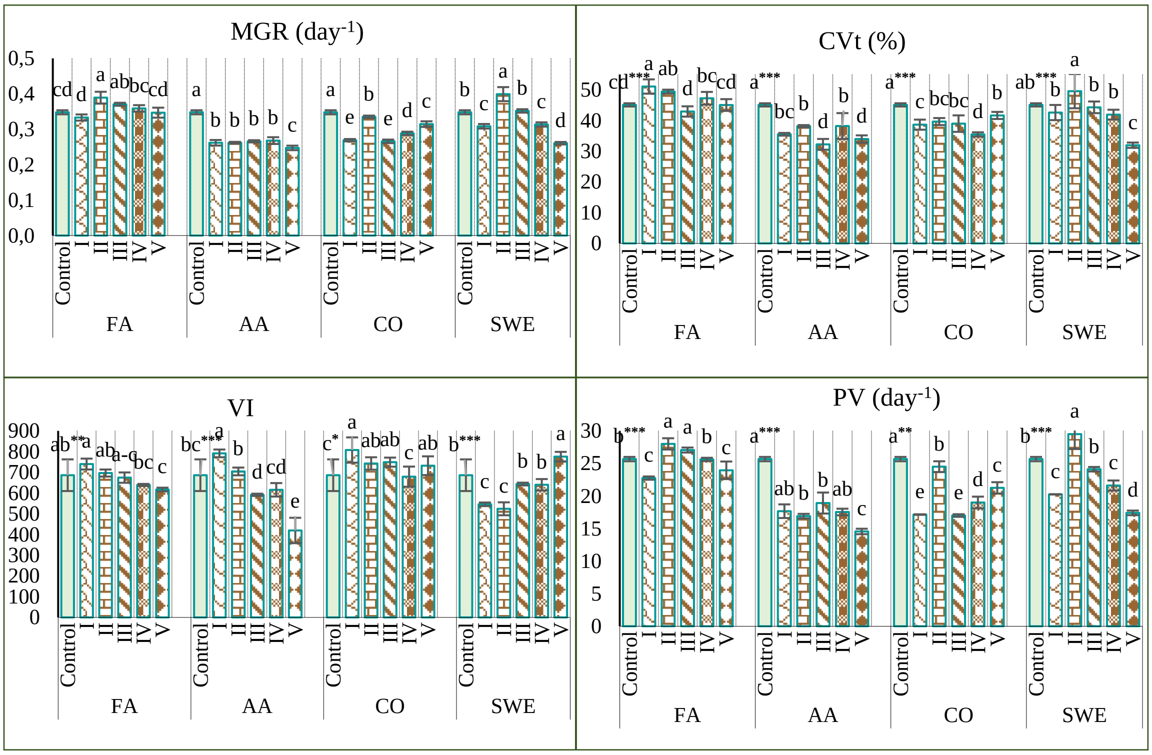

Figure 3. Effect of biostimulant applications on mean germination rate (MGR), coefficient of variation of germination time (CVt), vigour index (VI), peak value (PV)

The highest results in the vigour index were obtained from FA-I with 739.85, AA-I with 791.45, CO-I with 807,58 and SWE-V with 775.70. The lowest vigour index was found in the AA-V application with a value of 419.52 (Figure 3). The peak value (PV) is obtained by dividing the cumulative germination percentage for each day of measurement by the number of days since the start of the germination test. The daily maximum value is defined as the peak value (Thomson and El-Kassaby, 1993). The peak value was significantly altered by all biostimulant application doses. The highest peak values were found at FA-II (28.00 d^{-1}), FA-III (29.06 d^{-1}) and SWE-II (29.50 d^{-1}). Peak values were lower than the control (25.67 day^{-1}) for all doses of AA and CO biostimulants (Figure 3).

All biostimulant treatments showed significant differences in the hypocotyl length of radish sprout according to the dose. The highest hypocotyl length was recorded at dose I of FA, AA and CO treatments (49.02, 48.97 and 74.44 mm respectively) and at dose V of SWE treatment (45.87 mm). All doses of FA and CO treatments showed a higher hypocotyl length than the control (33.67 mm). However, at doses IV and V of the AA treatment and at I and II of the SWE treatment it was lower than the control (Figure 4). The effect of application doses on seedling length was found to be significant for all biostimulant treatments. The longest seedling length was recorded for FA treatment at dose I (77.59mm), AA treatment at dose I (81.82mm), CO treatment at dose I (81.81mm) and SWE treatment at dose V (81.51mm). Seedling length generally increased with all doses of CO, whereas FA, AA and SWE treatments showed variable results in seedling height compared to the control (Figure 4). Kaya et al. (2023) reported that the average shoot length of radish varieties varied between 4.13 and 8.28 mm, and the fresh seedling weight varied between 0.086 and 0.194 g $plant^{-1}$. According to the results of two experiments conducted by Khang (2011) with 1%, 2% and 4% doses of fulvic leaf fertilizer, it was observed that plant height increased in the germination of rice and radish seeds. With the exception of FA, stem diameter was significantly affected by the application doses of other biostimulants. With the exception of FA, the stem diameter was considerably influenced by the application doses of the other biostimulants. The highest stem diameter was reached at dose III with 1.27 in AA applications, at dose IV with 1.36 in CO applications and at dose I with 1.27 in SWE applications (Figure 4). Radish sprout fresh weight showed significant differences according to dose in all biostimulant treatments. The highest fresh sprout weight was 0.073 g $plant^{-1}$ at dose II for FA treatment, 0.082 g $plant^{-1}$ at dose I for AA treatment, 0.071 g $plant^{-1}$ at dose IV for CO treatment and 0.074 g $plant^{-1}$ at dose V for SWE treatment. Compared to the control (0.061 g $plant^{-1}$), the fresh weight of the sprouts was lower in the FA III and SWE II treatments. However, doses of all other biostimulants increased the fresh weight of the sprouts in comparison with the control (Figure 4). The effect of the biostimulants FA, AA, CO and SEE, applied at five different doses, on the seeds of radish is shown in Figure 5.

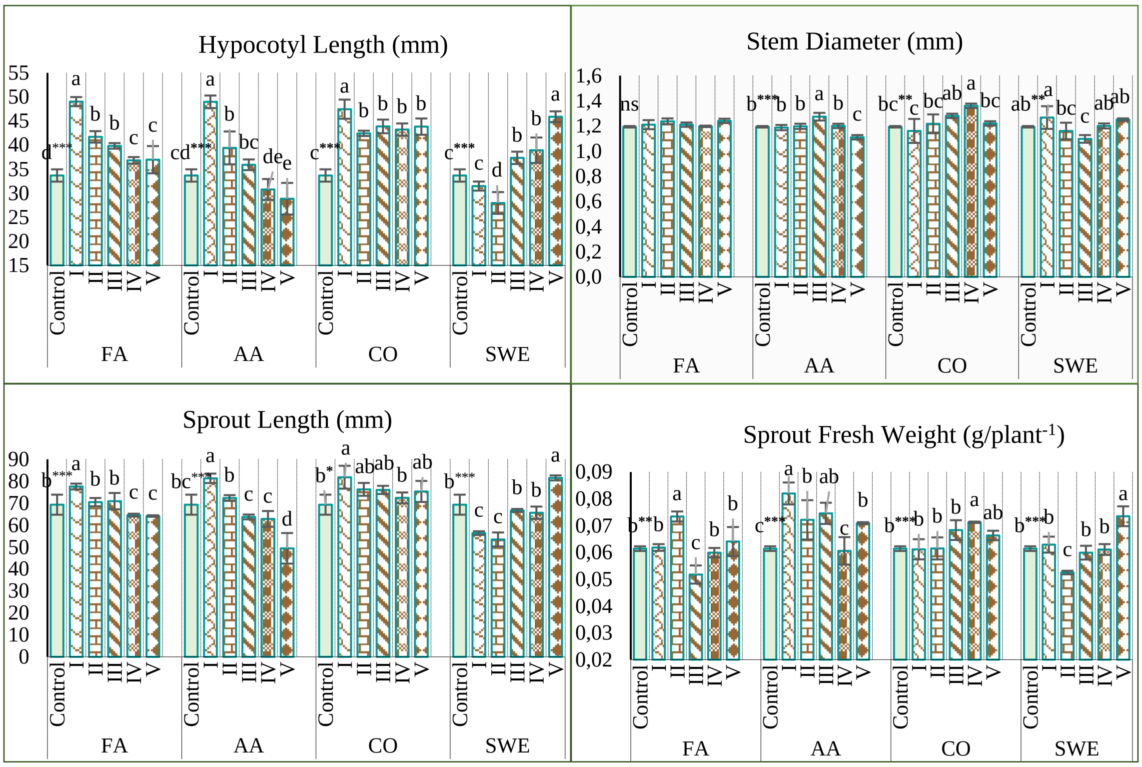

Figure 4. Effect of biostimulant applications on sprout length, stem diameter and sprout fresh weight.

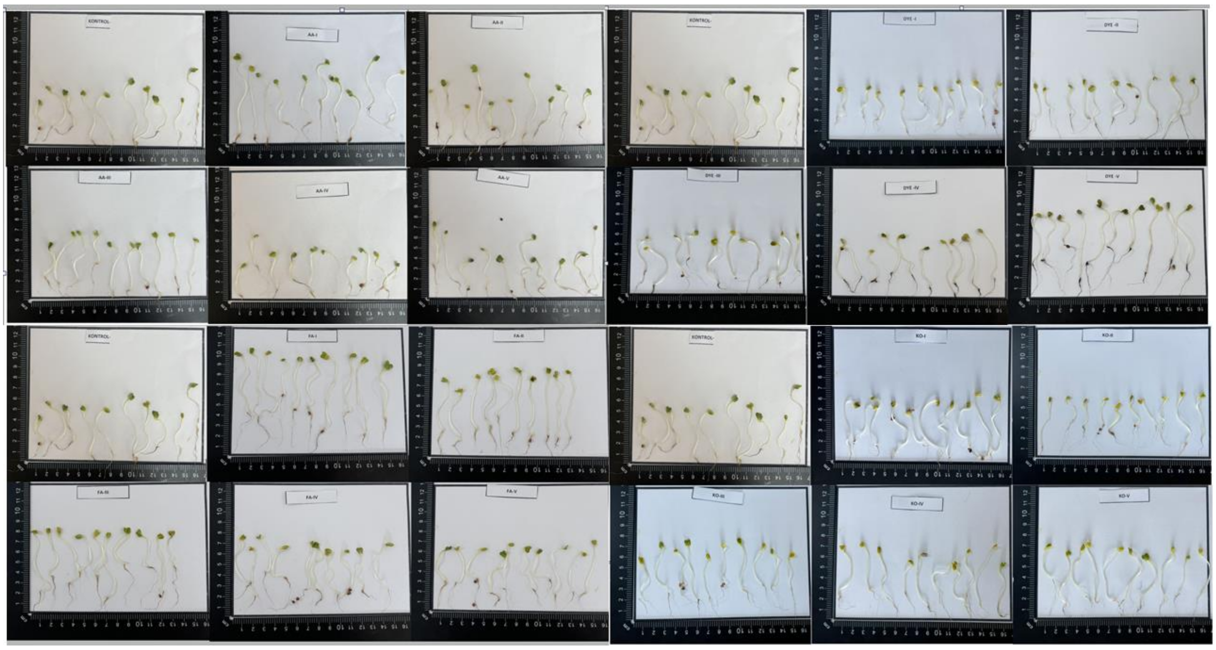

Figure 5. Radish sprouts germinated in five different doses of FA, AA, CO and SWE biostimulants

Conclusion

The varying doses of biostimulants showed different effects on germination and early growth characteristics of radish. Various responses were shown for different biostimulant doses, including stimulatory, inhibitory and neutral effects. Some treatment doses had a decreasing effect on germination rate, while some doses were not different from the control. For other germination traits (MGT, MGR, CVt, CVG, GI, T50 and PV), FA-II and SWE-II treatments showed better results than the control. On the other hand, biostimulant doses generally improved sprout growth traits compared to the control. Sprout fresh weight, an important indicator of the nutritional properties of biostimulants, gave the best results in FA-II, AA-I, CO-IV and SWE-V treatments. In this regard, it was clear that the efficacy of biostimulants was dependent on the biostimulant concentrations. Overall, this study demonstrated the importance and contribution of biostimulant type and concentration in radish seed germination, especially in developmental traits. Given the potential of biostimulant applications to improve seedling developmental traits, this study will guide future studies aimed at demonstrating the potential of biostimulants as an alternative to chemical fertilization for microgreen production.

Acknowledgement

We thank HUMICO BIOTECHNOLOGY CO.,LTD, Huang, China for providing biostimulants used in the study.

Funding

The research has not been funded or supported by any organisation or individual.

Statement of Conflict of Interest

I declare that there is no conflict of interest between the authors of this study.

Authors' Contributions

Raziye KUL designed and analyzed the research, Huriye ÖZDEMİR conducted the study. Raziye KUL and Huriye ÖZDEMİR worked on the preparation of the pictures and tables. All authors contributed to the writing of the article, participated in the publication process, and read and approved the article.

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International Conference on
Food, Agriculture and Animal Sciences
19-22 December 2024, Erzurum, TÜRKİYE

Effect of Volumetric Density and Skeletal Ratio on Soil Organic Carbon: The Palandöken Sample

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ABSTRACT: This study was carried out to investigate the relationships between soil organic carbon (SOC), bulk density and skeletal ratio at different altitudes in Palandöken Mountain, Erzurum and to compare SOC_s. Within the scope of the research, undisturbed soil samples were taken from three altitudes (2941 m, 2762 m, 2501 m) and three depth levels (0-10 cm, 10-20 cm and 20-30 cm) by random sampling method. SOC amounts were determined by Walkley-Black method, bulk weights by cylinder method and skeletal ratios by sieve method. The findings revealed that SOC amount was higher in the surface layer of the soil and at low altitude levels and decreased with increasing depth. A strong negative correlation (r=-0.83) was determined between bulk density and SOC and it was determined that soils with high SOC amount had lower bulk density. In addition, a weak negative correlation (r=-0.34) was observed between skeletal ratio and SOC. This situation reveals the negative effect of stone and coarse fractions on the transportation and accumulation of SOC. In addition, a positive relationship (r = 0.56) was observed between the skeleton ratio and bulk density; it was observed that the increase in stone and coarse fractions decreased soil porosity and increased bulk density. In addition, as a result of these analyses, it is predicted that the decrease in altitude increases the amount of SOC_s. These results provide important information in understanding the effects of soil properties at high altitudes on SOC accumulation. The study aims to contribute to sustainable soil management and carbon storage strategies.

Keywords: Soil Organic Carbon, Volumetric Density, Skeletal Ratio, Soil Organic Carbon Stock

1. INTRODUCTION

Soil plays a central role in the carbon storage capacity of terrestrial ecosystems and plays an important function in this ecosystem with the organic carbon it accumulates. SOC increases soil fertility and productivity and increases soil porosity by reducing soil density. This situation improves the water holding capacity and biological activities of soils. As a matter of fact, as SOC increases, the volume weight decreases and accordingly, it has an important effect in terms of providing physical stability in the upper soil layers and erosion control (Céspedes-Payret et al., 2017). Therefore, the variation and spatial distribution of SOC dynamics, which is one of the largest carbon pools of terrestrial ecosystems, is critical for land quality protection, farmland management, ecological landscaping and assessment of global climate change (Zhang et al., 2022). Spatial estimations of SOC should be performed to cover SOC stocks at different depths in the soil profile as well as in the surface layer of the soil (Jobbágy and Jackson, 2000).

SOC stocks at different depths of the soil profile in the surface and lower layers are associated with important processes such as surface runoff, water infiltration, erosion control and nutrient conservation (Kadlec et al., 2012). Dynamics in the lower layers are slower than in the surface layers (Balesdent et al., 2018). Plant root biomass has been reported to influence the vertical distribution of SOC and its conversion to carbon sinks (Jobbágy and Jackson, 2000). Therefore, analyzing the distribution of SOC along the soil profile is more important than horizontal properties for understanding the functional roles of soil layers and the relationships between them. Another important factor affecting the distribution of SOC in the profile is the soil skeleton consisting of stones, gravels and coarse fractions (Corti et al., 2002). Especially coarse fractions have the potential to direct SOC dynamics by influencing the transport and accumulation of SOC along the depth. However, the role and influence of this component in stony soils has often been overlooked (Singh et al., 2012). The limited research on the soil skeleton and the fact that the effects of coarse fractions on SOC are often neglected reveal the lack of knowledge in this field. However, some studies suggest that coarse fractions may play an important role in SOC accumulation and their contribution to the soil carbon cycle should be reconsidered (Rivard and De Kimpe, 1980). In particular, minerals such as Al- and Fe-oxides are known to be strong sorbents for SOC and play a critical role in SOC retention through organo-mineral interactions (Kaiser and Zech, 2000). However, information on the effects of soil skeleton on SOC in stony soils is scarce. This study was conducted on soil samples taken from different depths (0-10 cm, 10-20 cm and 20-30 cm) and aimed to investigate the effect of soil skeletal ratio and soil volume weight on SOC accumulation in soil profiles. The main objective of the study is to evaluate the role of soil skeletal fraction and volume weight in the transport and accumulation of SOC along the depth and to reveal the contribution of these relationships to the soil carbon cycle.

2. Material and Method

2.1. Description of the Study Area

The Palandöken Mountain, located approximately 5 km from Erzurum city center, were selected as the study area and surveys were carried out at three different elevations. Location 1 is located at an altitude of 2941 meters, southwest aspect (N 39° 50‘ 5’‘ - E 41° 17’ 37‘’) and has a slope of 40-45%. The 2nd location is located at an altitude of 2762 meters, facing north (N 39° 49‘ 47’‘ - E 41° 17’ 5‘’) and has a slope of 30-35%. The 3rd location is located at an altitude of 2501 meters, facing west (N 39° 50‘ 26’‘ - E 41° 16’ 41‘’) and has a slope of 25-30%. In these locations, rose hips (*Rosa canina* L.), juniper (*Juniperus* spp.), pine (*Pinus* *sylvestris* L.), birch (*Betula pendula* spp.), aspen (*Populus tremula* .L), elm (*Ulmus* spp.), and spindle (*Elaeagnus angustifolia* L.) species were commonly observed.

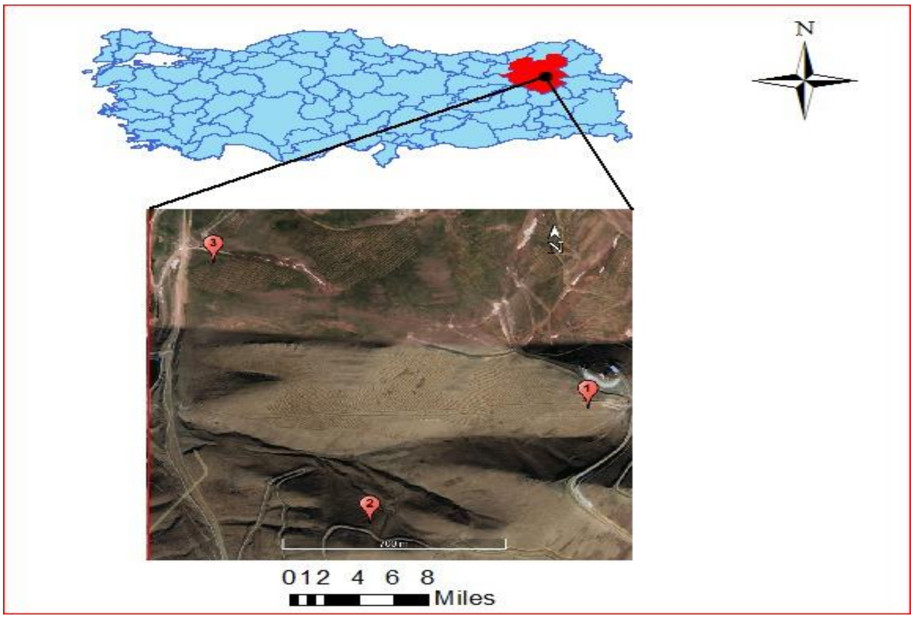

Figure 1. Location and Satellite Image of the Study Area

2.2. Soil Sampling

Soil samples were taken by random sampling method from the locations (1. 2. and 3.) determined at three different elevations (2941 m, 2762 m and 2501 m) in Erzurum Palandöken Mountain in July 2024. Nine undisturbed soil samples were taken from 0-10 cm, 10-20 cm and 20-30 cm depths using a 1000 cm³ cylinder. The samples were placed in plastic bags with labels with identifying characteristics and transported to the laboratory and made suitable for analysis. The sampling points were determined by considering the altitude, slope, aspect and vegetation characteristics of the region and were selected to investigate the potential effects on soil organic carbon (SOC) accumulation, soil skeleton ratio and bulk weight.

2.3. Soil Skeleton and Organic Carbon Calculations

2.3.1. Soil Skeleton Ratio

In order to determine the soil skeleton ratio, the soil samples were dried in an oven at 105°C for 24 hours. The dried samples were sieved using a sieve with a pore diameter of 2 mm and the coarse fractions remaining on the sieve were weighed using a precision balance. The total dry soil weight (W0) and the weight of coarse fractions remaining in the sieve (W1) were calculated using the following formula: (Corti et al., 2002).

Skelation ratio (%) = [W1/W0]×100

2.3.2. Calculation of Soil Organic Carbon (OC) Stocks

The %SOC values used in the calculation of SOC stocks were determined by the Walkley-Black method and the volume weight was determined according to Blake and Hartge (1986) (Walkey and Black 1934). In the calculation of SOC stocks, the amount of carbon in the soil depth (Mg C ha-¹) was calculated using the following formula (Tilaki et al., 2022).

$$SOC_s(Mg\ C\ ha^{-1}) = \frac{\%SOC}{100} \times Bd\left(\frac{mg}{m^3}\right) \times SD \times 10^4 \left(\frac{m^2}{ha}\right)$$

In the formula; %SOC: Percent soil organic carbon, Bd: soil volume weight, SD: Soil depth.

3. Results and Discussion

Soil properties such as SOC, SOC_s volume weight and skeleton ratio were analyses on soil samples. The evaluations of the determined soil properties are given in Table 1. According to Kacar (2009), the lowest organic carbon content was 1.78% in 10-20 cm depth of location 1, the highest carbon content was 3.31% in 0-10 cm depth of location 3, and the average organic carbon content was 2.61%. Organic skeleton ratios ranged between 39-79%, the highest skeleton ratio (78.51%) was determined at 20-30 cm depth of location 1, the lowest skeleton ratio (39.91%) was determined at 20-30 cm depth of location 2, and the average skeleton ratio of all soils was 60.41%. The bulk weight of all soils varied between 0,64- 1,29 g/cm^3. The lowest volume weight was 0,64 g/cm^3 at 0-10 cm depth of location 2, the highest volume weight was 1,29 g/cm^3 at 0-10 cm depth of location 1 and the average volume weight of all soil samples was 0,99 g/cm^3.

Table 1. Soil Skeleton Ratio, Volume Weight, Organic Carbon, Organic Carbon Stocks in the Study Areas

Location	Depth (cm)	Skeleton ratio (%)	Volume weight (g/cm^3)	Organic Carbon (%)	Organic Carbon Stock (Mg C ha^{-1})
1	0-10	68,36	1,29	2,46	31,73
	10-20	62,46	1,24	1,78	22,07
	20-30	78,51	1,15	1,94	22,31
2	0-10	57,47	0,64	3,27	20,92
	10-20	42,05	0,71	2,91	20,66
	20-30	39,91	0,99	2,42	23,96
3	0-10	59,88	0,78	3,31	25,81
	10-20	65,66	0,96	3,07	29,47
	20-30	69,44	1,16	2,34	27,14
Average		60,41	0,99	2,61	24,89

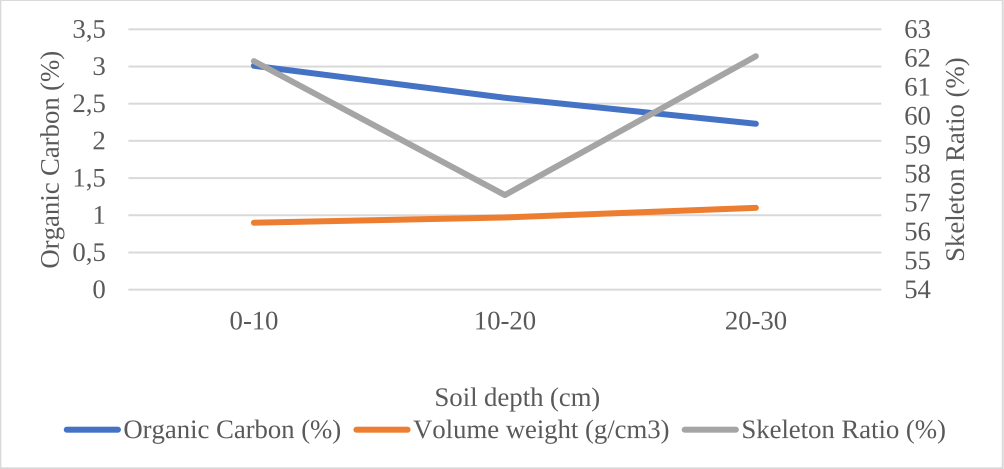

Figure 2. Figure 2. Average SOC, volumetric weight and skeletal ratios of different sampling points (1, 2, 3).

Figure 2 shows the average values (volume weight, skeleton ratio, organic carbon) of soil samples taken from 0-10 cm, 10-20 cm and 20-30 cm depths of locations 1, 2 and 3. It is expected that the skeleton ratio increases with soil depth. However, the low skeleton ratio of the soil samples taken from 10-20 cm depth at location 2 (Table 1) decreased the average skeleton ratio at 10-20 cm depth. This is thought to be due to the density of plant roots at this depth level.

In addition, it was observed that the volume weight increased gradually as the soil depth increased, whereas the organic carbon content decreased (Figure 2). The accumulation of organic carbon in the topsoil and its decrease in the deep layers is one of the main reasons for this situation. The increase in volume weight is associated with the decrease in the amount of organic matter and increase in the density of mineral components as the depth increases. These findings clearly demonstrate the inverse relationship between soil depth and physical and chemical properties.

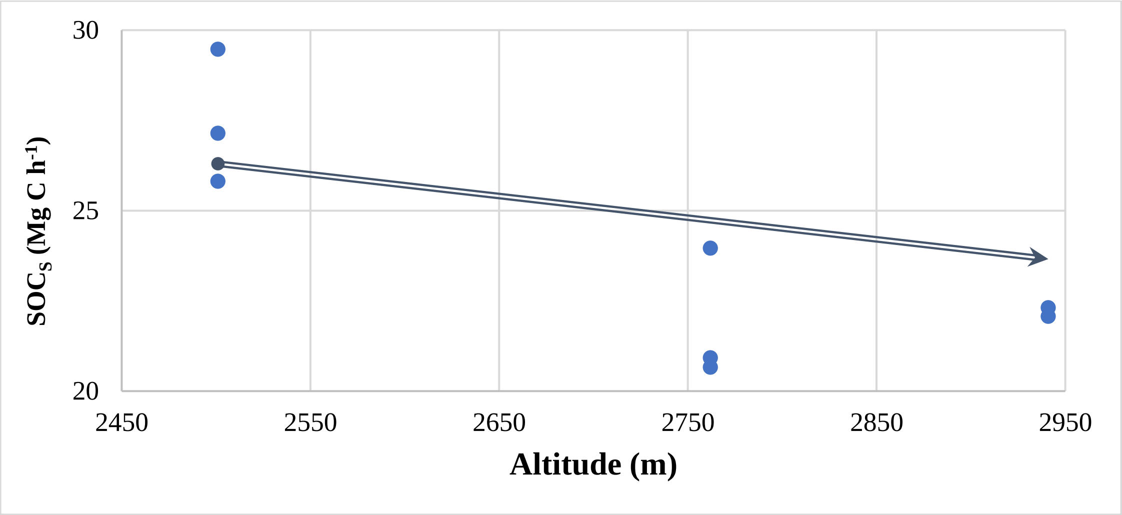

Figure 3. Relationship between Altitude and Soil Organic Carbon Stocks (SOC$_S$)

It is seen that SOCs tend to increase with decreasing altitude (Figure 3). However, the 0-10, 10-20 cm deep soil samples taken from the 2nd location were affected the trend line in SOCs calculations due to their low volume weight (Table 1).

Table 2. Correlation Matrix between Soil Properties

Features	Skeleton Ratio (%)	Volume weight (g/cm^3)	Organic Carbon (%)
Skeleton Ratio (%)	1.00	0.56	-0.34
Volume weight (g/cm^3)		1.00	-0.83
Organic Carbon (%)			1.00

According to the results of the correlation analysis presented in Table 2, a positive correlation was found between the skeleton ratio and volume weight (r = 0.56). This indicates that soil volume weight increases with the increase in stone and coarse fraction ratio. The increase in the skeleton ratio increases the volume weight by decreasing the soil voids and decreasing the porosity. In the studies, it is stated that the physical properties of stony soils have a tighter structure and therefore the volume weight increases. It supports the critical role of the skeleton ratio in the physical structure of the soil and similar results were observed in different soil types (Corti et al., 2002).

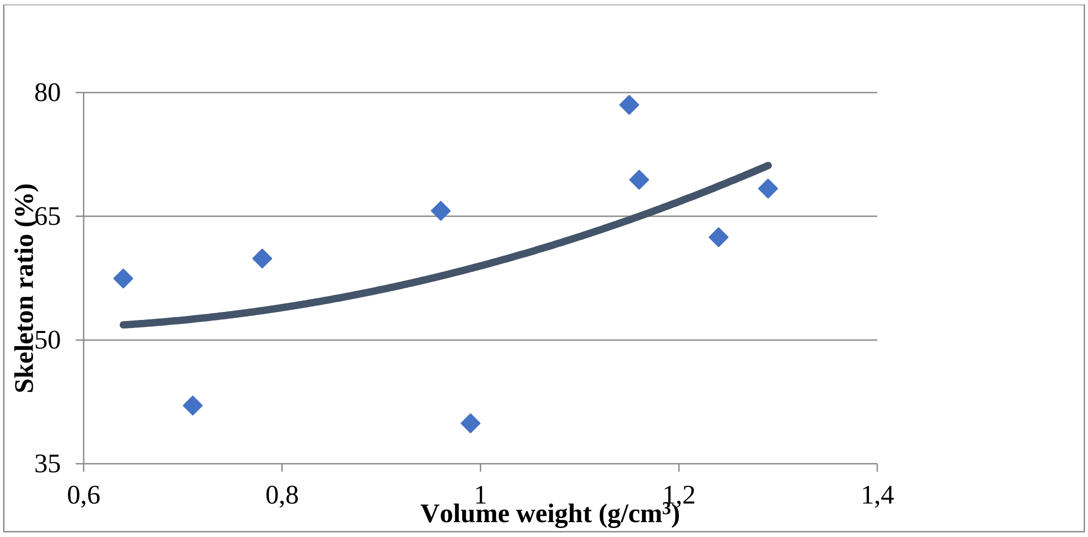

Figure 4. Relationship between volume weight and skeleton ratio

Table 2. A strong negative relationship was found between bulk density and organic carbon (r = -0.83). This result reveals that soils with high SOC content generally have lower volume weight (Figure 4). SOC increases the stability of soil aggregates and creates a hollow structure, which decreases the volume weight. This finding is in line with other studies in the literature describing the positive effects of organic matter on soil density (Céspedes-Payret et al., 2017).

Furthermore, Chen et al. (2024) emphasized that volume weight is a critical factor in estimating soil organic carbon stocks (Chen et al., 2024). The fact that soils with high organic carbon content have a looser structure once again reveals the importance of organic matter applications in terms of soil management.

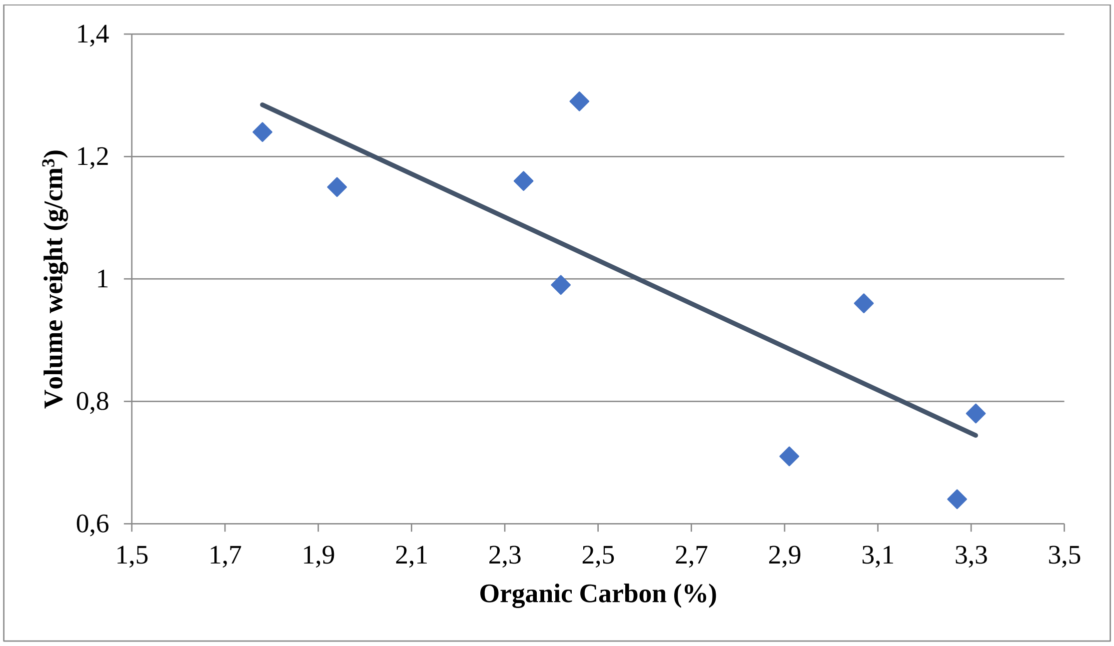

Figure 5. Relationship between organic carbon and volume weight

In Table 2, a weak negative correlation (r = -0.34) was found between skeletal ratio and organic carbon. This finding suggests that organic carbon accumulation may be restricted in soils with high skeletal ratio. Moreover, as seen in the graph, the increase in the skeletal ratio leads to a decreasing trend in the percentage of organic carbon (Figure 5). This relationship may have significant effects on soil properties and should be taken into consideration in terms of factors such as soil fertility, water holding capacity and workability.

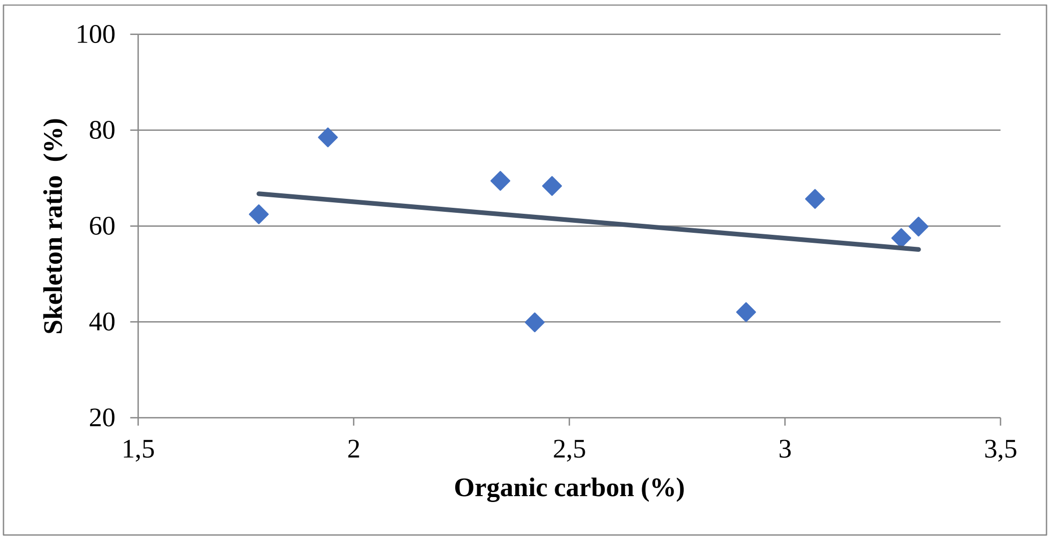

Figure 6. Relationship between organic carbon and skeleton ratio

The figure demonstrates a weak negative correlation (r = -0.34) between the skeleton ratio (%) and organic carbon (%). This suggests that higher skeleton ratios in soils may limit the accumulation of organic carbon. The data points indicate that as the skeleton ratio increases, the percentage of organic carbon tends to decrease, which aligns with the understanding that coarse soil fractions may impede organic carbon retention (Figure 6).

Six et al. (2002) proposed that stones and coarse fractions significantly influence the transport and accumulation of organic carbon within the soil profile. This observation highlights the potential challenges in carbon sequestration in stony soils. However, further research is required to explore the dynamics of this relationship under varying soil types, climatic conditions, and management practices. Understanding these dynamics, particularly in soils with high skeleton content, could provide valuable insights into the carbon cycle and contribute to more effective soil management strategies aimed at improving carbon storage.

4. Conclusion

In this study, the relationships between soil organic carbon (SOC), volume weight and skeleton ratio were investigated on undisturbed soil samples taken from different elevations (2941 m, 2762 m, 2501 m) and soil depths (0-10, 10-20, 20-30 cm) in Erzurum Palandöken Mountain. The results showed that SOC levels generally increased with decreasing altitude, but this trend was disrupted at the location where vegetation developed (2 locations). The excess of plant root biomass, which is thought to modify the trend, was found to lead to a decrease in volume weights and consequently affect SOCs.

A strong negative correlation (r = -0.83) was found between volume weight and SOC, and soils with high organic carbon content were generally found to have lower volume weight. On the contrary, a positive correlation (r = 0.56) was found between skeletal content and volume weight; an increase in stone and coarse fraction content decreased soil porosity and increased volume weight. A weak negative relationship (r = -0.34) was observed between skeletal fraction and SOC, suggesting that stone content has a limiting effect on organic carbon accumulation. In addition, further studies are recommended to understand the underlying causes of the relationship between skeletal ratio and soil organic carbon.

In conclusion, it is important to consider physical soil parameters such as bulk weight and skeletal ratio for the sustainability of soil organic carbon accumulation and storage processes in alpine belt ecosystems. These and similar studies may contribute to the development of both carbon management and sustainable soil management strategies.

Funding

The research was not supported by any organization.

Statement of Conflict of Interest

The author(s) should declare that they are no conflict of interest.

Authors' Contributions

Emre Çomaklı and Müdahir Özgül conceptualized the article idea, organized sample collection and analysis, conducted the research and compiled the data. Hüseyin Aydın contributed to the interpretation of the data, drawing graphs, creating tables and conducting analyses. In addition, Hüseyin Aydın drafted the all manuscript, Müdahir Özgül and Emre Çomaklı provided critical revisions, made necessary additions and supervised the overall preparation and completion of the manuscript.

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Organic Turnip Cultivation in Türkiye

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ABSTRACT: The continuous increase in the world population and the limited agricultural areas have made it necessary to increase the amount of product obtained from the unit area. This situation has put pressure on producers to use chemical fertilisers to increase production. However, the increasing use of chemical fertilisers has negatively affected sustainable agriculture. On the other hand, increasing global pandemics have further reinforced the importance of food security. Therefore, important countries of the world, including Türkiye, have turned to alternative methods in agricultural cultivation and the concept of organic agriculture has gained importance. However, some problems have emerged in terms of both government policies and agricultural practices in organic food production in Türkiye. This situation has caused various difficulties in organic turnip (*Brassica rapa* L.) production. As is well known, in addition to yield and economic return, the quality of the product is also very important. In this context, the importance of organic turnip has been proven by studies. In this study, it was aimed to provide a perspective on the current status of organic turnip cultivation in Türkiye and the challenges and solutions encountered in cultivation.

Keywords: Organic Turnip, Organic Agriculture, Production, Türkiye

INTRODUCTION

Turnip (*Brassica rapa* L.) is a plant belonging to the Brassicaceae family, the genus Brassica, the most economically important genus of this family, and the species *Brassica rapa*, which is consumed as a vegetable and forage plant (Raiola et al., 2018). Its cultivation is quite old (Cartea et al., 2011). Turnip, which is more resistant to cold than other vegetables, is a cool climate vegetable with highly nutritious properties. In addition to leaves and roots, flower buds can also be consumed by mixing with other vegetables. Its consumption as pickles and turnip juice is quite common (Fernandes et al., 2007; Haliloğlu et al., 2012; Azam et al., 2013).

As it is known, vegetables are important food sources for rational and healthy nutrition due to their active compounds and nutritional values, and especially vegetables whose roots and tubers are consumed have important nutritional value (Radovich, 2011; Barbu et al., 2022). Studies on turnips have shown that they have antimicrobial, antioxidant, antitumour, antidiabetic, painkiller, kidney and liver protective properties (Hong and Kim, 2008; Taveira et al., 2009; Li et al., 2010; Hosseini et al., 2013; Mohajeri et al., 2013). In addition, it has been proven that they contain good amounts of vitamin C and B6 and are rich in protein, fibre, thiamine, riboflavin and minerals (Ca, Mg, Fe and Zn) (Lyimo et al., 1991; Herbst, 2001; Choi et al., 2007).

Today's global epidemics and the diseases caused by these epidemics have led people to eat a healthy and balanced diet and to consume more fruits and vegetables in terms of nutritional and health benefits. However, the unbalanced distribution of food, waste and excessive increase in per capita consumption have increased the pressure on modern agriculture and led to more yield per unit area (Patel et al., 2020). This vicious cycle, which has continued from past to present, has forced the grower to produce more, more yield has been obtained from the unit area, but the quality has decreased. As production has increased worldwide, soil and environmental pollution have gradually worsened due to intensive agriculture and improper practices, leading to a growing search for sustainable and environmentally friendly alternative production techniques, driven by the effects of climate change. With these effects, the idea of organic agriculture has emerged and the countries of the world have started to talk about organic agriculture. The aim of organic agriculture is to correct the ecological balance that has been disturbed as a result of the traditional and conventional agricultural methods that have been applied and are still being applied, to minimise or not to use agricultural inputs and activities that cause the deterioration of this balance, to use natural preparations instead of fertilisers and pesticides that are harmful to soil, environment and human health (Kayahan, 2001; Kirazlar, 200; Demir et al., 2003). To address this, organic farming has been embraced globally, including in Türkiye, as a means of promoting sustainable agriculture. With the growing awareness of environmental issues and consumption, both the number and volume of organic products have been steadily increasing (Üçok et al., 2019).

Given the increasing awareness of the environmental impacts of conventional agricultural practices and the growing demand for sustainable and organic products, it can be hypothesized that organic turnip farming in Türkiye is on the rise, both in terms of the number of farmers involved and the production area allocated to it. This trend is likely influenced by the nutritional and health benefits of turnips, as well as their potential to thrive under organic farming conditions due to their resilience to cold climates and adaptability to various cultivation methods. Furthermore, the global focus on sustainable agriculture and the preference for environmentally friendly production techniques could play a significant role in shaping the dynamics of organic turnip farming in the region. In particular, Türkiye’s geographical and climatic advantages provide suitable conditions for organic turnip cultivation, can be enabling high yields with minimal environmental impact. Therefore, this study was carried out to evaluate the number of farmers engaged in organic turnip production, production area and production amount in Türkiye.

Materials and Methods

This study is based on extensive data collected from various publications, including scientific articles and published reports. Data from the Turkish Statistical Institute (TurkStat) and the FiBL Statistics database were used as primary sources for statistical analysis. The main indicators analysed are as follows: the current state of organic production globally and in Türkiye, as well as data on the number of producers, production area, and production quantity in organic turnip cultivation in Türkiye. The data on organic production and organic turnip production in Türkiye were visualised and supported through graphical illustrations. These graphs were specifically created to emphasise the production differences in organic production and organic turnip cultivation in Türkiye over the years. In addition, a polynomial regression analysis was conducted to investigate the relationship between the organic turnip production area and production quantity. The regression equation was formulated as follows:

$$\text{Production Quantity} = -6.9408 + 5.7108(\text{Production Area}) - 0.3341(\text{Production Area}^2)$$

Results and Discussions

The first agricultural inputs, such as seeds, seedlings, and saplings, were obtained from nature during the earliest stages of agriculture, and the agricultural development process advanced further with the introduction of inputs such as water and animal manure. However, this progress also caused environmental degradation. Traditional agricultural activities persisted for centuries, but by the 1700s, the use of chemical fertilisers disrupted the biological and chemical balance of soils. Consequently, the resistance of cultivated plants to diseases and pests declined, prompting the development and use of chemical preparations to counteract these issues. A significant increase in yield was achieved, and with the industrial revolution, industrialised production replaced traditional agricultural practices (Sürmeli, 2003). Over time, these changes led to a rapid and almost unsustainable deterioration of the natural balance (Ak, 2004).

The concept of organic agriculture began to emerge as a response to these environmental challenges, and the International Federation of Organic Agriculture Movements (IFOAM) was established in Germany in 1972. Since the 1980s, organic agriculture has evolved into a commercial sector in response to the growing consumer demand (Dalbeyler and Işın, 2017). Worldwide, significant progress has been made in organic farming. For example, while only 15 million hectares were devoted to organic farming in 2000, this area expanded to 96.4 million hectares by 2022. Furthermore, current data shows that organic farming is now practiced in 188 countries. Organic farming occupies approximately 2% of the world's total agricultural land, with Liechtenstein (43%), Austria (27.5%), and Estonia (23.4%) leading in terms of land share.

There has also been a substantial increase in the number of organic producers globally. The number of producers rose from 200,000 in 1999 to 4.5 million in 2022. India has the highest number of organic producers (2,480,859), followed by Uganda (404,246) and Thailand (121,540). From an economic perspective, the organic agriculture market is expanding rapidly. The United States leads the market with a share of EUR 58.6 billion within the global organic agriculture market, valued at EUR 134.8 billion, followed by Germany (EUR 15.3 billion) and China (EUR 12.4 billion) (FIBL, 2024).

In many countries, farmers took the lead in the development of organic agriculture. However, in Türkiye, the initial promotion and cultivation efforts were driven by private companies (Aksoy and Altındişli, 1999; Demiryürek, 2004). The establishment of the Ecological Agriculture Organization (ETO) in 1992 marked a significant step in this direction. As the global recognition of organic farming grew, many countries included it on their policy agendas and introduced laws to foster its development. Reflecting this growing importance, Türkiye passed the Organic Agriculture Law in 2004 and the Regulation on the Principles and Practices of Organic Agriculture in 2010. Moreover, data collection on organic agriculture began in 2002, and a systematic record-keeping process has been in place ever since.

An analysis of organic agriculture data in Türkiye reveals fluctuations in the number of producers with TR certification, as well as in organic production areas and outputs, due to commercial factors such as marketing and costs. The number of producers increased from 313 in 1990 to 26,181 by 2013 (including those in the transition process), despite some fluctuations during the 2001-2008 period. Between 2013 and 2023, the number of producers initially increased until 2018 but then experienced a steady decline, with the number reaching 34,358 in 2023.

Similarly, the total organic production area, which includes both cultivated areas and areas collected from nature, exhibited fluctuations between 2002 and 2009, followed by a steady increase during 2009-2013. However, from 2013 to 2023, the total area showed an overall decreasing trend despite occasional increases in certain years. The organic production area, which was 89,827 hectares in 2002, expanded sixfold to 558,838 hectares by 2013 but subsequently declined to 224,913 hectares in 2023.

The organic product output in Türkiye, which was 310,125 tonnes in 2002, steadily increased until 2012. While production decreased slightly in 2013, the period from 2013 to 2023 saw alternating years of increase and decrease due to fluctuations. In 2023, organic product production amounted to 1,028,888 tonnes, marking an approximate 11% decrease compared to the previous year. However, compared to 2013, this represents a 12% increase, and compared to 2002, an impressive 231,766% growth was observed (Figure 1).

Regarding the Turkish organic market, current data indicate that approximately 59,000 tonnes of organic products were exported, generating an income of 164 million dollars. Imports, on the other hand, were recorded at 10,233 tonnes (Ministry of Agriculture and Forestry, 2024).

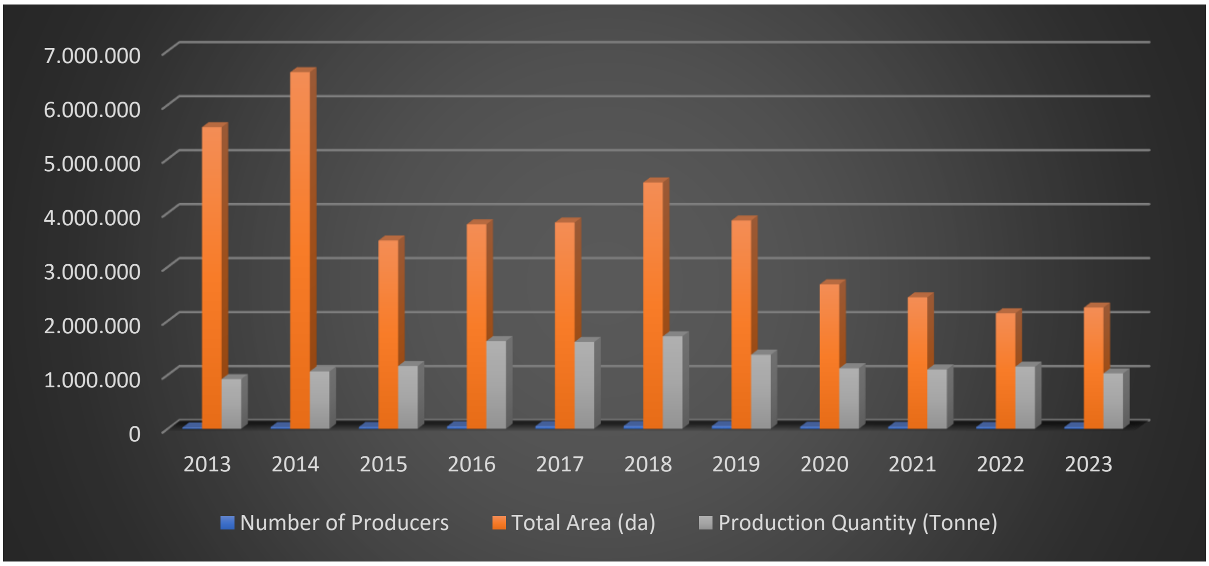

Figure 1. Türkiye Organic Crop Production Data of the Last 10 Years

When the data on organic turnip production in Türkiye are analysed, it is evident that no information exists regarding the number of producers until 2021 and the total production area until 2020. Although the number of producers involved in organic turnip cultivation is very limited, records indicate the presence of organic turnip growers in the provinces of Afyonkarahisar, Balıkesir, Bursa, Çanakkale, İstanbul, İzmir, Sakarya, and Zonguldak, albeit in small numbers. Based on the most recent data, the number of organic turnip producers in 2023 was highest in Bursa and Zonguldak provinces, each with two producers, while one producer each was recorded in İstanbul and Sakarya. Although organic turnip growers were present in Afyonkarahisar, Balıkesir, Çanakkale, and İzmir in previous years, no data were recorded for these provinces in 2023 (Figure 2).

One of the most significant challenges in organic agriculture, including organic turnip cultivation, is the lack of organisation among producers (Kahveci and Ataseven, 2020).

Additionally, producers often struggle to find a market for their organically grown turnips, forcing them to sell their products at prices much lower than their value, thereby incurring financial losses. Another critical issue is the ambiguity of the regulations determining the limits and processes for support schemes related to organic agriculture, particularly at the beginning of the production year. This lack of clarity negatively impacts production planning. Furthermore, area-based organic agriculture subsidies are often insufficient, especially for small-scale producers. To address these challenges, it is essential to transition away from the area-based support model. Instead, establishing organic agriculture production zones and implementing product-based support mechanisms should be prioritised to ensure the sustainability and growth of organic agriculture (Anonymous, 2024).

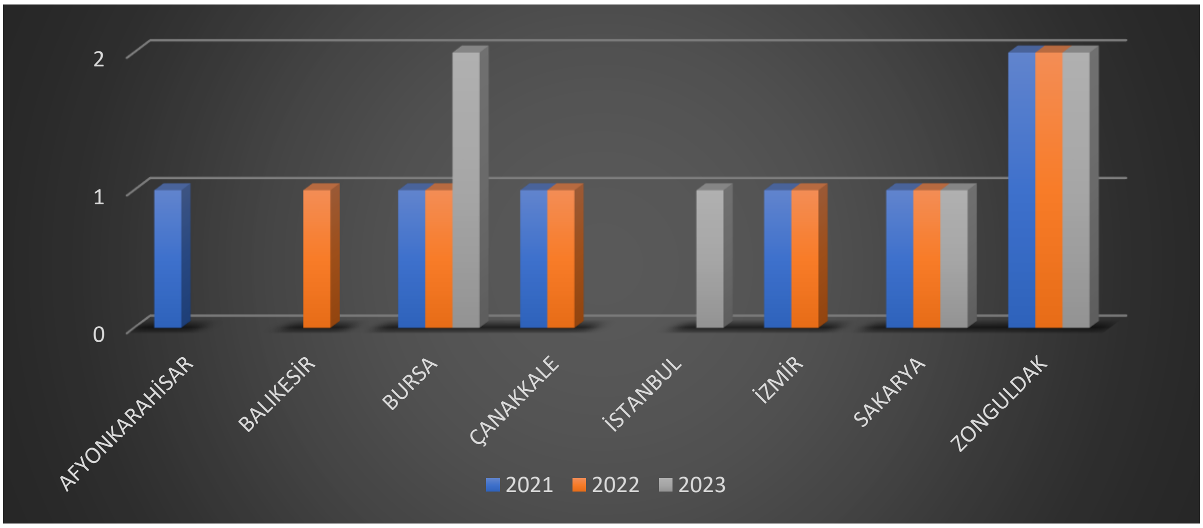

Figure 2. Number of Organic Turnip Producers in Türkiye

An examination of the total area (da) of organic turnip cultivation reveals that production takes place in Afyonkarahisar, Balıkesir, Bursa, Çanakkale, İstanbul, İzmir, Sakarya, and Zonguldak provinces. Despite fluctuations, consistent cultivation has been observed in Bursa, İzmir, and Zonguldak from 2020 to 2023. Upon analysing the areas under organic turnip cultivation, it is clear that Bursa (0.10 da) has the largest production area as of 2023, while Sakarya (0.03 da), İzmir (0.01 da), and Zonguldak (0.01 da) also have relatively small cultivation areas (Figure 3).

The small and fragmented structure of organic farms in Türkiye contributes to the cultivation of crops on limited areas, often located close to conventional farming areas (Akyüz and Theuvsen, 2021). Furthermore, it is critical to support research and development projects aimed at the development of varieties and stems suitable for organic farming, the identification of areas conducive to organic agriculture, and the encouragement of farmers to adopt organic production with regionally appropriate species and varieties. These efforts should leverage Türkiye's diverse ecological conditions and rich genetic resources (Anonymous, 2024). Such initiatives are crucial, as they directly impact the ability of organic turnip farmers to expand their operations. It is believed that a sustained increase in the total cultivation area could be achieved if the necessary regulatory and support measures are implemented effectively.

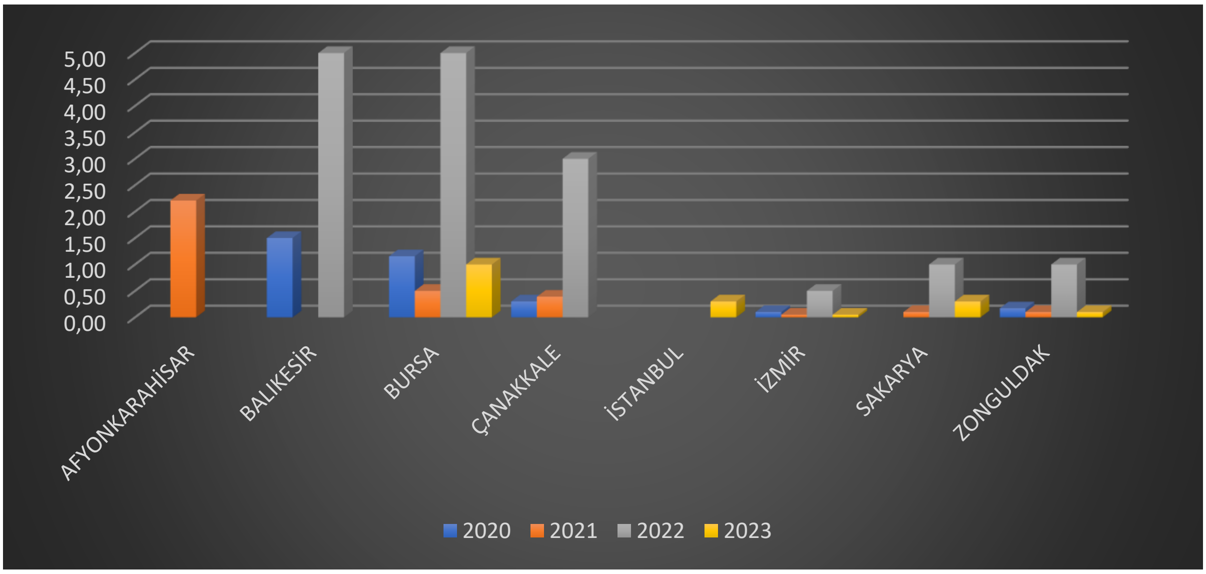

Figure 3. Provinces of Organic Turnip Cultivation in Türkiye and Total Production Area (da)

The analysis of organic turnip production data reveals that records of cultivation have been collected from the provinces of Afyonkarahisar, Aydın, Balıkesir, Bursa, Çanakkale, Erzurum, Eskişehir, İstanbul, İzmir, Manisa, Sakarya, and Zonguldak. As shown in Figure 4, with the exception of Zonguldak, there were years where cultivation did not occur in some other provinces. However, despite fluctuations, it can be observed that organic turnip cultivation has been consistently carried out in Zonguldak province every year. In 2015, no data on organic turnip cultivation was found. When examining the amount of organic turnip production, it is evident that Bursa province had the highest production amount in 2023, with 1.5 tonnes. Bursa is followed by Sakarya (0.30 tonnes), İzmir (0.20 tonnes), Zonguldak (0.13 tonnes), and İstanbul (0.01 tonnes) (Table 4). As can be seen in the tables, although production data are available for Aydın, Erzurum, Eskişehir, and Manisa provinces, the area of production and the number of producers are not available. This situation indicates that there is no comprehensive database and transparent flow of information about organic agriculture in Türkiye. One of the primary reasons for the low turnip production amounts is the low yield during the initial years of organic cultivation. As shown in Table 4, producers tend not to continue regular production due to lower yields compared to conventional farming, often abandoning the practice because of these initial challenges. To ensure sustainable production, producers should be supported and educated on sustainable soil management and crop fertility practices. By identifying the causes of decreased production, solutions can be developed to increase production levels (Karabaş and Gürler, 2015; Arslan, 2022).

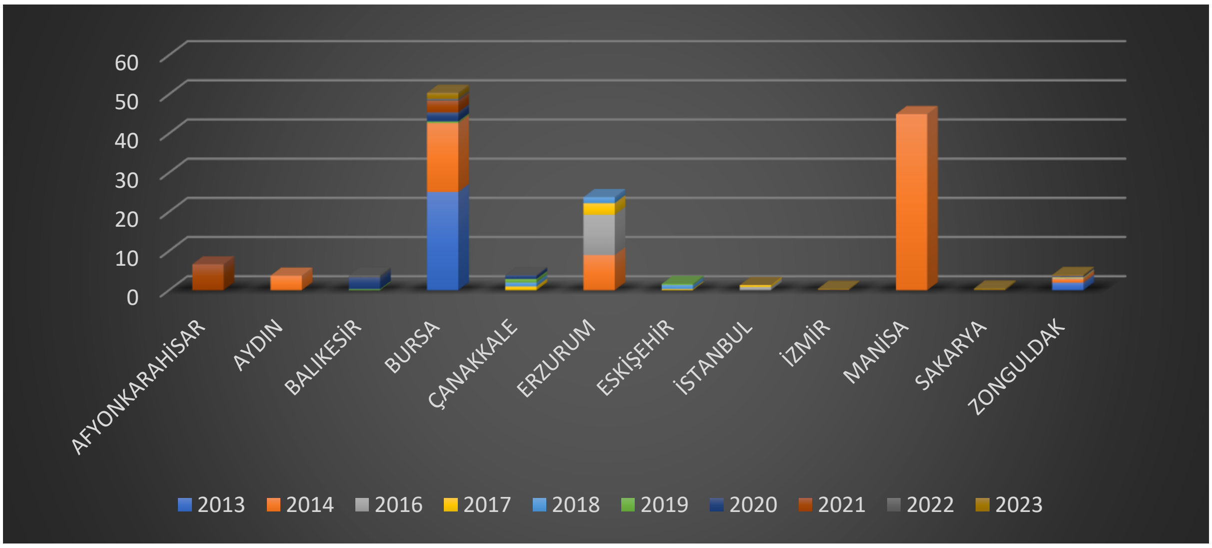

Figure 4. Provinces and Production Amount of Organic Turnip in Türkiye (Tonnes)

Furthermore, Türkiye is home to 42 organic agriculture control and certification organizations. According to the latest data, these organizations are distributed as follows: 20 in Izmir, 5 in both Istanbul and Ankara, 3 in Mersin, 2 in Antalya, and 1 each in Yalova, Kayseri, Denizli, Adana, Gaziantep, Aydın, and Afyonkarahisar (Ministry of Agriculture and Forestry, 2024). This geographical concentration of control and certification bodies increases the cost for producers cultivating organic turnips outside these regions (Acıbuca et al., 2018). As a result, many producers are discouraged from continuing organic turnip cultivation. Additionally, the high prices of organic products, combined with the relatively low income levels of consumers, have prevented domestic demand from reaching the desired levels (Çınar and Göktaş, 2019). The significant price gap between conventional and organic products often leads consumers to choose conventional options (Ece, 2008). It is believed that improving consumer income levels and raising awareness about organic products could stimulate demand for organic turnips and, in turn, boost production.

Moreover, a Polynomial Regression Analysis was conducted using the R statistical program to assess the relationship between the production volume over the last four years and the total production area.

Upon reviewing the descriptive statistics, it is evident that the total area varies between 1.75 and 15.50 decares (mean = 5.957), while the production amount ranges from 1.302 to 9.867 tonnes (mean = 4.948) (Table 1).

Table 1. Descriptive statistics of the variables used in the model

Variable	Minimum	Maksimum	Mean
Total Area	1,750	15.500	5.957
Production Quantity	1.302	9.867	4.948

The results of the polynomial regression analysis of organic farming data reveal a non-linear relationship between area and production volume. The coefficient of determination (R^2) of the model was calculated at 0.9085, indicating that approximately 91% of the variability in the dataset is explained by the model. The adjusted R^2 value was determined to be 0.7254.

This equation suggests that the production amount initially increases with an increase in area ($\beta = 5.7108$), but as the area continues to expand, production tends to decrease in line with the law of diminishing returns ($\beta = -0.3341$). This finding implies that there may be an optimal enterprise size in organic farming.

The residual values of the model range from -1.527 to 1.426, demonstrating that the predictive power of the model is reasonable. However, the small size of the dataset (n=4) and the P-value of the F-statistic being 0.3025 ($P > 0.05$) suggest that the statistical significance level of the results is limited (Table 2.).

Table 2. Results of Polynomial Regression Analysis

Variable	Katsayı	Standart Hata	t değeri	*P* değeri
Constant Term	-6.9408	5.4623	-1.271	0.424
Total Area	5.7108	2.2964	2.487	0.243
Total Area^2	-0.3341	0.1267	-2.637	0.231

**Model Statistics: - $R^2 = 0.9085$, - Corrected $R^2 = 0.7254$. - F-statistic = 4.963 (df: 2,1)

Conclusion

Due to its geographical location, Türkiye holds significant potential for both domestic and international markets. With the rise of organic agriculture, the Turkish agricultural economy has undergone a qualitative transformation since the early 2000s. However, it is evident that this potential has not been fully utilized. While organic agriculture is on the rise globally, it has shown a declining trend in Türkiye. Although there has been considerable progress since the initial records in 2002, recent years have seen a gradual decrease in the rate of growth. There are several reasons for this trend, and these reasons are interrelated.

Organic turnip cultivation, which is gaining increasing importance from both an economic and health perspective, has also been affected by this trend. While it occupies a significant place in global production, it has not attracted the attention it deserves in Türkiye. One of the primary reasons for this underperformance is the challenges faced by producers in transitioning to organic farming. Lower yields and higher costs compared to conventional agriculture are significant obstacles, making it difficult for producers to sustain organic turnip production. These economic challenges, coupled with inadequate knowledge dissemination among producers regarding sustainable agricultural practices, hinder the expansion of organic turnip cultivation.

Moreover, the high prices of organic products, combined with the relatively low income levels of consumers, have limited the demand for organic products in Türkiye. The price disparity between conventional and organic products often drives consumers toward conventional options. It is believed that improving consumer income levels and increasing awareness about the health benefits and environmental advantages of organic products will likely drive greater demand for organic turnip consumption, thereby boosting production.

The growth of organic agriculture in Türkiye is not only dependent on increasing production volumes but also on enhancing regulatory frameworks, developing targeted strategies, and providing more robust support to producers. Identifying suitable areas for organic cultivation and directing producers to these areas with appropriate varieties and species tailored to organic farming conditions are critical steps in fostering the growth of the sector. Türkiye’s diverse ecological conditions and rich genetic resources present a unique advantage for developing sustainable organic farming solutions.

Additionally, the 42 organic agriculture control and certification organizations in Türkiye play a pivotal role in enabling producers to market their products domestically and internationally. However, the complex and costly certification processes pose significant barriers, especially for small-scale farmers. Streamlining these certification processes and making them more accessible and supportive for producers could help foster the growth of organic turnip production.

Furthermore, the results of the polynomial regression analysis highlight a non-linear relationship between production area and output. Initially, as the area of production increases, output increases as well, but beyond a certain point, further increases in production area may lead to diminishing returns. This suggests that there may be an optimal farm size for organic farming, where efficiency and productivity are maximized.

In conclusion, organic farming, and in particular organic turnip cultivation, holds significant potential for Türkiye. However, to fully realize this potential, it is essential to address the challenges faced by producers, including the need for better education, more accessible certification, and greater market support. Efforts to improve consumer awareness and raise income levels will also be critical in boosting domestic demand for organic products. A well-coordinated approach, involving regulatory bodies, producers, and consumers, could enable Türkiye to establish itself as a key player in the global organic farming sector. With the right measures in place, organic turnip production could contribute significantly to the development of sustainable agriculture in Türkiye.

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Estimation of Agricultural Mechanization Levels in Erzurum and Its Districts Using ARIMA Model

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ABSTRACT: It is well known how important agricultural mechanization is in increasing the productivity and quality of agricultural products. Tractors are used as the main power source for operating other agricultural machinery, apart from self-propelled machines. Therefore, making predictions about tractor availability and mechanization levels is important for developing future planning. In this study, data for Erzurum province and its districts from 1995 to 2023, obtained from the Turkish Statistical Institute (TUIK), have been forecasted for the years 2024-2028, considering five different agricultural mechanization level indicators. The 5-year future forecasts were determined using the ARIMA model, which is frequently used in time series analysis of agricultural data and capable of making accurate predictions. According to the analysis results, the number of tractors across Erzurum reached its highest level with a 25.49% increase between 2018 and 2023, and is expected to increase by 8.59% over the next five years. By 2028, it is expected that the number of tractors in the province will be 15,508, the average tractor power will be 43.75 kW, the tractor power per unit area will be 1.58 kW ha^{-1}, the area per tractor will be 27.2 ha tractor^{-1}, the number of tractors per 1000 hectares of land will be 36.50 tractors 1000 ha^{-1}, and the number of equipment per tractor will be 5.71 equipment tractor^{-1}. By 2028, the highest increase in the number of tractors is expected to be in the district of Karaçoban, with a rate of 56.23%, while the highest decrease is anticipated in the district of Tekman, with a rate of 38.51%. In the northern districts of the province, small increases in the number of tractors are expected by 2028, depending on the land and crop patterns. Significant differences are expected in the number of tractors in the central and surrounding districts where field farming is intensively practiced by the year 2028.

Keywords: Agricultural Mechanization Level, ARIMA Model, Erzurum

INTRODUCTION

With the rapidly increasing population worldwide and global climate change, especially in recent years, access to basic food items has become more difficult as a result of pandemics, political, and economic crises. Increasing productivity and quality in plant production depends not only on fundamental input factors such as selecting seeds suitable for climate and geographical conditions and providing plant nutrients, but also on current technology investments and the effective use of agricultural mechanization technology per unit of time.

Recent developments and applications in agricultural machinery and technology are important for the sustainability of agricultural production.

In agricultural mechanization planning, the appropriate selection and proper planning of tractor-equipment combinations, which constitute the majority of operational costs, are crucial for economic profitability (Bilim et al., 2014). The use of machinery in agriculture is important for incorporating new areas into cultivation, performing operations effectively in a short time, and increasing employment opportunities through advancements in the agricultural machinery manufacturing industry (Ertekin et al., 2021).

Today, with the advancement of agricultural mechanization, the effective use of agricultural tools and machinery in field applications has gained importance. The most fundamental component of the development level of agricultural mechanization is the availability of tractors. Increasing the use of machinery in agricultural production and raising the mechanization level to the average of developed countries will contribute to Türkiye's industrial growth (Altuntaş, 2020). Agricultural production, which is influenced by economic and climatic conditions in the short term, can also be affected by the annual and long-term availability of tractors and agricultural machinery in enterprises (Civelek, 2021). The most important indicators defining the level of agricultural mechanization include the quantitative and qualitative status of the tractor fleet, its development over the years, its relationship with agricultural machinery, its density per unit of agricultural land, and its power level (Özgüven et al., 2010). Agricultural mechanization, however, varies depending on geographic and topographic structure, climatic conditions, the crops produced, and even the economic structure (Koçtürk and Avcıoğlu, 2007). To objectively discuss the mechanization status of regions with differing agricultural structures, it is useful to compare these criteria across regions (Evcim et al., 2015). Therefore, it is believed that examining the levels of agricultural mechanization on a regional basis, identifying deficiencies, and finding solutions to the encountered problems will contribute to regional production and the increase in the level of mechanization.

The estimated number of tractors expected in the coming years is valuable for the healthier planning of activities that tractor, equipment, and spare parts dealers and manufacturers will carry out in the following years (Civelek, 2021). The estimation of the presence of tractors, which are used as a power source in agricultural mechanization, is a difficult problem to determine because it depends on many variables, such as the economic situation of the businesses, land size, equipment availability, agricultural activities carried out, and users' personal preferences.

By predicting the level of mechanization in agricultural production for the future, strategies and policies can be developed that are aligned with the desired outcome of increasing the level of mechanization (Malaslı et al., 2016). It is essential to plan the predicted scenarios well for public and private sector organizations to improve or update their current situation for the future (Hamleci, 2017). Many researchers have conducted studies on these topics. (Gül et al., 2023; Dertlioğlu and Altuntaş., 2022; Gül et al., 2022; Aybek et al., 2021; Altuntaş, 2020; Kuzu et al., 2020; Abdikoğlu, 2019; Malaslı et al., 2016;). The studies conducted have shown that in predicting the number of tractors, the univariate ARIMA model provides statistically reliable results in the short term compared to multivariate models (Biondi et al., 1998).

This study aims to examine the level of agricultural mechanization in the province and districts of Erzurum between 1995 and 2023, and to predict agricultural mechanization indicators along with tractor presence for the years 2025-2028.

Material and Method

In the study, data for the years 1995-2023 regarding cereals, other crop fallow and vegetable areas, two-axle tractor numbers, and agricultural tools and machinery for the province and districts of Erzurum were obtained from the Turkish Statistical Institute (TUIK). The 5-year forecasts for the variables for the years 2024-2028 were obtained using the Autoregressive Integrated Moving Average (ARIMA) Model, which is commonly used in agricultural time series and is an accurate model for short-term forecasting. This model, proposed by Box and Jenkins in the 1970s, consists of AR, I, and MA components. The AR (Autoregressive) model represents the Autoregressive process, I represent the integration indicating the order of differencing, and MA represents the Moving Average model. In the ARIMA (p, d, q) model, p represents the order of the autoregressive model, d represents the number of differencing, and q represents the order of the moving average model (Yıldırım and Alkan 2018; Uzundumlu et al. 2019). The ARIMA model, which is generally used for stationary series, is also applied to non-stationary series by performing differencing to make them stationary. The differencing operation, which represents a single integer order, usually takes the values of 1 or 2. The stationarity of time series is determined by unit root tests (Duru, 2007). When the time series of the variables representing the level of mechanization for the province and districts of Erzurum was examined, it was found that the variables were stationary and suitable for the ARIMA model.

The ARIMA (p, d, q) model is expressed as a combination of the differencing and the ARMA (p, q) model (Ma et al., 2018). The ARIMA model is expressed as follows (Shumway et al. 2017).

$$x_t = \alpha + \emptyset_1 x_{t-1} + \emptyset_2 x_{t-2} + \cdots + \emptyset_p x_{t-p} + \theta_1 \varepsilon_{t-1} + \theta_2 \varepsilon_{t-2} + \cdots + \theta_q \varepsilon_{t-q} + \varepsilon_t$$

x_t represents the value of the time series at time t, ∅(i) represents the autoregressive (AR) parameters, x(t-i) represents past observations, θ_i represents the moving average (MA) parameters, ε_(t) represents the error term, p represents the order of the autoregressive model, d represents the order of differencing, and q represents the order of the moving average model. (Zhang, 2003). The ARIMA model was analyzed using the Least Squares Method, taking into account the Eviews software package, which is frequently used for data analysis and forecasting in statistics and econometrics. The Augmented Dickey-Fuller (ADF) test for stationarity was performed on each series for the province and districts of Erzurum, and it was found that the series are stationary. The most suitable ARIMA model for the series was determined by making various trials, in addition to the software's suggestion, and a different ARIMA model was identified for each parameter and district. The ARIMA model determined for each parameter was analyzed, and the mechanization level forecasts for the years 2024-2028 for the province and districts of Erzurum were made.

Table 1 shows the agricultural production areas for the province and districts of Erzurum. The district with the largest agricultural area in Erzurum is Horasan, with 675588 decares, while the district with the smallest production area is Uzundere, with 25115 decares. (Table 1).

Table 1. Agricultural production areas of Erzurum province and districts (TUIK 2023)

District Name	Field crops area (da)	Fallow area (da)	Vegetable production area (da)	Total area (da)
Merkez	324881	26823	1068	352772
Aziziye	245199	41334	639	287172
Aşkale	170293	37614	0	207907
Horasan	657626	17862	100	675588
Hınıs	178042	22127	350	200519
Karayazı	388987	14017	0	403004
Karaçoban	127866	13504	34	141404
Köprüköy	243461	3073	0	246534
Narman	219317	8628	26	227971
Oltu	74045	25069	834	99948
Olur	33709	4931	622	39262
Pasinler	355480	6460	5677	367617
Pazaryolu	39851	13528	503	53882
Tekman	186840	7207	0	194047
Tortum	121018	27732	2291	151041
Uzundere	13305	11050	760	25115
Çat	172050	18082	0	190132
İspir	74335	9049	1796	85180
Şenkaya	139886	12887	230	153003
TOTAL	**3766191**	**320977**	**14930**	**4102098**

Tractors are classified into six groups based on their power values, and the average power values provided in Table 2 have been used to determine the total power value (Kuzu et al., 2021; Gül et al., 2022; Gül et al., 2023). The indicator of the number of equipment per tractor is determined by the numerical data of the implements and machinery used with two-axle tractors, including soil preparation tools and machinery, planting, maintenance and fertilization machinery, plant protection machinery, harvesting and threshing machinery, as well as some other machinery. The agricultural tools and machinery used in the calculation are provided in Table 3.

Table 2. Average power value groups of tractors

Tractor Group	Average Power (HP)
Tractor Two Axle (1-10 HP)	5.5
Tractor Two Axle (11-24 HP)	17.5
Tractor Two Axle (25-34 HP)	29.5
Tractor Two Axle (35-50 HP)	42.5
Tractor Two Axle (51-70 HP)	60.5
Tractor Two Axle (Greater than 70 HP)	85

Table 3. Agricultural tool and machines used in calculations

Agricultural tools and machinery	Agricultural tools and machinery
Ear Tractor Plow	Corn Silage Machine
Moldboard Plow	Corn Shelling Machine
Disc Tractor Plow	Selector (Fixed or Mobile)
Disc Stubble Plow (Vanvey)	Feed Preparation Machine
Ear Stubble Plow	Stalk Chopping Machine
Soil Rotavator (Rotavator)	PTO-Driven Pulverizer
Cultivator	Atomizer
Roller	Centrifugal Pump
Disc Harrow (Discarrows)	Deep Well Pump
Tine Harrow	Trailer (Agricultural Wagon)
Combination Harrow (Mixed Harrow)	Water Tanker (Used in Agriculture)
Hay Rake	Subsoiler
Tractor-Pulled Grain Seeder	Rototiller
Combined Grain Seeder	Stone Collection Machine
Potato Planter	Soil Leveling Machine
Farm Manure Spreader	Bed Forming Machine
Chemical Fertilizer Spreader	Soil Auger
Reaper	Pneumatic Seeder
Combine Harvester	Universal Seeder (Including Beet Seeder)
Baler	Stubble Seeder
Threshing Machine	Stalk Thresher and Threshing Machine (Batöz)
Potato Digger	Stalk Collection and Straw Making Machine
Combined Potato Harvester	Straw Transfer-Unloading Machine
Beet Digger	Feed Distributor Trailer
Combined Beet Harvester	Bucket (Used in Agriculture)
Tractor-Pulled Grass Mower	Stone Crushing Machine
Silage Machine	

The mechanization level for each year from 1995 to 2023 has been determined using the number of two-axle tractors, total tractor power, cultivated land areas, and agricultural tools and machinery used in Erzurum province and districts, based on the national and international criteria listed below. The criteria used to determine the mechanization level are presented below.

1. Average tractor power (kW),
2. Tractor power per cultivated area (kW ha^{-1}),
3. Agricultural area per tractor (ha tractor^{-1}),
4. Number of tractors per thousand hectares of agricultural land (tractor 1000 ha^{-1}), and
5. Number of equipment per tractor (equipment tractor^{-1}).

The statistical relationship between agricultural mechanization criteria and the number of tractors was analyzed using correlation analysis in the IBM SPSS 2022 software.

Results and Discussion

To determine the level of agricultural mechanization, the total area of cereal, fallow, and vegetable farming, the number of two-axle tractors, and the agricultural tools and machinery intensively used in agricultural activities from 1995 to 2023 in the province have been considered. In the study, five criteria were considered to determine the mechanization indicators: average tractor power (kW), tractor power per cultivated agricultural area (kW ha^{-1}), cultivated agricultural area per tractor (ha tractor^{-1}), number of tractors per 1000 hectares of cultivated area (tractor 1000 ha^{-1}), and number of equipment per tractor (equipment tractor^{-1}).

As the number of tractors increases, the tractor power per unit area also increases, and a statistically positive relationship has been identified between them (Pearson Correlation: 0.909** P=0.000). As the number of tractors increases, the area per tractor decreases, and a statistically negative relationship has been found between them (Pearson Correlation: -0.824** P= 0.000). The number of tractors per 1000 hectares increases, and a statistically positive relationship has been found between them (Pearson Correlation: 0.870** P= 0.000). Similarly, the number of equipment per tractor also increases, and a statistically positive relationship has been found between them (Pearson Correlation: 0.885** P= 0.000), which is highly significant.

The changes in the number of tractors and mechanization indicators for the province between 1995 and 2023, along with the forecasted values for the next five years using the ARIMA model, are presented in Table 4. For the average number of tractors in Erzurum province, the ARIMA (2,1,1) model was used, while the ARIMA (0,1,1) model was applied for tractor power per unit area, area per tractor, number of tractors per 1000 hectares, and the number of equipment per tractor. For the districts, the most suitable and significant ARIMA models were selected and analyzed. Accordingly, between 1995 and 2023, the number of tractors in Erzurum has generally increased, despite small decreases in some years. In 2023, there are 1460185 two-axle tractors in the country, and Erzurum, with 13461 tractors, makes up 0.92% of this total. The average tractor power in Erzurum province (43.00 kW) is higher than the national average (41.42 kW). Based on this result, it can be said that higher horsepower tractors are more preferred in Erzurum, the Pasinler, and Güzelova plains due to intensive agriculture and the province's rugged terrain. In 2023, 2.02% of the total field crops, fallow land, and vegetable areas in the country are located in Erzurum. In Erzurum, the tractor power per unit area in 2023 is 1.41 kW ha^{-1}, which is below the national average. Based on this result, it can be said that Erzurum province is not being used effectively in terms of both cultivated area and the efficient use of total tractor power. In 2023, the cultivated area per tractor in Turkey averages 13.88 ha $tractor^{-1}$, while in Erzurum province, it is determined to be 30.47 ha $tractor^{-1}$. Although the proportion of agricultural land in Turkey is low, it can be said that the agricultural land per tractor in Erzurum is relatively high. In 2023, the number of tractors per 1000 hectares is 72.03 (tractors 1000 ha^{-1}) for the national average, while for Erzurum province, it is determined to be 32.81 (tractors 1000 ha^{-1}), which is more than twice as high. The number of tractors per 1000 hectares in the Northeast Anatolia agricultural region, which includes Erzurum province, was determined to be 40.23 (tractors 1000 ha^{-1}) in 2019 (Aybek ve ark., 2020). Although Erzurum province has a small cultivated area in terms of tractors per 1000 hectares, it can be said that it has not shown an increase parallel to the national average. Between 2008 and 2017, a decrease in the number of equipment per tractor was observed in Turkey (Abdikoğlu, 2019). In Erzurum, however, an increase in the number of equipment per tractor was observed between 2008 and 2017 (Table 4). Table 4 Tractor the number of, power and mechanization level values in 1995-2023 periods and projection for 2024-2028 years in Erzurum province.

Table 4. Tractor the number of, power and mechanization level values in Erzurum province.

Years	**Tractor the number of**	**Mechanization level indicators**				
		Average tractor power (kW)	**kW ha^{-1}**	**ha $tractor^{-1}$**	**tractor $1000ha^{-1}$**	**equipment $tractor^{-1}$**
1995	5124	38,35	0,68	56,42	17,73	4,60
1996	5296	38,09	0,70	54,35	18,40	4,56
1997	6045	37,50	0,78	47,94	20,86	4,85
1998	6529	35,48	0,85	41,75	23,95	4,58
1999	6707	37,35	0,88	42,23	23,68	4,66
2000	7197	37,03	0,97	38,05	26,28	4,65
2001	7301	36,94	0,96	38,54	25,95	4,74
2002	7662	37,81	0,63	60,15	16,62	4,50
2003	7941	38,07	0,81	47,17	21,20	4,55
2004	8101	38,17	0,82	46,73	21,40	4,78
2005	8487	38,13	0,85	44,64	22,40	4,81
2006	8606	38,41	0,88	43,63	22,92	4,99
2007	8657	38,43	1,01	38,22	26,17	5,00
2008	9003	39,03	0,85	45,74	21,86	5,14
2009	8813	39,29	0,97	40,57	24,65	5,19

2010	9575	40,07	1,11	35,95	27,82	5,02
2011	9802	40,63	1,14	35,70	28,01	5,11
2012	9689	40,64	1,04	39,12	25,56	5,21
2013	10264	41,13	1,18	34,79	28,74	5,21
2014	10387	41,30	1,20	34,40	29,07	5,29
2015	10273	41,81	1,24	33,69	29,68	5,52
2016	10463	41,98	1,27	32,97	30,33	5,49
2017	10598	42,00	1,31	32,00	31,25	5,46
2018	10726	42,03	1,33	31,58	31,67	5,45
2019	11546	42,03	1,40	29,93	33,41	5,26
2020	11539	42,03	1,41	29,91	33,43	5,49
2021	12574	42,45	1,55	27,37	36,53	5,32
2022	13276	42,98	1,37	31,44	31,81	5,54
2023	13461	43,00	1,41	30,47	32,81	5,56
Forecast						
2024	**14282**	**43,13**	**1,48**	**29,81**	**34,50**	**5,58**
2025	**14614**	**43,28**	**1,50**	**29,16**	**35,00**	**5,61**
2026	**14920**	**43,44**	**1,53**	**28,51**	**35,50**	**5,64**
2027	**15217**	**43,60**	**1,56**	**27,85**	**36,00**	**5,68**
2028	**15508**	**43,75**	**1,58**	**27,20**	**36,50**	**5,71**

According to the forecast results for Erzurum province, considering the years 2024-2028, the number of tractors in the province is expected to increase by 15.21% by 2028, reaching a total of 15508 tractors compared to 2023. According to the change in tractor numbers over the years, the average tractor power fluctuated until 2005, and it has been increasing from that year until 2023. The average tractor power is expected to increase by 1.74% by 2028, reaching 43.75 kW. While fluctuations are observed in the values of the mechanization indicators over the years, it is expected that by 2028, the tractor power per cultivated area will be 1.58 kW ha^{-1}, the cultivated area per tractor will be 27.20 ha tractor^{-1}, the number of tractors per 1000 hectares will be 36.50 tractors 1000 ha^{-1}, and the number of equipment per tractor will be 5.71 equipment tractor^{-1}.

The changes in the number of tractors in Erzurum and its districts between 1995 and 2023 were used to estimate the number of tractors for the next five years (2024-2028) using a predictive model. Accordingly, the increases and decreases in tractor numbers have been predicted for the province and its districts in the coming years. According to the data for 2023, the highest increase in tractor numbers over the next five years is expected to be in Karaçoban district, with an increase of 1242 tractors, representing a 56.23% rise. On the other hand, the largest decrease is expected in Tekman district, with a reduction of 307 tractors, representing a 38.51% decrease. No significant changes are expected in the districts of Oltu, Pazaryolu, and Şenkaya over the next five years. In Erzurum, it is expected that Pasinler district, which has the highest number of tractors with 17.15%, will experience a decrease of 1.85%, resulting in 2226 tractors. Meanwhile, Uzundere district, which has the least number of tractors (0.49%) and the smallest cultivated agricultural area, is projected to see an increase of 28.64%, reaching 85 tractors. In Horasan district, which has the largest share of cultivated agricultural land, the number of tractors is expected to increase by 10.32% over the next five years, reaching 1,821 tractors (Tables 5 and 6).

Table 5. Tractor the number of projection for 2024-2028 years in Erzurum and district province.

Years	Center	Aşkale	Aziziye	Çat	Hınıs	Horasan	İspir	Kçoban	Kyazı	Kköy	Narman
2024	1474	658	704	244	855	1676	268	861	531	994	515
2025	1515	652	673	246	881	1708	272	937	512	1016	516
2026	1514	647	652	250	907	1743	275	1025	501	1040	517
2027	1569	642	637	255	933	1782	277	1126	495	1064	518
2028	1639	638	627	261	959	1821	279	1242	491	1089	518
change	**18,35**	**-4,05**	**-12,85**	**7,77**	**15,52**	**10,32**	**-15,23**	**56,23**	**-12,88**	**11,68**	**-6,29**
%	**10,29**	**4,94**	**5,35**	**1,80**	**6,17**	**12,27**	**2,44**	**5,91**	**4,19**	**7,24**	**4,11**

Table 6. Tractor the number of projection for 2024-2028 years in Erzurum and district province (Continue).

Years	Oltu	Olur	Pasinler	Pyolu	Şenkaya	Tekman	Tortum	Udere	Erzurum
2024	348	283	2298	146	801	431	316	70	14282
2025	347	285	2289	146	802	450	329	74	14614
2026	346	288	2280	146	802	455	335	77	14920
2027	345	290	2273	146	802	344	347	81	15217
2028	344	292	2266	146	803	307	354	85	15508
change	**-0,39**	**4,44**	**-1,85**	**-0,03**	**0,35**	**-38,51**	**15,73**	**28,64**	**15,21**
%	**2,56**	**2,08**	**17,15**	**1,08**	**5,94**	**3,71**	**2,27**	**0,49**	**100,00**

It is expected that the average tractor power in the majority of Erzurum and its districts will exceed the national average. (Table 6). In Pasinler district, which has the most tractors among the districts, a decrease in average tractor power is expected over the next five years. In addition to having a large share of cultivated agricultural land, an increase in average tractor power is expected in Horasan district over the next five years. Based on this result, it can be said that high-powered tractors may enter the inventories of businesses in Horasan district. It is forecasted that the average tractor power will increase in parallel with the increase in the number of tractors in the central districts of Erzurum, Köprüköy, and Olur. As a result of this, it can be said that the level of mechanization will increase (Tables 7 and 8).

Table 7. Average tractor power (kW) for 2024-2028 years in Erzurum and district province.

Years	Center	Aşkale	Aziziye	Çat	Hınıs	Horasan	İspir	Kçoban	Kyazı	Kköy	Narman
2024	46,41	44,57	43,50	45,40	43,82	40,79	40,82	42,79	44,67	38,55	45,95
2025	46,84	44,61	43,61	45,37	43,71	40,83	40,85	41,79	44,86	38,09	45,93
2026	47,27	44,64	43,75	45,35	43,62	40,85	40,88	40,95	45,03	39,22	45,92
2027	47,70	44,68	43,87	45,33	43,56	40,86	40,92	40,25	45,25	39,58	45,91
2028	48,13	44,72	43,99	45,31	43,51	40,87	40,94	39,65	45,44	39,95	45,90

Table 8. Average tractor power (kW) for 2024-2028 years in Erzurum and district province. (Continue).

Years	Oltu	Olur	Pasinler	Pyolu	Şenkaya	Tekman	Tortum	Udere	Erzurum
2024	45,07	43,56	39,66	45,38	45,07	49,25	37,32	39,57	43,13
2025	45,07	43,65	39,24	45,61	45,07	49,06	37,18	38,83	43,28
2026	45,07	43,72	38,95	45,80	45,07	48,89	37,05	38,32	43,44
2027	45,07	43,78	38,74	45,97	45,07	48,73	36,92	37,97	43,60
2028	45,07	43,83	38,59	46,10	45,07	48,58	36,80	37,72	43,75

Although the tractor power per unit area in Erzurum is below the Turkish average, it is projected to increase during the 2024-2028 period. Although the number of tractors in Aşkale district is expected to decrease, the average tractor power and tractor power per unit area are anticipated to increase. This situation arises from producers shifting towards higher power group tractors for their operations. Despite the decrease in the number of tractors, the increase in average power and tractor power per unit area indicates more efficient utilization of tractors and an improvement in the effectiveness of mechanization. On a district basis, it is estimated that in Olur, along with an increase in the number of tractors and average power, the tractor power per unit area will exceed both the Erzurum and Turkey averages. In this case, it can be said that the mechanization level in the Olur district will increase. In the Uzundere district, although the number of tractors is expected to increase, the average tractor power and tractor power per unit area are projected to decrease. It has been stated that the increase in mechanization levels will be influenced by the rise in the number of tractors and power values, as well as the slight decrease in cultivated agricultural areas. (Aybek et al., 2020). Uzundere district, having the smallest agricultural area in the province, is projected to experience a decline in mechanization levels due to a decrease in tractor power per unit area in the future projections, suggesting that producers will tend to prefer smaller power group tractors (Tables 9 and 10).

Table 9. Tractor power per unit of cultivated area (kW ha^{-1}) of projection for 2024-2028 years in Erzurum and district province.

Years	Center	Aşkale	Aziziye	Çat	Hınıs	Horasan	İspir	Kçoban	Kyazı	Kköy	Narman
2024	1,82	1,39	1,12	0,54	1,87	1,01	1,45	2,43	1,00	1,51	1,12
2025	1,85	1,36	1,08	0,51	1,93	1,03	1,37	2,44	1,00	1,50	1,13
2026	1,88	1,33	0,99	0,48	1,99	1,05	1,33	2,46	1,01	1,50	1,14
2027	1,91	1,30	0,98	0,46	2,05	1,06	1,30	2,47	1,01	1,50	1,14
2028	1,93	1,29	0,98	0,44	2,11	1,08	1,28	2,48	1,01	1,50	1,15

Table 10. Tractor power per unit of cultivated area (kW ha^{-1}) of projection for 2024-2028 years in Erzurum and district province. (Continue).

Years	Oltu	Olur	Pasinler	Pyolu	Şenkaya	Tekman	Tortum	Udere	Erzurum
2024	1,56	3,18	2,54	1,30	2,25	1,17	0,77	0,96	1,48
2025	1,55	3,23	2,55	1,34	2,19	1,11	0,75	0,86	1,50
2026	1,55	3,28	2,55	1,35	2,15	1,08	0,74	0,78	1,53
2027	1,55	3,32	2,56	1,36	2,13	1,07	0,73	0,72	1,56
2028	1,55	3,36	2,56	1,37	2,12	1,06	0,72	0,66	1,58

In Erzurum and its districts, the agricultural land per tractor has remained below the Turkish average from 1995 to 2023, and the same scenario is predicted for the next five years. In a study, the agricultural land per tractor in Turkey for the year 2020 was determined to be 16.03 (Saygılı and Çakmak., 2021). As of 2023, Erzurum and its districts remain below the Turkish average, and it is predicted that they will continue to be below the national average for the next five years. The district of Pasinler, with the highest number of tractors, is expected to be closest to the Turkish average in 2028, with a value of 14.67 (ha tractor-1). The highest increase in land per tractor is expected in the district of Çat. In the districts of Pazaryolu and İspir, the cultivated area per tractor is predicted to decrease linearly over the next five years. Although the number of tractors is decreasing in the districts of Aziziye and Aşkale, a fluctuation in the cultivated area per tractor is expected in Aşkale, while an increase is anticipated in Aziziye (Tables 11 and 12).

Table 11. Agricultural area per tractor (ha tractor^{-1}) of projection for 2024-2028 years in Erzurum and district province.

Years	Center	Aşkale	Aziziye	Çat	Hınıs	Horasan	İspir	Kçoban	Kyazı	Kköy	Narman
2024	26,62	38,23	40,96	68,94	22,71	39,82	25,22	18,78	64,41	26,39	38,98
2025	31,39	38,31	41,11	112,90	21,27	38,71	24,53	19,66	59,07	27,34	38,65
2026	29,04	38,38	43,18	146,32	19,83	37,61	23,85	20,42	55,02	28,16	38,83
2027	30,19	38,43	43,89	171,73	18,39	36,50	23,16	21,09	51,94	28,86	38,94
2028	29,62	38,48	44,48	191,05	16,94	35,40	22,48	21,68	49,60	29,46	39,01

Table 12. Agricultural area per tractor (ha tractor^{-1}) of projection for 2024-2028 years in Erzurum and district province (Continue).

Years	Oltu	Olur	Pasinler	Pyolu	Şenkaya	Tekman	Tortum	Udere	Erzurum
2024	32,35	16,73	14,96	42,70	21,56	40,05	51,16	60,83	29,81
2025	34,72	18,65	14,87	42,59	22,48	40,58	55,31	79,37	29,16
2026	36,37	20,01	14,79	42,53	22,83	40,80	58,66	94,47	28,51
2027	37,53	20,96	14,73	42,49	22,97	40,90	61,36	10,68	27,85
2028	38,34	21,64	14,67	42,46	23,02	40,94	63,54	11,68	27,20

Another indicator of agricultural mechanization, the number of tractors per 1000 hectares, is expected to increase linearly across the entire Erzurum province over the next five years. The district of Olur, which has the highest value in Erzurum province, is expected to increase by 7.08% to reach 76.37 (tractors 1000 ha-1). Although the most agricultural activities are carried out in the district of Horasan, small increases in the number of tractors per 1000 hectares are expected. An increase is expected in the districts of Erzurum Center, Aşkale, Hınıs, Karayazı, Narman, Pasinler, Oltu, and Pazaryolu, while decreases are anticipated in the other districts (Tables 13 and 14).

Table 13. Agricultural area per tractor (tractor 1000 ha^{-1}) of projection for 2024-2028 years in Erzurum and district province.

Years	Center	Aşkale	Aziziye	Çat	Hınıs	Horasan	İspir	Kçoban	Kyazı	Kköy	Narman
2024	39,58	24,07	24,16	11,62	41,96	24,83	36,21	54,64	20,27	39,44	24,57
2025	39,89	24,26	23,47	10,73	43,20	25,23	34,82	53,26	24,12	39,34	24,78
2026	40,21	24,43	22,94	10,00	44,45	25,63	34,02	52,05	26,20	39,25	24,93
2027	40,53	24,59	22,54	9,41	45,70	26,02	33,56	51,00	27,10	39,16	25,04
2028	40,85	24,73	22,23	8,93	46,96	26,42	33,29	50,08	27,30	39,09	25,11

Table 14. Agricultural area per tractor (tractor 1000 ha^{-1}) of projection for 2024-2028 years in Erzurum and district province (Continue).

Years	Oltu	Olur	Pasinler	Pyolu	Şenkaya	Tekman	Tortum	Udere	Erzurum
2024	34,52	72,54	64,29	28,72	50,06	25,30	21,13	21,53	34,50
2025	34,52	73,64	64,69	29,58	48,70	25,08	21,72	18,07	35,00
2026	34,53	74,64	65,04	30,04	47,86	24,98	22,31	15,56	35,50
2027	34,53	75,55	65,35	30,28	47,35	24,93	22,90	13,74	36,00
2028	34,53	76,37	65,61	30,41	47,03	24,91	23,48	12,41	36,50

The number of implements per tractor used in agricultural activities across Erzurum is expected to increase by 2.7% compared to 2023, reaching 5.71 (equipment tractor-1). In the districts of Horasan and Pasinler, where agricultural activities are carried out over large areas, an increase is expected over the next five years. However, in the district of Karayazı, which ranks second in terms of agricultural land, a decrease in the number of equipment per tractor is anticipated. Considering the challenging geographical conditions and the economic situation of the producers in the Eastern Anatolia Region, it has adverse effects on the supply and use of equipment (Erkmen and Bastaban., 1988). The fact that the number of equipment per tractor in Erzurum province is below the Turkish average and that the level of mechanization is not increasing rapidly can be explained by this situation. Although a decrease in the number of tractors is expected in the district of Aşkale, an increase in the number of equipment per tractor is anticipated. This situation can be interpreted as a potential increase in the number of tools and machinery over the next five years. (Tables 15 and 16).

Table 15. Number of equipment per tractorof projection for 2024-2028 years in Erzurum and district province (equipment tractor-1).

Years	Center	Aşkale	Aziziye	Çat	Hınıs	Horasan	İspir	Kçoban	Kyazı	Kköy	Narman
2024	6,22	4,86	5,18	3,25	7,30	5,46	5,12	6,20	5,05	4,56	4,66
2025	6,22	5,00	5,09	5,26	7,41	5,57	5,38	6,08	4,87	4,49	4,74
2026	6,22	5,09	5,04	6,55	7,52	5,64	5,15	5,97	4,56	4,44	4,83
2027	6,22	5,16	5,02	7,37	7,63	5,68	5,24	5,87	4,74	4,39	4,92
2028	6,22	5,21	5,01	7,90	7,74	5,71	5,20	5,77	4,64	4,35	5,01

Table 16. Number of equipment per tractorof projection for 2024-2028 years in Erzurum and district province (equipment tractor-1). (Continue)

Years	Oltu	Olur	Pasinler	Pyolu	Şenkaya	Tekman	Tortum	Udere	Erzurum
2024	3,62	3,54	5,51	5,30	5,54	11,79	2,56	16,92	5,58
2025	3,65	3,53	5,55	4,93	5,58	8,11	2,53	21,37	5,61
2026	3,66	3,53	5,60	4,91	5,63	6,71	2,50	24,15	5,64
2027	3,67	3,52	5,63	4,92	5,67	6,03	2,48	25,87	5,68
2028	3,68	3,52	5,66	4,91	5,72	5,71	2,47	26,95	5,71

Conclusion

It is very important for the forecasting studies conducted to determine future agricultural mechanization criteria to be included in the literature as a significant topic for agricultural producers, official organizations, and the agricultural machinery sector. With the agricultural mechanization criteria forecast values, taking preventive measures for future agricultural production and implementing subsidies are expected to make producers more competitive in the market with a wide product range, improve their welfare levels, and contribute to the employment and economy of Erzurum province. In this study, the mechanization level data of Erzurum Province and its districts over the last 29 years have been calculated, and forecasts have been made for the next five years based on this data. According to the results obtained, it is forecasted that over the next five years, the number of four-wheel tractors, along with the average tractor power, tractor power per hectare (kW ha^{-1}), the number of tractors per 1000 hectares of cultivated land (tractor 1000 ha^{-1}), and the number of equipment per tractor (equipment tractor^{-1}) will increase, while the cultivated area per tractor (ha tractor^{-1}) will decrease. The increase in the level of mechanization is highly valuable in terms of improving efficiency and quality in agricultural production. In this study, where future projections are made using the ARIMA model, it is predicted that the agricultural mechanization criteria across Erzurum will not show rapid improvement over the next five years.

Acknowledgement

We thank the 6th International Conference on Food, Agriculture and Animal Sciences for giving us the opportunity to attend this scientific event.

Funding

No Funding

Statement of Conflict of Interest

There is no conflict of interest between the authors.

Authors' Contributions

M.Ç. contributed to the collection of data and writing of the article, and N.E.T. contributed to the analysis of data.

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Diagnosis of Bacterial Strains Causing Disease in Lettuce Plant (*Lactuca sativa*)*

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ABSTRACT: This study was conducted to determine the isolation, diagnosis and characterization of bacteria causing disease in lettuce varieties in Erzurum province. For this purpose, 41 bacterial strains were isolated and purified as a result of the isolations made from diseased lettuce samples taken from different areas in Erzurum city center. HR test and pathogenicity tests were performed on the obtained strains in tobacco and 20 strains were found to be positive as a result of HR tests. As a result of pathogenicity tests, 30 strains were found to be positive. Classical and molecular methods will be used for definitive diagnosis and characterization of strains determined to be pathogenic. According to the literature review; only *Xanthomonas campestris* pv. *vitians* was found to be the only bacteria causing disease in lettuce varieties in Erzurum province and no studies were found regarding other pathogens. In the light of the current data, it is thought that there may be new bacterial pathogens in lettuce in Erzurum province. Therefore, this study aims to identify bacteria that may cause yield and quality losses in lettuce varieties in Erzurum province and is of great importance as it will provide important data for combating these diseases.

Keywords: *Lactuca sativa*, Bacteria, Plant Disease

INTRODUCTION

The first written sources about lettuce cultivation belong to Herodotus, who said that it was eaten in a Persian court in 550 BC. It is known that lettuce culture was first made in Egypt in 4500 BC and that its homeland was the Caucasus, Anatolia, Turkestan and Iran. Lettuce was brought to the New World by Christopher Columbus. In the following 400 years, Batavia type lettuce, known as loose-headed crisp, was cultivated in the USA. The most primitive forms were consumed by animals and used for oil production. With the breeding studies carried out in the following years, different types of lettuce and lettuce emerged, and it was reported that the ancestor of today's cultivated forms came from the wild form L. serriola species. China ranks first in lettuce and lettuce production worldwide, while the USA ranks second and India ranks third. India is followed by Spain, Italy, Iran, Japan, Turkey, Mexico and Germany, respectively. Yield is calculated in units. Lettuce is a one-year, cool-climate vegetable. In lettuce types with a short growing period of 2-3 months, it has become possible to produce 12 months of the year in a row with varieties that have been improved for different seasons in the open and under cover. Lettuce and lettuce are cool, warm climate vegetables that are partially resistant to cold and require humid weather conditions. Summer cultivation is also possible in

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* Bu çalışma yüksek lisans öğrencisi Mustafa ÖZGERİŞ'in Erzurum İlinde Marul Çeşitlerinde Hastalığa Neden Olan Bakterilerin İzolasyonu Tanısı ve Karakterizasyonu isimli projenin bir kısmından hazırlanmıştır.

regions with cool summers. In this respect, it is possible to grow summer varieties in the plateau area, which is 1000-1500 m in the summer months. Although the most suitable temperature for lettuce cultivation is between 15.5 ºC and 18.3 ºC, the transition from the vegetative phase to the generative phase begins at temperatures above 18 ºC. They are also quite resistant to frost. In open cultivation, plants can withstand low temperatures of -4-5 ºC without much damage. In a study, according to MIS diagnostic results, 40 candidate plant growth promoting rhizobacteria (PGPR) and plant growth promoting endophytic (PGPE) bacteria belonging to the genera *Pantoea* (33 isolates), *Bacillus* (6 isolates) and *Paenibacillus* (1 isolate) were investigated for their effects on disease severity and lettuce development. All isolates were identified with MIS (Microbial Diagnostic System) and Biolog systems, and their phosphate solubilization and nitrogen fixation abilities were tested. All isolates grew in nitrogen-free (N-free) medium and their nitrogen fixation abilities were evaluated as positive. It was also found that the isolates could solubilize phosphate in insoluble form at values ranging from 40.95 to 227.20 µg ml^{-1}. (Karagöz and Kotan 2010).

During the 2015 and 2016 growing season, the status of disease agents that caused problems in early seedling and harvest periods in randomly selected fields where important lettuce (*Lactuca sativa* L.) cultivation areas of Hatay province were determined. As a result of the isolations made from plant samples showing typical disease symptoms, *Pectobacterium carotovorum* subsp, *pectobacterium* and *Enterobacter cloacae* were determined as bacterial disease agents causing soft rot symptoms in the root area, and *Xanthomonas campestris* pv. *vitians* was determined as spots on the leaves. (Soylu et al. 2017).

Malaysia produces many types of vegetables. Cameron Highland in Pahang state is the main region for lettuce (*Lactuca sativa* var. *romana*) production. In a recent study, *Pectobacterium* spp. was determined to be responsible for more than 15% damage to lettuce both in the field and in storage. During 2010, *Pectobacterium carotovorum* isolates were collected from different greenhouses and fields and analyzed in the laboratory. Nine isolates were purified and characterized by morphological, biochemical and molecular methods. Pathogenicity studies on lettuce using 4 strains showed high susceptibility to *P. carotovorum*. This was the first record in the literature of a bacterial pathogen causing disease in lettuce in Malaysia (Nazerian, et.al. 2013).

Collection of Diseased Plant Samples And Bringing Them to the Laboratory

For the research, plant materials showing signs of disease on lettuce in Erzurum Province were collected, each one labeled separately and brought to the laboratory in polyethylene bags.

Isolation and Storage of Bacteria

Standard Trypticase Soy Broth Agar (TSBA), Nutrient Agar (NA), Yeast Dextrose Carbonate Agar (YDC) media will be used for isolations. After the diseased plant materials, vegetables and fruits were washed in tap water, they were kept in a container containing 70% ethyl alcohol for 5 minutes and then sterilized superficially and then passed through sdH_2O. Small pieces were cut from the areas containing both diseased and healthy tissue and kept in sterile tubes containing 2 ml of sdH_2O for 1 hour, and dilutions were prepared by diluting them 5 times. 100 µl of each dilution was taken with a pipette, transferred to standard media and spread on the surface with a glass rod. The cultures were incubated at 25℃ and pure cultures were obtained by re-cultivation of each developing colony.

A separate code number was given to each purely obtained isolate, and information about the isolation (isolated plant, location, date, etc.) was recorded; and it was stored at -86°C in stock media containing 30% glycerol and Lauryl Broth (LB) mixed at a 1:1 ratio until diagnosis and characterization procedures.

Hypersensitivity (HR) Test in Tobacco

Purified bacterial isolates were streaked onto NA media and left for incubation. Bacteria taken from 24-hour cultures with a loop and transferred to sdH_2O were mixed in a vortex device and the concentration of the prepared mixture was adjusted to 10^8 CFU/ml. The resulting solution was taken with a sterile syringe as 2 cc and injected into the veins of tobacco (*Nicotina tabacum* L. var. *Samsun*) leaves. The applied plants were kept in plant growth cabinets at 90% humidity for 24-48 hours and it was monitored whether dead tissue (necrosis) formed in the inoculated areas. Isolates that formed dead tissue were evaluated as HR positive (+), and those that did not were evaluated as HR negative (–). sdH_2O was used in control plants (Klement et. al. 1967; Lelliot et al. 1987).

Pathogenicity Test

Lettuce varieties from which pathogens were isolated were grown and used for pathogens. In the studies conducted, pathogen solutions prepared at a concentration of 10^8 CFU/ml in liquid nutrient medium were injected into the above-ground parts of the plants with a syringe and kept in polyethylene bags under humid conditions for 2 days. At the end of this period, the bags were removed and the plants were monitored for 7 days to determine whether they caused disease. sdH_2O was used as control (Schaad et al. 2001)

Results and Discussion

Erzurum ilinde farklı alanlardan hastalık belirtisi görülen marul çeşitlerinden yapılan izolasyonlar sonucunda 41 farklı bakteri straini elde edilmiştir. Elde edilen strainlere ait konukçu, HR ve patojenite test sonuçları Tabl 1'de verilmiştir. Tüm strainlere HR ve patojenite testi yapılmış olup, elde edilen sonuçlara göre, 20 strainin HR test sonucu pozitif iken patojenite testleri sonucunda 30 strain pozitif sonuç vermiştir. Her iki test sonucuna göre pozitif olan strainlerin klasik ve moleküler yöntemler kullanılarak kesin ve karakterizasyonu yapılacaktır.

Table 1. Host, HR and pathogenicity test results of bacterial strains isolated from different lettuce varieties

Strain No	Host	HR Test	Pathogenicity test
MF-1	Lettuce	-	-
MF-2	Lettuce	-	-
MF-3	Lettuce	-	-
MF-4	Lettuce	+	+
MF-5	Iceberg lettuce	+	+
MF-6	Iceberg lettuce	-	-
MF-7	Iceberg lettuce	-	-
MF-8	Iceberg lettuce	-	-
MF-9	Iceberg lettuce	-	-
MF-10	Curly lettuce	-	-
MF-11	Curly lettuce	-	-
MF-12	Curly lettuce	-	-
MF-13	Lettuce	+	+
MF-14	Lettuce	+	+
MF-15	Lettuce	-	-
MF-16	Lettuce	-	-
MF-17	Iceberg lettuce	+	+
MF-18	Iceberg lettuce	+	+
MF-19	Iceberg lettuce	+	+
MF-20	Lettuce	+	+
MF-21	Lettuce	+	+
MF-22	Lettuce	+	+
MF-23	Lettuce	-	-
MF-24	Iceberg lettuce	+	+
MF-25	Iceberg lettuce	+	+
MF-26	Curly lettuce	-	-
MF-27	Curly lettuce	+	+
MF-28	Curly lettuce	+	+
MF-29	Lettuce	+	+
MF-30	Lettuce	+	+
MF-31	Lettuce	-	-
MF-32	Iceberg lettuce	+	+
MF-33	Iceberg lettuce	+	+
MF-34	Iceberg lettuce	+	+
MF-35	Curly lettuce	+	+
MF-36	Lettuce	-	-
MF-37	Lettuce	+	+
MF-38	Lettuce	+	+
MF-39	Iceberg lettuce	-	-
MF-40	Iceberg lettuce	-	-
MF-41	Iceberg lettuce	-	-

In a recent study conducted in Japan, new bacterial diseases causing rot in lettuce were identified and according to the results obtained, it was determined that these strains belonged to the *Pseudomonas* genus and that there were two new types of strains*: Pseudomonas aegrilactucae* sp. nov. for MAFF 301350T, *Pseudomonas aegrilactucae* sp. nov. and for MAFF 302030T and MAFF 302046, *Pseudomonas morbosilactucae* sp. nov. (Swada et al. 2022). In a study conducted in Malaysia, *Pectobacterium carotovorum* bacteria was identified in lettuce (Nazerian, et.al. 2013). According to the literature review; only *Xanthomonas campestris* pv. vitians was found to be the only bacteria causing disease in lettuce varieties in Erzurum province and no studies were found regarding other pathogens (Şahin 2000). Therefore, this study is of great importance for the diagnosis and characterization of bacterial diseases in lettuce plants in Erzurum province.

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Genetic Resources of Alfalfa

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ABSTRACT: Differences occur between populations and individuals through the processes of evolution and adaptation to ecology. The genetic diversity formed in this process is reflected in the genomic structure. The richer the genetic diversity within a population, the greater its adaptation to environmental changes and its potential for hybridisation. Therefore, the study of genetic diversity provides important clues in understanding the origin and evolution of plants. It also provides benefits in terms of conservation of biodiversity and sustainability of biological resources. Legume forage crops such as alfalfa are used in animal diets for their nutritional benefits and protein production. Alfalfa is the most widely cultivated perennial forage legume globally, grown on more than 35 million hectares in more than 80 countries. Genetic resources in forage species are categorised into three groups: cultivated populations, populations originating from natural grasslands or partially controlled environments, and wild, spontaneous populations. The genetic resources of alfalfa consist mostly of local cultivars and historically cultivated populations. The aim of this study was to investigate the genetic resources of alfalfa.

Keywords: Alfaalfa, Genebank, Genetic Resource, Accession, Wild Relative, Forage

INTRODUCTION

Legume fodder crops are utilized in animal diets by grazing, fresh consumption post-harvest, or as hay or silage, owing to their nutritional benefits. Legume fodder crops serve as a significant protein source in production operations. Alfalfa (*Medicago sativa* L.) is the most extensively cultivated perennial forage legume for feed production globally. Alfalfa is recognized for its superior fodder quality and beneficial impact on soil fertility (Kebede et al., 2016). Its economic importance is significant owing to its biomass output (Annicchiarico et al., 2011). Alfalfa is cultivated throughout over 35 million hectares in more than 80 nations on every continent globally. It is cultivated in many climatic and compositional circumstances, spanning from semi-arid to humid places (Sayed et al., 2022).

Alfalfa is a globally significant crop owing to its nutritional value as animal feed and its environmental advantages (El-Ramady et al., 2020). Numerous agricultural crops possess plant genetic resource (PGR) collections preserved by national and international genebanks (Tyagi and Agrawal, 2015). Extensive alfalfa germplasm collections are preserved in seed form in gene banks throughout. The identical genebanks are additionally accountable for numerous other cultivated species and wild relatives of clover crops (CWR) within the genus *Medicago*. Upon acquisition, these taxonomically varied collections are actively handled and necessitate regeneration operations to ensure optimal storage and viable seeds for longevity. Extensible database software platforms are always enhancing their functionalities to facilitate public access to information related to accessioning. When resources and policies permit, PGR are allocated to stakeholders in the public, non-profit, and private research sectors. The majority of PGRs have been thoroughly characterized and assessed for significant phenotypic, agronomic, and genetic features (Irish and Greene, 2021). Significant genetic variety has been recognized in many big collections; nevertheless, the accessions of Alfalfa and numerous *Medicago* species are challenging to evaluate due to their predominantly heterozygous outcrossing polyploid populations. The accession numbers for diversity and CWR collections are far lower; yet, the potential benefit of integrating essential features from germplasm into these gene pools has been established. Historically, the cultivation of alfalfa and other *Medicago* spp. forages has profited from the diversity preserved in PGR collections.

Different Genetic Resource Types in Forage Plants

Genetic resources in forage species have been categorised in three different groups (Prosperi, 1996).

Cultivated populations: These populations are well defined and carefully maintained by seed producers in terms of ecological adaptation, thus preserving phenotypic and genotypic traits.

Populations originating from natural meadows or partially controlled environments: The human influence on these plants can vary; multiple reproductive cycles typically occur under natural conditions. In many instances, these communities comprise many sources, hence jeopardizing their natural preservation.

Wild, spontaneous populations: Wild, spontaneous populations are typically scarce and found in uncontrolled environments. Their in situ conservation is heavily dependent on habitat preservation.

Alfalfa Gene Resources

The genetic resources of *Medicago sativa* subsp. *sativa* mostly consist of local varieties and historically cultivated populations. Wild populations are present for *Medicago sativa* subsp. *falcata* and associated diploid subspecies. The majority of native breeds and cultivated populations in temperate regions were gathered, analyzed, and utilized for breeding during the initial phases of alfalfa farming. This constituted the initial pool from which numerous types were selected.

The fundamental germplasm utilized for alfalfa breeding in the USA aligns with the phases of genetic diversity introduction to North America (Barnes et al., 1977; Barnes, 1988). These sources exhibit considerable disparities in agronomic value and physiological characteristics, particularly in winter hardiness and dormancy, which subsequently influence biomass production and genotype × environment interactions for production and adaptation. Significant disparities exist among germplasm sources regarding nutritional value at comparable phenological stages; for instance, Indian and Flemish germplasm exhibited more crude protein content than Turkestan and Peruvian germplasm during the late flowering stage (Lenssen et al., 1990).

In Egypt, germplasm from the Siwa region specifically signifies populations historically grown by farmers in tiny irrigated fields with minimal seed exchange among them. Genotypes from these regions are highly desirable due to their resilience to elevated temperatures and summer growth (Veronesi et al., 2010).

Chinese farmers have emphasized alfalfa for its capacity to yield high protein production in arid environments. Certain scholars have examined the extant variety within traditionally cultivated populations, particularly in Northwest China (Wei 2004; Hu et al., 2000). Synthetic varieties resemble foreign germplasm and differ from local ecotypes, indicating the potential for variety introductions in breeding programs. This underscores the necessity to gather and assess local demographics for prospective applications.

Alfalfa Crop Wild Relatives

Wild relatives of plants (CWR) are widely used genetically by plant breeders. The productive alfalfa cultivars grown today were obtained by transferring some traits from wild relatives. These traits include cold hardiness, aluminium tolerance, aphid (*Empoasca fabae* [Harris]) resistance (Irish and Greene, 2021). Table 1 provides information on the primary, secondary and tertiary gene pools for alfalfa and its wild relatives, the estimated number of accessions in collections worldwide, and related traits used or potentially used in crop breeding.

Table 1. Some information on gene pools for alfalfa and its wild relatives (Irish and Greene, 2021)

Genepool	Taxon	Accessions	Trait
Primary	*M.s.* subsp.*falcata* (L.) Arcang.	1390	Readily hybridizes,with many traits introgressed. Examples include cold,drought, and grazing tolerance,which have been incorporated from subsp. falcata (Boe et al. 2020), and insect resistance from the glandular hair trait in subsp.viscosa/glomerata (Sorensen et al., 1994)
	M.s. subsp.*falcata* var. *viscosa* (Rchb.) Posp.	30	
	M.s. subsp. *glomerata* (Balb.) Rouy	98	
	M.s. nothosubsp. *varia* (Martyn) Arcang.	2280	
Secondary	*M. s.* subsp. *caerulea* (Less. ex Ledeb.) Schmalh.	369	Cold, drought, and salt tolerance (Small 2011), and aluminum tolerance (Milic et al. 2018)
	M. s. nothosubsp. *Tunetana* Murb.	28	-
Tertiary	M.arborea L.	158	Disease resistance (Renfro and Sprague 1959; Armour et al. 2008), yield (Irwin et al. 2010)
	M. cancellata M. Bieb.	58	Disease resistance (Borges et al. 1975)
	M. daghestanica Rupr. ex Boiss.	36	Disease resistance,fertility,cold tolerance (McCoy and Bingham 1988)
	M. hybrida (Pourr.) Trautv.	24	Disease resistance
	M. littoralis Rohde ex Loisel.	36	Disease resistance
	M. marina L.	238	Drought and salt tolerance (McCoy and Bingham 1988; Scippa et al.2011)
	M. murex Willd.	619	Disease resistance (Elgin and Ostazeski 1982)
	M. papillosad Boiss.	62	Disease resistance,drought tolerance (Quiros and Bauchan 1988)
	M. murex Willd.	619	Disease resistance (Elgin and Ostazeski 1982)
	M. papillosad Boiss.	62	Disease resistance,drought tolerance (Quiros and Bauchan 1988)
	M. pironae Vis.	44	Fertility, cold tolerance, disease resistance (McCoy and Bingham 1988)
	M. rigidula (L.) All.	3084	Insect resistance (Quiros and Bauchan 1988)
	M. rhodopeai Velen.	40	-
	M. rupestris M. Bieb.	35	-
	M. ruthenica (L.)Trautv.	167	Alkalinity, drought, and salt tolerance (Wang et al. 2008)
	M. saxatilis M.Bieb.	38	-
	M. sphaerocarpos BertoL.	35	Drought tolerance, disease resistance
	M. suffruticosa Ramond ex DC.	76	Disease resistance
	M. tenoreana Ser.	59	Disease resistance
	M. truncatula (L.) Mill.	9571	Disease resistance (O'Neill and Bauchan 2000)

Other Medicago species inside the tertiary gene pool can significantly contribute to alfalfa plant breeding (Annicchiarico et al., 2015). Varied ploidy levels restrict the application of wild clover genotypes in breeding (McCoy and Bingham, 1988; McCoy and Echt, 1993). This can be addressed using procedures like colchicine administration, hybridization, protoplast culture, and embryo rescue (McCoy and Echt 1993; Bingham et al., 2013), as well as protoplast fusion methods (Pupilli et al., 1992).

Alfalfa Gene Banks

There are many gene banks focusing on clover in the world such as National Plant Germplasm System USA, Australian *Medicago* Genetic Resource Centre Australia, ICARDA Syria, Vavilov Institute Russia. Genetic resources of perennial *Medicago* species are maintained by many countries. Due to past exchanges of genetic material between research institutes, the conservation of cultivars and local breeds is ensured by several genebanks.

Alfalfa is the most economically important species in *Medicago* and therefore large collections are predominantly found in genebanks in countries such as the USA, Australia and Russia where the crop is of economic importance. Table 2 summarises information on the number of alfalfa accessions currently held in the ten largest genebanks responsible for this crop. Three of these organisations (the US NPGS, Plant Germ Plasm Promotion and Testing Research Unit [PGITRU], South Australian Research and Development Institute [SARDI], Australian Pasture Gene Bank [APG] and Nikolai I. Vavilov Plant Industry Research Institute [VIR]) account for just over 55% of the more than 21000 alfalfa germ plasm accessions in the world. In most countries, crop-specific PGR management responsibilities are associated with a single or primary organisation, but collections may be held in more than one location. Detailed access-related passport information for many of the collections is available through Genesys (https://www.genesys-pgr. org/) or publicly available online genebank-specific databases.

Table 2. Country, genebank/organization, site, and estimated number of alfalfa (*Medicago sativa* L.) and subordinate taxa accessions held in germplasm collections

Country	**Genebank/organization**	**Accessions**
USA	National Plant Germplasm System, Plant Germplasm Introduction and Testing Research Unit	4083
AUS	South Australian Research and Development Institute, Australian Pastures Genebank	3843
RUS	Nikolai I. Vavilov Research Institute of Plant Industry	3647
GBR	Genetic Resources Unit, Institute of Biological, Environmental and Rural Sciences, Aberystwyth University	1023
HUN	Centre for Plant Diversity	914
LBN	International Centre for Agricultural Research in Dry Areas	890
DEU	External Branch North of the Department Genebank, IPK, Oil Plants and Fodder Crops	743
ITA	Applied Biology Department, University of Perugia	697
CZE	Research Institute of Crop Production	635
ROM	National Agricultural Research and Development Institute	546
OTHER	Composite of 54 international organizations	4011
Total		21032

While not as significant as alfalfa in crop production, 16 perennial and annual *Medicago* species are grown, alongside numerous wild species utilized for fodder. The Genesys germplasm database indicates that there are somewhat more than 47000 *Medicago* species PGRs preserved in gene banks, excluding M. sativa. The three organizations with the most extensive collections of non-alfalfa *Medicago* species are: APG (5276 accessions), ICARDA (9144 accessions), and PGITRU (4695 accessions).

Funding

The study was not supported by any institution or organisation.

Statement of Conflict of Interest

There is no conflict of interest between the authors.

Authors' Contributions

MAN designed and analyzed the research, MFS studies arranged. All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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Foliar Application of Folic Acid on Cabbage Seedlings Grown under Restricted Irrigation Conditions Can Alleviate the Negative Effects

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ABSTRACT: Exacerbated by climate change, drought is a significant abiotic stress in the crop production sector that profoundly affects food security worldwide. White cabbage is classified as a moderately drought-sensitive crop. The role of folic acid (FA) or its derivatives (folates) in plant sensitivity to drought stress remains unclear. The study aimed to evaluate the potential of folic acid in enhancing specific growth parameters and physiological attributes of drought tolerance in cabbage seedlings. In this investigation, the effects of FA as a foliar application at 0, 100, and 200 µM (FA0, FA1, and FA2, respectively) were examined on white cabbage seedlings grown under full-irrigation (I0) and restricted irrigation (I1) treatment, which was adjusted to 50% of the I0 treatment. Drought stress adversely affected the plant growth properties of cabbage seedlings, whereas FA treatments mitigated the adverse effects of drought stress on the plant growth properties of cabbage seedlings. Under restricted irrigation, plants treated with 100 µM FA (FA1) had higher plant height, stem diameter and leaf area, while plants treated with 200 µM FA (FA2) had higher plant dry weight and plant dry matter content. Plant fresh weight increased with FA treatments under restricted irrigation, but no significant difference was observed between doses. On the other hand, leaf relative water content (LRWC), which decreased under restricted irrigation conditions, increased with FA applications regardless of the dose, while electrical conductivity (EC), which increased under the same conditions, decreased with 100 µM FA (FA1) application. Leaf number, root fresh weight, root fresh weight, root dry weight, root dry matter content and chlorophyll value (SPAD) were not affected by FA treatments under both restricted and full irrigation conditions. In conclusion, foliar spray of folic acid in cabbage can be recommended as a potential application to alleviate drought stress.

Keywords: *Brassica oleracae,* Folic Acid, Restricted Irrigation, Plant Growth Properties, LRWC, EC

INTRODUCTION

Increasing environmental stresses resulting from the impact of climate change elicit a range of responses in plants, including alterations in growth rate, productivity, cellular metabolism, and gene expression (Muhammad et al., 2024). One of the adverse effects of climate change is soil water deficit, which leads to drought stress (Shinde et al., 2024). Rosa et al (2022) based on their review in global agricultural landscapes for 130 primary crops; they estimated that exposure to water scarcity is highly dependent on geographical location and month of the year, with 76% of global agricultural land facing water scarcity for at least one month per year and another 42% of these lands facing five months per year.

Drought conditions trigger numerous significant events at morphological, physiological, and biochemical levels that can cause severe plant metabolism dysfunction (Anjum et al., 2011; Sanchez-Reinoso et al., 2018). As posited by Yildirim et al. (2021), insufficient hydration in plants has been demonstrated to engender a reduction in photosynthesis, which consequently results in a decrease in vegetative growth. Moreover, the stem and leaves of plants exhibit greater sensitivity to water stress compared to the roots. In addition to alterations in metabolism, such as cell division and cell elongation, drought causes loss of turgor, deterioration in enzyme activities, and decreased photosynthesis efficiency (Bhargava and Sawant, 2013; Osakabe et al., 2014). The effect of drought is known to vary according to the severity and duration of the stress experienced, as well as the response of the plants (Farooq et al., 2009).

Cabbage (*Brassica oleracea* var. *capitata* L.) belongs to the family Brassicaceae, mainly spread on the northern extratropical region of the globe, and originated from wild types growing on the European coasts of the Atlantic and the Mediterranean (Leik, 1989). Brassica vegetables, including cabbage, include many economically important species grown worldwide (Pavlović et al., 2018). Since Brassica crops are mainly cultivated commercially in Mediterranean, semi-arid and arid environments, their growth, and consequently the crop yield and quality, can be greatly impaired by drought (Zhang et al., 2014). Future projections are even worse, since a gradual, but consistent, increase in aridity and drought is estimated for most of the Mediterranean region (Daliakopoulos et al., 2014). Cabbage production is strongly influenced by environmental conditions. The growth and yield of white cabbage have been shown to be affected by drought (Maggio et al., 2005; Seidel et al. 2017), classified it as a moderately drought-sensitive plant. Despite this sensitivity, white cabbage has been shown to tolerate limited water availability to a certain extent (Pavlović et al., 2018), although the exact resilience mechanisms are not yet fully understood.

Vitamin B9 (folic acid; FA) and its derivatives (folates) are significant contributors to the metabolism of both carbohydrates and nitrogen (Stakhova et al., 2000). Furthermore, folic acid plays crucial roles in plants, serving as a cofactor in one-carbon metabolism and participating in the synthesis of nucleic acids and amino acids (Alsamadany et al., 2022). Additionally, it possesses antioxidant properties and can mitigate oxidative damage induced by abiotic stresses (Cui et al., 2018; Gliszczyńska-Świgło, 2007). Exogenous application of folic acid has been demonstrated to function as a regulator of plant responses to various abiotic stresses, including drought, salinity, and metal exposure. In this context, exogenous folic acid plays a significant role in mitigating the deleterious effects of abiotic stresses such as drought (Poudineh et al., 2015; Ibrahim et al., 2021; Alsamadany et al., 2022; Khan et al., 2022), salinity (Kilic et al., 2016; Alsamadany et al., 2022; Al-Elwany et al., 2022), and metal toxicity. Moreover, a number of earlier studies have indicated that the foliar application of folic acid may promote vegetative growth in numerous plant species, including those such as wheat (Mohamed, 2013), potato (Ibrahim et al., 2015) and faba bean (Dawood and El-Metwally, 2018). A review of the literature on foliar applications of folic acid revealed that there were no studies on its use to improve drought tolerance in cabbage. To address this gap in knowledge, the present study investigated the effects of foliar applications of folic acid on select developmental and physiological characteristics of cabbage seedlings grown under limited irrigation conditions. The results of this study are expected to provide a valuable resource for future research on this topic.

Material and Method

The study was carried out in the greenhouses of Atatürk University, Plant Production Application and Research Centre, and in the laboratories of the Department of Horticulture of the Faculty of Agriculture. Seeds of the commercial standard variety "Yalova 1" of white head cabbage, treated with thiram to prevent possible fungal diseases, were used as plant material in this study.

The study was conducted as a pot experiment under controlled greenhouse conditions (average temperature 25°C and humidity 60%). Cabbage seeds were sown in multi-well trays containing a mixture of peat and perlite (1:1, v/v) and seedlings were transplanted after 30 days into 1.5 L pots with a 2:1 (v:v) soil:peat mixture. The study was designed as a completely randomised factorial design with two factors; two irrigation level treatments (I0 and I1) and three doses of folic acid (FA0, FA1 and FA2). There were three replications and 5 pots per replication.

Seedlings of homogeneous size and morphology, aged two weeks, were segregated into two primary groups. One group received irrigation equivalent to field capacity for the control treatment (fully irrigated; I0), while the other group was subjected to restricted irrigation conditions, receiving 50% of the I0 treatment (I1). The volumetric determination of irrigation water application and soil moisture content in the pots was conducted utilizing a portable moisture meter. Within each major group, pots were subdivided into three subgroups to administer folic acid ($C_{19}H_{19}N_7O_6$) at concentrations of 0 (FA0), 100 (FA1), and 200 µM (FA2) (Alsamadany et al., 2022). Seedlings were subjected to foliar application of FA five times at 15, 20, 25, 30, and 35 days post-transplantation. The plants in the control group were treated with foliar rainwater. The volume of applied solution was 10 mL per plant per application. Tween-20, a non-ionic surfactant, was incorporated at 0.05% (v/v) in all foliar treatments.

To evaluate the impacts of the irrigation levels and FA applications on cabbace seedlings, some measurements, weighing and observations were carried out. In the study, plant height, leaf number, stem diamerter, leaf area, plant fresh and dry weight, root fresh and dry weight, plant and root dry matter content, leaf relative water content (LRWC), SPAD values, and electrical conductivity (EC) were determined. SPAD value is measured with portable SPAD-502 chlorophyll meters, which express the relative chlorophyll content. The total leaf area of each plant was determined by the leaf area meter (CID Bio-Science, USA).

The electrical conductivity (EC) of the samples was determined according to method described by Kaya et al. (2003). Disks (1 cm in diameter) were obtained from two randomly selected plants and placed in glass bottles containing 30 ml of pure water. The samples in bottles were subjected to a 24-hour shaking process in a shaker. Thereafter, the electrical conductivity of the soaking water was measured, and the permeability (damage rate) of the cell membranes was determined (EC1). The samples were subsequently subjected to autoclaving at 121°C for 20 minutes to ensure complete lysis of the cells and tissues. This was followed by the second measurement (EC2). The EC value was thus determined by calculating the percentage of EC1/EC2.

For LRWC, leaf discs were taken from two randomly selected plants and their fresh weight (FW) was determined by weighing immediately. Then, the discs were placed in glass bottles filled with pure water for 24 h. Then, excess water was removed using blotting paper and the discs were weighed again to determine their turgor weight (TW). The discs were then dried in an oven set at 72 ºC for 48 h and then weighed again to determine their dry weight (DW). Leaf relative water content (LRWC) was calculated according to the following formula (Shams et al., 2019):

$$\text{LRWC} = [(\text{FW} - \text{DW}) / (\text{TW} - \text{DW})] \times 100$$

The data were analyzed by using the SPSS 27 package program, and the difference between the means was determined by Duncan multiple range tests.

Results and Discussion

Figure 1, Table 1, and Table 2 illustrate the effects of folic acid on the growth and physiological characteristics of cabbage seedlings subjected to water deficit.

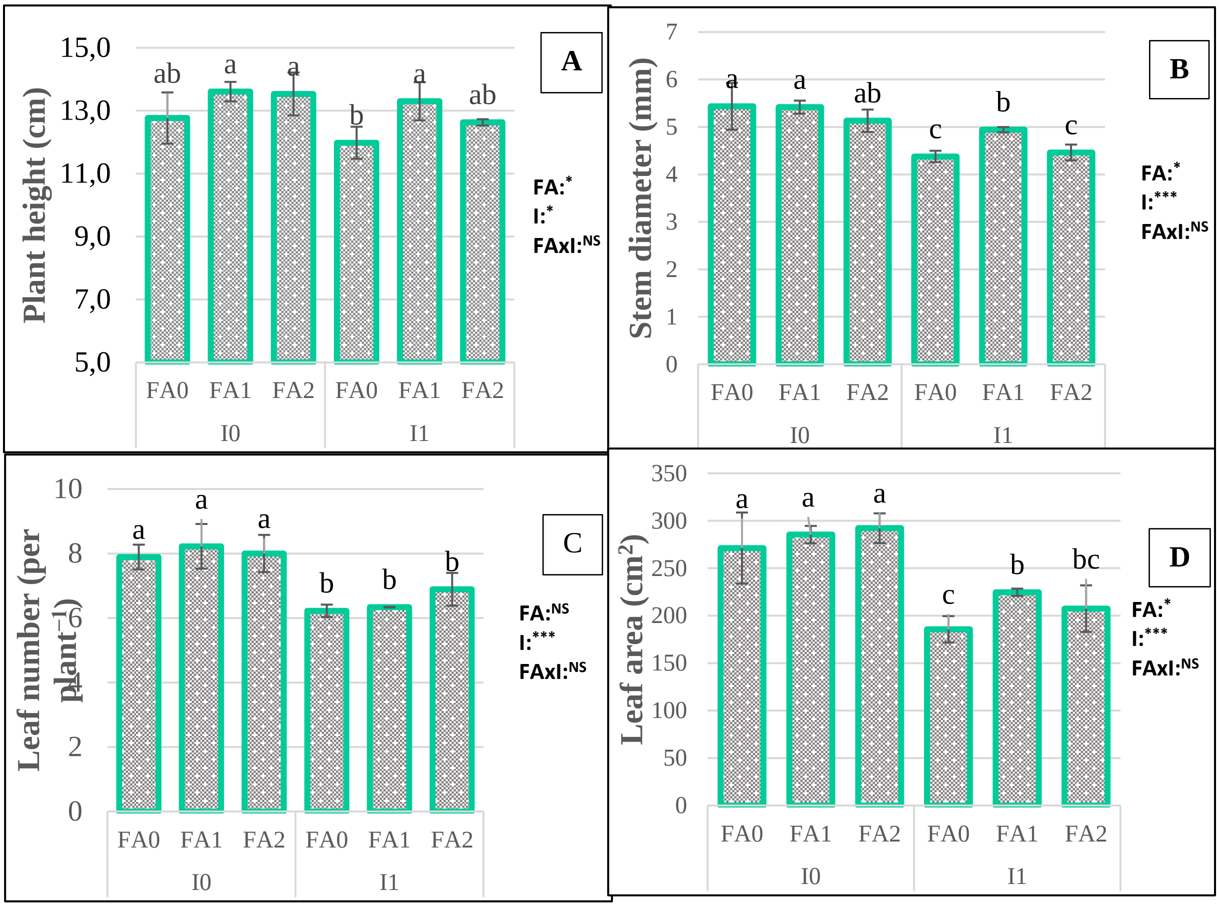

Figure 1. Effect of foliar application of 0 (FA0), 100 (FA1), and 200 µM (FA2) on (A) plant height (cm), (B) stem diameter, (C) leaf number, (D) leaf area in I0 and I1. Graph values are the mean ± SE of three replicates. Bars exhibited with different letters indicated a significant difference between means ($p \leq 0.05$).

The effects of folic acid doses and irrigation levels on plant height, stem diameter, number of leaves and leaf area were found to be significant at the $p<0.05$ level, except for FA treatments for stem diameter. Cabbage seedlings exposed to water deficit showed a significant decrease in plant height, stem diameter, number of leaves and leaf area by 6.19%, 19.49%, 21.17% and 31.56% compared to the control plants under well-irrigated conditions. As reported by Fathi and Tari (2016), drought stress during the vegetative period has multifaceted effects on plant development, including leaf and stem development, photosynthesis and accumulation of plant components. The study findings were consistent with the results of Jang et al. (2024), who reported drought stress-induced decrease in leaf area, fresh weight, and leaf water content of Chinese cabbage seedlings. Samancıoğlu et al. (2016) also confirmed that low irrigation levels reduce the growth parameters of cabbage seedlings. However, foliar application of folic acid has been shown to mitigate the adverse effects of deficient irrigation on the growth characteristics of cabbage seedlings (Figure 2). In plants experiencing water stress and treated with folic acid, FA1 and FA2, significant increases in plant height (11.02 and 5.43%), stem diameter (12.79 and 1.83%), and leaf area (21.02 and 11.74%) were observed compared to the control (F0). Folic acid treatments had no statistically significant impact on cabbage seedlings' leaf number, regardless of watering conditions (Figure 1). Gorelova et al. (2017) documented the significant regulatory role of folates in plant growth and development processes. In the study by Aljuaid et al. (2022), the application of folic acid was found to significantly improve the shoot fresh-weight of plants subjected to stress, particularly at concentrations of 0.1 and 0.2 mM, in comparison to untreated plants. A similar outcome was reported in a study conducted in coriander, where foliar FA application was found to enhance plant growth under conditions of deficient irrigation (Khan et al., 2022).

Table 1. Effect of 0 (FA0), 100 (FA1) and 200 µM (FA2) foliar applications on plant fresh weight, plant dry weight, plant dry matter content, root fresh weight, root dry weight and root dry matter content at I0 and I1.

Irrigation	Folic acid	Plant fresh weighth (g)	Plant dry weighth (g)	Plant dry matter content (%)	Root fresh weight (g plant^{-1})	Root dry weight (g plant^{-1})	Root dry matter content (%)
I0	FA0	15.37±0.56 a	3.40±0.18 a	22.18±1.13 a	4.44±0.94 a	3.45±0.09 a	14.05±1.38 b
	FA1	15.54±0.44 a	3.59±0.16 a	23.13±0.95 a	4.20±0.25 a	3.42±0.03 a	14.46±0.09 b
	FA2	15.39±1.39 a	3.41±0.20 a	22.14±1.42 a	4.81±0.40 a	2.94±0.07 a	13.08±0.64 b
I1	FA0	8.91±0.13 c	1.80±0.07 c	20.20±0.58 b	2.26±0.13 b	1.85±0.04 b	17.02±1.84 a
	FA1	9.16±0.68 b	1.97±0.08 bc	21.54±2.14 ab	2.36±0.38 b	2.05±0.05 b	17.92±1.76 a
	FA2	9.43±0.41 b	2.12±0.07 b	22.5±0.59 a	2.02±0.13 b	1.52±0.04 b	18.90±1.09 a
Falic Acid (FA)		*	*	*	NS	NS	NS
Irrigation (I)		***	***	**	***	***	***
FA× I		NS	NS	NS	NS	NS	NS

Table values are the mean ± SE of three replicates. Means with different letters in the same column indicate a significant difference (p ≤ 0.05).

On the other hand, a marked decline in plant fresh weight, plant dry weight and plant dry matter content was observed, amounting to 42.03%, 47.06% and 8.93%, respectively, as a consequence of the restricted irrigation. Concurrently, the fresh and dry weights of the cabbage seedlings' roots decreased by 49.10% and 46.38%, respectively, while root dry matter content exhibited an increase of 21.14%. Our results are consistent with those of the study by Şahin et al. (2018), which found that severe drought stress caused a 46.11-48.29% decrease in the relative fresh and dry weights of plant shoots. On the other hand, as a result of restricted irrigation, plant fresh weight, plant dry weight and plant dry matter content of cabbage seedling decreased significantly by 42.03%, 47.06% and 8.93%, respectively. Meanwhile, the restriction of irrigation led to a decline in the fresh and dry weights of cabbage seedlings' roots by 49.10% and 46.38%, respectively, while root dry matter content exhibited an increase of 21.14%. However, folic acid foliar application significantly increased plant fresh weight under restricted irrigation conditions, though no differences were observed between doses. The most favourable outcomes were observed for plant dry weight and plant dry matter content of cabbage seedlings, with 17.78% and 11.39%, respectively, attained in the 200 µM FA (FA2) treatment under restricted irrigation conditions. Conversely, the impact of folic acid on root fresh weight and root dry weight of seedlings under restricted irrigation conditions was found to be insignificant. (Table 1). Khan et al. (2022) reported that foliar application of folic acid to coriander plants under IR75 and IR50 irrigation regimes resulted in higher plant fresh biomass (28% and 131%) and dry biomass (63% and 66%) in comparison to plants not treated with folic acid.

Table 2. Effect of 0 (FA0), 100 (FA1) and 200 µM (FA2) foliar applications on plant fresh weight, plant dry weight, plant dry matter content, root fresh weight, root dry weight and root dry matter content at I0 and I1.

Irrigation	**Folic Acid**	**SPAD**	**LRWC (%)**	**EC (%)**
I0	FA0	50.07±0.88 c	89.27±0.65 b	43.63±1.11 d
	FA1	47.69±1.07 d	90.31±3.45 b	39.26±0.86 e
	FA2	47.43±1.09 d	94.87±2.98 a	41.31±1.4 e
I1	FA0	59.04±0.15 a	67.35±1.95 d	64.02±1.24 a
	FA1	54.62±0.59 b	74.78±1.43 c	55.26±1.19 c
	FA2	55.16±0.88 b	72.52±0.95 c	57.79±1.06 b
Falic Acid (FA)		***	***	***
Irrigation (I)		***	***	***
FA× I		**NS**	**	**

Table values are the mean ± SE of three replicates. Means with different letters in the same column indicate a significant difference ($p \leq 0.05$).

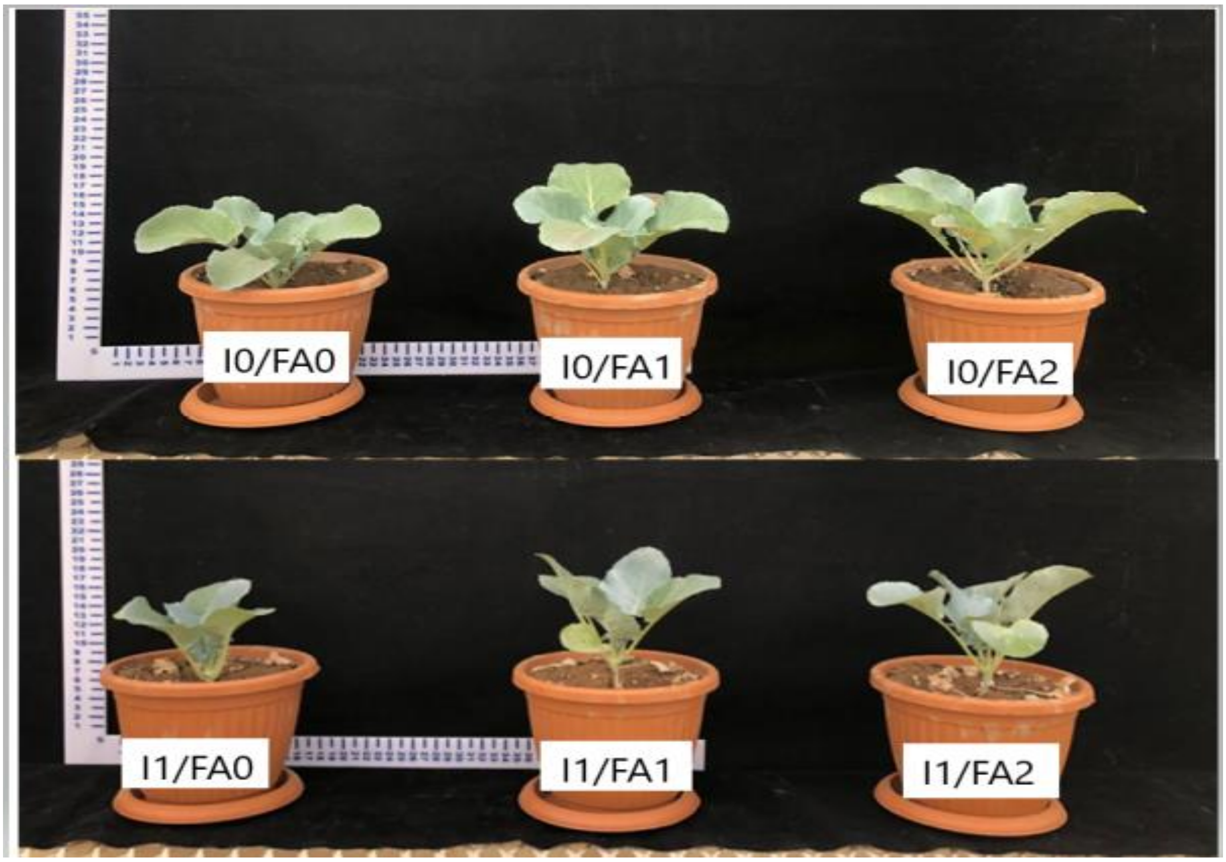

Figure 2. Response of cabbage seedlings to folic acid applications under varying irrigation conditions. I0: 100% irrigation; I1, 50% irrigation; FA0, 0 µM FA; FA1, 100 µM FA; FA2, 200 µM FA

Conclusion

The study's findings indicated that a restricted irrigation treatment resulted in a decline in several pivotal parameters of cabbage seedlings' growth. The parameters that demonstrated a decline included plant height, stem diameter, leaf number, leaf area, plant fresh and dry weight, plant dry matter content and root fresh and dry weight. Also, restricted irrigation increased root dry matter content, SPAD value and EC, while decreasing LRWC. However, folic acid application increased plant height, stem diameter, leaf area, plant fresh and dry weight and plant dry substance content in cabbage seedlings under restricted irrigation conditions. The best results in terms of plant height, stem diameter and leaf area were observed at 100 µM FA (FA1) folic acid dose in the restricted irrigation group. A folic acid dose of 200 µM (FA2) was found to be most effective in increasing plant dry weight and dry matter content in the drought-affected group. Furthermore, it was observed that folic acid sprays, irrespective of the dose, enhanced plant fresh weight, which had been diminished by the effects of drought. The study concluded that foliar application of folic acid in cabbage can be recommended as a possible intervention to reduce the effects of drought stress.

Acknowledgement

I would like to thank my student Şevval Dinçsoy, who contributed to the conducted of the study, and the Atatürk University Plant Production Application and Research Center, which provided greenhouse facilities.

Funding

The research has not been funded or supported by any organisation or individual.

Statement of Conflict of Interest

I declare that there is no conflict of interest between the authors of this study.

Authors' Contributions

Raziye Kul carried out all stages such as designing, conducting, analyzing the research, preparing pictures and tables, and writing the article.

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Origin and Evolution of Alfalfa

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ABSTRACT: Cultivated alfalfa (*Medicago sativa* ssp. *sativa*) is a crossing and autotetraploid (2n = 4x = 32) perennial forage crop selected from the M. sativa species complex, which includes both diploid and tetraploid interfertile subspecies. There are two possible centres of diversity and origin for alfalfa. These are Asia Minor/Caucasia and Central Asia. As a member of a relatively extensive complex, the evolution of alfalfa and related taxa can be traced using morphological traits and the cytogenetic status of ploidy and subsequent hybridisation between taxa. Morphological traits such as flower colour, pod shape and pod glandular hairs have been used to determine the evolution of alfalfa. Similarly, autotetraploidy within the complex has been linked to the evolution of alfalfa and related taxa. This research is summarised in order to provide a reference for the collection and use of alfalfa genetic resources and for the improvement of alfalfa breeding efforts.

Keywords: Alfaalfa, Origin, Evolution, Forage Crops, Ploidy, Taxon

INTRODUCTION

Alfalfa, one of the oldest domesticated forage crops, has played an important economic and cultural role in the history of human development. With its high nutritional value, alfalfa is among the most valuable forage crops used in animal nutrition worldwide. Apart from animal nutrition, alfalfa has many positive effects on economic, environmental and plant production. Alfalfa (*Medicago sativa* ssp. *sativa*) is a perennial, foreign fertilised and autotetraploid (2n = 4x = 32) forage plant. It has a species complex including diploid and tetraploid interfertile subspecies (Lesins and Lesins 1979; Barnes et al., 1988). It shows a wide range of phenotypic variation due to factors such as polyploidy and hybridisation. In the process of adaptation to different ecological conditions, alfalfa genetic resources have been enriched as a result of natural and artificial selection (Wang and Şakiroğlu, 2021). Therefore, studying the origin, evolution and genetic diversity of alfalfa is only useful in understanding the history of race formation.

The Origin of Alfalfa

Alfalfa (*Medicago* L.) is a large genus that includes valuable forage crops. There are about 60 species in this genus (Açıkgöz, 2001). Many alfalfa species are cultivated as forage crops in large areas (Veronesi et al., 2010). Most of these species are annual. Perennial alfalfa species are more important as forage plants (Annicchiarico et al., 2015). Perennial alfalfa varieties grown in the world today have developed from two main species. The first one, common alfalfa (*Medicago sativa* subsp. *sativa* L.), is a species with violet-purple flowers, small crown, taproot and generally tends to grow upright. It has pods that rotate around its axis 1-5 times in a spiral. The second species, yellow-flowered alfalfa (*Medicago sativa* subsp. *falcata* L.), is a yellow-flowered plant with yellow flowers, which grows in a recumbent position, has branching roots and a deep root crown (Figure 1). Its pods have a typical sickle shape (Li and Brummer, 2012). The hybrid alfalfa (*Medicago sativa* subsp. *varia* (Martyn) Arcang. Syn: *Medicago media* Pers.) has flowers ranging in colour from yellow to violet. Its pods show a shape between two species (Açıkgöz, 2001).

Figure 1. *Medicago sativa* subsp. *sativa* L. in the upper part and *Medicago sativa* subsp. *falcata* L. in the lower part

The date and place of domestication of alfalfa is uncertain. It is probably domesticated in more than one place (Small, 2011). Alfalfa is mentioned in the literature in a Babylonian text written around 700 BC. In this text, alfalfa is listed under axpasti, a name of Iranian origin, by the gardener of the Babylonian King Mardukbalidin (Hendry, 1923).

Therefore, the centre of origin of alfalfa is generally attributed to Asia Minor/Caucasia (a region including the highlands of northwestern Iran, Armenia, Georgia and eastern Turkey) and Central Asia (the highlands of Kazakhstan, Uzbekistan and Afghanistan) (Şakiroğlu and İlhan 2021; Small 2010; Small and Brookes 1984; Lesins and Lesins 1979). From the proposed centres of origin (Asia Minor and Central Asia) it spread to Greece and the wider Middle East, and then to Rome (Small 2010; Michaud et al., 1988).

The Evolution of Clover

Morphological Features

In the evolution of alfalfa, flower colour and pod shape are two morphological characteristics. The basic flower colour for the whole *Medicago* genus is yellow and the pods are flat. Purple flower colour is a new evolutionary event seen in certain taxa (Şakiroğlu and İlhan 2021). Differences in floral morphology were probably linked to changes in the behaviour of pollinators resulting in genetic isolation and subspeciation (Quattrocchio et al., 1999).

In the pre-genome era, the biochemical composition of floral colour pigmentation was investigated for the classification of taxa. The yellow colour of petals has been attributed to flavonoids, while violet petals have been attributed to anthocyanin content (Steiner et al., 1992; Small and Brookes 1984; Barnes 1966). Taxa with purple flower colour also have curved pods, making the two traits interrelated. Varieties worldwide have purple flowers with a few yellow-flowered varieties. Modern cultivated alfalfas have purple flowers, as yellow-flowered taxa are less resistant to winter hardiness (Sakiroglu et al., 2011; Small 2010).

Another trait, the inheritance of pod glandular hairs, has a different pattern among taxa and can be separated from the other two traits. The evolution of fruit hairs in alfalfa pods has been linked to the biology and geography of Rychius species (Small 1985). Similar information has been reported for the evolution of coiled pods as a result of selective evolution around the Caucasus to adapt to seed chalcid (Bruchophagusroddi) invasion (Small and Brookes 1982).

Figure 2. Pod Glandular Hairs of Alfalfa

Poiliploidi

Polyploidy is common in plant evolution. *Medicago sativa* is a polyploid complex consisting of two ploidal levels, diploid ($2n = 2x = 16$) and tetraploid ($2n = 4x = 32$). There are weak hybridisation barriers at the same level and between ploidal levels (Quiros and

Bauchan, 1988; Foster and Prentice, 1987; McCoy, 1982; Bingham, 1968). Flower colour, pod shape and pod pubescence are the main morphological characters that distinguish the three main diploid members of this species; the diversity of these characters and ploidal level characterise the other members (Table 1). Taxonomic treatment of *M. sativa* has long been contradictory in terms of ranking and nomenclature. Some researchers have ranked most taxa in *M. sativa* as distinct species (Lesins and Lesins 2012), while others have recognised most of them as subspecies (Şakiroğlu and Brummer, 2011; Quiros and Bauchan, 1988). The morphological variability resulting from the crossing ability among members of this species has been considered as the reason for the confusion and proliferation of names throughout the long taxonomic history of M. sativa (Quiros and Bauchan, 1988).

Among the members of the complex, the diploid subspecies (2n = 2x = 16) are: *M. sativa* subsp. *glomerata* (yellow flowers, curled fruits, glandular hairs present), *M. sativa* subsp. 2x *falcata* (yellow flowers, flat fruits, no glandular hairs), *M. sativa* subsp. *caerulea* (purple flowers, curled fruits, no gland hairs) and the natural hybrid between diploid subsp. *falcata* and subsp. *caerulea*, *M. sativa* subsp. hemisikla (variegated flowers, semi-curled fruits, no gland hairs). The tetraploid subspecies (2n = 4x = 32) are: *M. sativa* subsp. glutinosa (yellow flowers, curled fruits, tetraploid analogue of subsp. glomerata with glandular hairs), *M. sativa* subsp. *sativa* (purple flowers, curled fruits, tetraploid analogue of subsp. caerulea without glandular hairs), *M. sativa* subsp. 4x *falcata* (yellow flowers, flat fruits, no glandular hairs) and *M. sativa* subsp. *varia* (tetraploid hybrid between subsp. *sativa* and subsp. *falcata* with variegated flowers, semi-curled fruits, no glandular hairs) (Small 2010; Quiros and Bauchan 1988; Lesins and Lesins 1979; Stanford et al., 1972).

Table 1. Principal characters used in distinguihing members of *Medicago sativa* (Havananda et al., 2011)

Taxa	Ploidy	Flower color	Pod shape	Pod pubescence
M. sativa subsp. *caerulea*	Diploid	Violet	Coiled	Simple or glabrous
M. sativa subsp. *sativa*	Tetraploid	Violet	Coiled	Simple or glabrous
M. sativa subsp. *falcata*	Di-, tetraploid	Yellow	Straight or sickle	Simple or glandular
M. sativa subsp. *glomerata*	Di-, tetraploid	Yellow	Coiled	Glandular
M. sativa subsp. × *hemicycla*	Diploid	Segregated or variegated	Curved or loosely coiled	Simple
M. sativa subsp. × *varia*	Tetraploid	Segregated or variegated	Curved or loosely coiled	Simple
M. sativa subsp. × *tunetana*	Tetraploid	Segregated or variegated	Coiled	Glandular

Hybridisation between Taxon

Differentiation in wild clover germ plasm has occurred through isolation and subspeciation. However, differentiation has occurred by extensive hybridisation both within ploidy levels and between ploidy levels (Lesins and Gillies 1972). These hybridisations can be seen at both the genome and morphological levels. For example, at the diploid and tetraploid levels some hybrids show intermediate patterns in flower colour and pod shape. The diploid hybrid subsp. hemicycla and the tetraploid hybrid subsp. varia are variegated flowers (intermediate product of yellow and purple flowers) and semi-spiral fruits (Havananda et al., 2011; Small 2010).

Self-incompatibility

Self-incompatibility, or self-sterility, is a process that promotes allogamy in plants, marked by the inability to produce seeds following self-pollination, even when functioning male and female gametes are present (Vogel ve Lamb 2007). Alfalfa and its relatives possess external reproductive mating mechanisms that inhibit the formation of inbred seeds and, consequently, inbred lines, which are linked to inbreeding depression during self-fertilization. Alfalfa demonstrates significant inbreeding depression mostly owing to the loss of dominance or the disruption of epistatic interactions (Li and Brummer 2009; Şakiroğlu and Brummer 2007). This has facilitated the extensive adaptability of alfalfa and its relatives to a wider ecogeography and significant genetic diversity. Previous investigations have demonstrated that single or multiple genome duplications have led to the existing autotetraploid species. Repeated hybridizations in the sympatric areas of Eurasia, succeeded by isolation, have produced hybrid taxa. The fitness benefits of tetraploids, including enhanced resistance to diseases and pests, as well as greater tolerance to abiotic conditions, have facilitated their further dispersion. Humans recognized these advantages, resulting in a subsequent global anthropogenic dispersion (Vyšniauskienė et al., 2013; Soltis et al., 2004).

Funding

The study was not supported by any institution or organisation.

Statement of Conflict of Interest

There is no conflict of interest between the authors.

Authors' Contributions

MAN designed and analyzed the research, MFS studies arranged. All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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International Conference on
Food, Agriculture and Animal Sciences
19-22 December 2024, Erzurum, TÜRKİYE

Overview of Meat Consumption in Türkiye

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ABSTRACT: The purpose of this study is to calculate per capita meat consumption and protein intake for cattle, sheep, and poultry in Türkiye over a 10-year period. The calculations are based on FAOSTAT's meat production, export, and import data from 1961 to 2022, as well as population data. The findings indicate that yearly per capita buffalo meat consumption declined from 577.17 grams in the 1960s to 89.83 grams in 2021–2022, whereas beef consumption rose from 3.20 kilograms to 14.43 kilograms. During the same timeframe, sheep meat consumption declined from 7.59 kg to 3.78 kg, and goat meat consumption fell from 1.68 kg to 1.01 kg. Chicken meat consumption rose from 2.24 kg to 20.12 kg, and turkey meat consumption went from 113.61 g to 568.16 g; however, goose meat consumption declined from 42.21 g to 37.01 g, and duck meat consumption fell from 21.43 g to 6.74 g. In the 1960s, sheep contributed 47% of the protein derived from these animals' meat, followed by cattle at 22%, chicken at 15%, goat at 11%, buffalo at 4%, and turkey, goose, and duck collectively at 1.5–2%. During the period of 2021-2022, chicken constituted 53% of the protein, with cattle at 35%, sheep at 10%, goat at 2%, and turkey at roughly 1%. The protein intake per person from these meats increased from 8.5–12 g in 1961–2000 to 27.60 g in 2021–2022. Until 2000, animal food consumption was insufficient in terms of protein. Although the consumption of animal food was sufficient in subsequent years, changes in consumption patterns may have led to issues, such as weight gain. For this reason, consumers can become healthier by consuming meat and its products more consciously.

Keywords: Nutrition, Meat Consumption, Protein Needs, Health, Consumer Awareness

INTRODUCTION

The rapid growth of the global population has resulted in several challenges related to nutrition and food security in various regions around the world. Furthermore, a number of factors, including the need to keep pace with developing technology and save time (Aydogdu and Kucuk, 2018), have led to a situation in which many individuals are unable to consume adequate and balanced nutrition (Aydogdu and Kucuk, 2018). This has resulted in a range of adverse health outcomes, including obesity, high blood pressure, diabetes, cardiovascular and musculoskeletal disorders, and cancer. (Bilici et al., 2012). A satisfactory quality of life is contingent upon the attainment of adequate nutrition and regular physical activity. This combination also serves to reduce the risk of developing numerous chronic diseases while simultaneously enhancing one's physical performance level (Fernández-Lázaro and Seco-

Calvo, 2023). The overarching objective of studies on adequate and balanced nutrition is to facilitate the well-being of individuals (Saygın & Demirbaş, 2018).

Adequate and balanced nutrition comprises the daily intake of nutrients in the proportions that the body requires. Among these elements, carbohydrates and fats provide the energy the body requires for optimal functioning, while proteins facilitate the renewal of cells and tissues. To provide context, each food group is a distinctive source of specific nutrients. Cereals and legumes are the primary sources of carbohydrates and protein, while vegetables and fruits are considered rich sources of minerals and vitamins. Nuts and oilseeds are essential for meeting the body's micronutrient requirements, and foods of animal origin provide the quality proteins that individuals require (Leitzmann, 2009). Adequate protein intake is crucial for maintaining muscle mass and facilitating cellular regeneration (Bauer et al., 2013).

Amino acids combine to form proteins. The body's ability to digest food determines its protein quality, and the composition of amino acids directly influences this quality. In other words, the presence of all essential amino acids in a protein source signifies that its digestibility rate is 100%. This suggests that the protein in question is of a high quality. The aforementioned classification also encompasses proteins derived from animal sources, as evidenced by the findings of Philips et al. (2015) and Özer et al. (2016). Vitamin B12, which is present in meat but absent from plant nutrients, plays a pivotal role in the development of the nervous system and red blood cells in the brain (Jakobsen et al., 2017). Additionally, meat serves as a significant source of minerals, including copper (Cu), iron (Fe), magnesium (Mg), and zinc (Zn) (Menezes et al., 2018).

The Food and Nutrition Board (FNB) of the US National Academy of Sciences has established a minimum daily protein requirement for a normal, healthy adult (not pregnant or lactating) of 0.6 g per kilogram of body weight. However, the FNB has incorporated a safety margin of 33% into this minimum, establishing the recommended daily protein intake for healthy adults at a minimum of 0.8 g per kilogram of body weight (Kovesdy et al., 2013; Kovesdy and Kalantar-Zadeh, 2016). Although there is a lack of precise data regarding the proportion of this ratio derived from animal sources (Camilleri et al., 2013), studies have indicated that it is at least 33% (Flachowsky et al., 2017). The percentage of protein derived from animal sources is estimated to be between 40 and 50% (Ünlüsoy et al., 2010; Şimşek, 2018), while studies have indicated that the figure may be as high as 51-66% (Lonnie et al., 2018).

The average daily calorie intake per capita has increased from 2196 kcal in 1961 to approximately 2985 kcal in 2022. This is due to a rise in per capita income worldwide, as well as increases in crop and animal product yields. Plant products accounted for 84.6% of these calories in 1961, while cereals accounted for 49.5%. By 2022, these proportions had decreased to 82.4% and 42.8%, respectively. During the same period, the European Union saw a decrease in the proportion of energy in crop production from 74.4% to 68.8%. China saw a similar trend, with the figure dropping from 96% to 80.4%. Japan also exhibited a notable decline, with the proportion falling from 90.1% to 80.4%. In the USA, the proportion increased from 64.9% to 72.0%, while in Russia it increased from 73.8% in 1992 to 74.0% in 2022. In Türkiye, the proportion of individuals meeting their energy needs from crops and cereals decreased from 84.3% and 55.8% to 81.5% and 36.9% in the same years (FAOSTAT, 2024).

Accordingly, the present study sought to ascertain the daily animal protein levels that could be obtained through per capita consumption of buffalo, sheep, goat, cattle, chicken, duck, goose, and turkey meat over the ten years between 1961 and 2022.

Materials and Methods

Material

The Food and Agriculture Organization Statistics (FAOSTAT) statistical database provided the data used in the study. We also consulted national and international literature, including articles, papers, books, online resources, and master's and doctoral theses, to support the study's findings.

Method

This study used data from FAOSTAT on meat production, exports, and imports, as well as population data from Türkiye, to figure out how much meat each person in Türkiye ate each year and how much animal protein they got from eating buffalo, sheep, goat, cattle, chicken, duck, goose, and turkey meat each year from 1961 to 2022. We used the average values of buffalo (21.2%), sheep (20.2%), goat (21.1%), cattle (22.5%), chicken (22.3%), duck (19.8%), goose (20.6%), and turkey (22.6%) meat to calculate the animal protein value (USDA, 2024). Note that this calculation did not include processed meat products and offal.

Research and Discussion

Meat production, exports and imports in Türkiye

The number of water buffaloes in Türkiye has decreased significantly over the past six decades, from 1.14 million in 1961 to 170 thousand heads in 2022. This represents a notable decline in the country's ranking, which has fallen from 9-10th in the world in the 1960s to 18-20th in the 2020s. Furthermore, while Türkiye accounted for 1.34% of global buffalo meat production in 1961, this figure declined to 0.20% in 2022 (Uzundumlu and Özdemir, 2024). Türkiye recorded no exports or imports of buffalo meat between 1961 and 2022.

While Türkiye's beef production accounted for 0.34% of the global total in 1961, this figure increased to 2.26% by 2022 (FAOSTAT, 2024). There was a notable increase in beef imports between 1984 and 1996. In 1985, 1987, and 1995, Türkiye imported between 35 and 45 thousand tons of beef (FAOSTAT, 2024). In 2018, Türkiye imported approximately 55,700 tons of beef, 80% of which came from Poland and the remaining 20% from other EU countries such as Bosnia and Herzegovina, Serbia, Ukraine, and Hungary. In the same year, Türkiye exported 110 tons of beef to countries including the United Arab Emirates, Qatar, and Iraq. The country of Türkiye generated a revenue of $1.1 million from these exports, while expenditures on imports reached $160 million. The average purchase price of beef in Türkiye was approximately $4-5 per kilogram, while the average sale price was $9-11 (ITC, 2024).

Türkiye is the ninth largest sheep-producing country in the world, with a total of 35 million sheep in 1961 and 45 million in 2022 (FAOSTAT, 2024). In recent years, there has been no import of ovine animals from Türkiye to any country. In 2018, Türkiye exported 48 tons of ovine meat to countries like Qatar, the United Arab Emirates, Iraq, and Oman, resulting in a revenue of $1.2 million. Türkiye sold sheep meat at an average price per kilogram (ITC, 2024).

Türkiye is currently the third largest goat producer in the world, with a population of 24.5 million in 1961 and the 22nd largest, with a production of 11.6 million heads in 2022 (FAOSTAT, 2024). In recent years, Türkiye has not imported ovine meat from any country. However, it has exported 5,208 tons of ovine meat in 2022 and 390 tons in 2023 to countries including Qatar, Kuwait, the United Arab Emirates, Iraq, and Oman. This has generated revenues of $32.2 million and $5.4 million, respectively. In 2022, the average price of a kilogram of sheep meat in Türkiye was $6.2, rising to $13.7 in 2023 (ITC, 2024).

With 27 million chickens and a 0.7% share in 1961, Türkiye ranked 26th. By 2022, this had risen to 11th place with 361 million heads of chickens and a share of 1.4%. While Türkiye ranked 14th with 500,000 geese and a 1.4% share in 1961, it ranked 8th with 1.38 million geese and a 0.38% share in 2022 (FAOSTAT, 2024). The most significant factor contributing to this shift is the expansion of goose production in China. In 1961, China accounted for 41% of the global goose population but only produced 87% of the world's goose meat. By 2022, China had increased its goose production by over 10 times, becoming the dominant player in the global goose meat market (Dumlu, 2024). Türkiye does not have a significant share in global duck production, with figures standing at 600,000 (0.3%) in 1961 and 420,000 (0.04%) in 2022. With regard to turkey production, while Türkiye was the sixth largest producer in 1961, accounting for 1.7 million turkeys and 0.8% of the global production, it became the twelfth largest producer in 2022, with 3.2 million turkeys, and 1.4% of the global production (FAOSTAT, 2024). In 2022, Türkiye imported 63,189 tons of poultry meat from countries such as Romania, Iraq, Lebanon, and Uzbekistan. On the other hand, Türkiye exported 665 thousand tons of poultry meat to countries such as Iraq, Iran, Libya, Hong Kong, the United Arab Emirates, Congo, Vietnam, and Georgia. Türkiye generated $1 billion in revenue from these exports while spending $105 million on imports. The country purchased poultry meat at approximately $1.67 per kilogram and sold it at $1.50 (ITC, 2024).

Meat Consumption per Capita

In order to ascertain the per capita meat consumption, it is necessary to consider the total meat production, the quantity of meat imported, and the quantity of meat exported. It is also assumed that there is no wastage or spoilage and that the meat is consumed exclusively by humans. The chart below presents the resulting calculation.

Table 1. Annual per capita meat consumption in Türkiye according to 10-year averages (g) (FAOSTAT, 2024)

Meat Types	1961-1970	1971-1980	1981-1990	1991-2000	2001-2010	2011-2020	2021-2022
Buffalo	577,17	365,21	263,06	101,96	69,09	70,38	89,83
Cattle	3.196,24	2.921,96	6.144,96	5.769,98	7.826,15	12.830,11	14.425,40
Sheep	7.592,72	7.099,73	5.517,67	1.951,95	2.858,14	3.307,60	3.779,53
Goat	1.676,87	1.575,82	1.369,77	298,55	743,00	883,58	1.008,27
Chicken	2.243,49	4.192,88	6.241,99	7.663,06	13.387,29	19.623,03	20.119,53
Goose	42,21	49,37	56,43	71,11	43,04	31,83	37,01
Duck	21,43	21,53	20,81	21,90	10,71	6,52	6,74
Türkiye	113,61	133,97	156,94	141,47	429,51	551,17	568,16
Total	15.463,70	16.360,47	19.771,64	16.019,99	25.366,92	37.304,74	40.035,63

The mean annual consumption of buffalo meat per capita for the period 1961-1970 was 577.17 g, which decreased to 365.21 g in the 1970s, 263.06 g in the 1980s, and 101.9 In the 1990s, consumption decreased to 6 g, while in the 2000s, it fell to 69.09 g. Following the introduction of support and incentives in the 2010s, consumption increased to 70.38 g in the 2010s and 89.83 g in 2021–2022. As stated by Guerrero-Legarreta et al. (2020), buffalo meat represents a promising option for meeting the increasing demand for foods rich in essential proteins and low in fat for human consumption. However, production and per capita consumption in Türkiye have decreased by a factor of five over the past six decades.

The average annual consumption of beef per capita for the period 1961–1970 was 3.20 kg, rising to 2.92 kg in the 1970s and then declining to 6.15 kg in the 1980s, a period during which incentives and supports were provided. The average annual consumption of beef per capita decreased to 5.77 kg in the 1990s, then decreased further to 7.83 kg in the 2000s. The average annual consumption of beef increased to 12.83 kg in the 2010s and further increased to 14.43 kg in the 2021-2022 period. As stated by Saygın and Demirbaş (2018), the prevalence of red meat is high in countries such as Argentina (55.4 kg), Brazil (37.5 kg), the USA (37.2 kg), Uzbekistan (28.5 kg), and Australia (28.2 kg), which have extensive pasture areas where feed resources are cultivated and animal husbandry is developed. Red meat plays an essential role in human nutrition, particularly in Türkiye due to its geographical location and cultural structure. However, media news and information pollution can erode consumer confidence and have a detrimental impact on consumption. Consequently, unscientific statements by non-experts may lead to a reduction in demand for red meat, which is crucial for human nutrition and Türkiye's cultural identity (Ergün and Bayram, 2021).

The mean annual consumption of sheep's meat per capita, as calculated from the data for the years 1961–1970, exhibited a decline from 7.59 kg to 7.10 kg in the 1970s and subsequently to 5.52 kg in the 1980s. The average annual consumption of sheep meat per capita was 1.95 kg in the 1990s, 2.86 kg in the 2000s, 3.31 kg in the 2010s, and 3.78 kg in 2021-2022. In a recent publication, Aydenizöz (2024) highlighted the suitability of sheep breeding in Türkiye, citing the country's favorable geographical structure and extensive pastures. The author underscored the significance of ovine breeding in the country's agricultural landscape. However, misguided policies and the imposition of higher prices have prompted a shift in consumer preferences, which has led to a decline in sheep breeding activities and inadequate protection of local breeds, thereby creating obstacles to the sustainable development of sheep farming.

The mean annual goat meat consumption per capita for the period 1961-1970 was 1.68 kg, declining to 1.58 kg in the 1970s and 1.37 kg in the 1980s. The average consumption of goat meat per capita was 0.30 kg in the 1990s, 0.74 kg in the 2000s, 0.88 kg in the 2010s, and 1.01 kg in 2021–2022. In their 2020 study, Şirin et al. observed that goat breeding in Türkiye is an animal production activity that is typically conducted in mountainous regions unsuitable for other activities. They further noted the success of goat breeding in the Mediterranean and Southeastern Anatolia regions in converting feed into milk compared to other animal production. The advantages of this breed include the variety of feed these animals can consume, the ability to establish goat enterprises with relatively small capital, high fertility, resistance to disease factors and adverse conditions, well-suited body and hoof structures for grazing and mountainous life, and superior utilization of feed raw materials with a high cellulose content compared to other species. As Aydenizöz (2024) notes, misguided agricultural policies and price hikes present significant challenges to the sustainability of small ruminant farming. These policies have the potential to alter consumer preferences, diminish the viability of small ruminant breeding enterprises, and leave local breeds vulnerable to extinction.

The mean annual per capita consumption of chicken meat for the period 1961-1970 was 2.24 kg, rising to 4.19 kg in the 1970s and 6.24 kg in the 1980s. The average annual per capita consumption of chicken meat was 7.66 kg in the 1990s, 13.39 kg in the 2000s, 19.62 kg in the 2010s, and 20.12 kg in the 2021-2022 period. As Yerlikaya et al. (2024) have observed, chicken meat has become a popular protein source in both developed and developing countries due to a number of factors, including its high protein content, low fat content, health awareness, and affordable price. A growing body of evidence suggests that the consumption of chicken meat is on the rise in developing countries such as Türkiye, particularly among low-income households. This trend points to a preference for chicken as a protein source among large families, given its cost-effectiveness.

The mean annual consumption of goose meat per capita for the period 1961-1970 was 42.21 g, rising to 49.37 g in the 1970s and 56.43 g in the 1980s. The average consumption of goose meat per capita increased from 11 g in the 1990s to 43.04 g in the 2000s, to 31.83 g in the 2010s, and reached 37.01 g on average in 2021–2022, with the support provided. According to Aksoy and Uzundumlu (2024), low domestic demand, elevated prices, and a lack of consumer information lead to the underrepresentation of geese, a type of poultry that can withstand harsh weather conditions, in the Turkish poultry market. Specifically, the exclusive production and consumption of goose meat in certain provinces, despite its nutritional benefits, has caused it to lag behind its alternatives.

The mean annual consumption of duck meat per capita for the period 1961-1970 was 21.43 grams. This figure increased to 21.53 grams in the 1970s, decreased to 20.81 grams in the 1980s, and then increased again to The average annual consumption of duck meat per capita was 21.90 grams in the 1990s, 10.71 grams in the 2000s, 6.52 grams in the 2010s, and 6.74 grams in the 2021-2022 period, according to the aforementioned average. Duck meat consumption is not a common practice in Turkish society, and many consumers are unaware of its taste. In their study, İlter and Altıner (2022) asserted that China is the dominant producer of goose and duck meat. However, China's large population and high poultry demand prevent it from meeting domestic demand, leading to the importation of duck and goose meat from countries with higher production levels. As Keskin (2017) stated in his master's thesis, although accelerating the daily production of young Peking ducks with their rapid development growth rate, good feed use, ease of maintenance, low disease risk, and high prices in luxury restaurants provides a very important social and economic plus, it is difficult for the public to switch from chicken to duck meat due to traditional family farming in rural areas and urbanization that has resulted in a shift away from older culinary traditions and a corresponding decline in popularity of duck meat.

The mean annual consumption of turkey meat per capita for the period 1961-1970 was 113.61 g, rising to 133.97 g in the 1970s, 156.94 g in the 1980s, and 178.86 g in the 1990s. In the 1990s, consumption was 141.47 g; in the 2000s, 429.51 g; in the 2010s, 551.17 g; and in 2021-2022, 568.16 g. Kálmán and Szőllősi (2023) asserted that according to FAOSTAT data, the annual per capita consumption of turkey meat for 2021 was 9.56 kg in Israel, 6.95 kg in the USA, 5.12 kg in France, 4.45 kg in Italy, and 0.73 kg globally. Additionally, they posited that shifts in consumer preferences, labor shortages, and an aging population impact poultry production, which is labor-intensive and necessitates expertise. Furthermore, they highlighted that avian influenza outbreaks in recent years can result in substantial economic losses and that antibiotics used in poultry production may erode confidence in poultry products. Additionally, Arslan et al. (2020) posited that turkey farming can enhance the income of low-income households in rural areas with low-cost production, as turkeys feed on waste from unused fields and unharvested plant parts. Furthermore, they suggested that it offers a means of safeguarding biodiversity as a natural pest control measure against harmful locusts.

Proteins from Meat Consumption per Capita

The table below shows the estimated per capita meat consumption and the corresponding daily protein intake from meat, assuming equal animal and human consumption and no losses.

Meat Types	**1961-1970**	**1971-1980**	**1981-1990**	**1991-2000**	**2001-2010**	**2011-2020**	**2021-2022**
Buffalo	0,34	0,22	0,15	0,06	0,04	0,04	0,08
Cattle	1,97	1,80	3,74	3,56	4,81	7,86	10,99
Sheep	4,22	3,95	3,05	1,08	1,59	1,82	2,83
Goat	0,97	0,92	0,79	0,17	0,43	0,51	0,72
Chicken	1,36	2,54	3,79	4,66	8,13	11,97	12,62
Goose	0,03	0,03	0,03	0,04	0,03	0,02	0,03
Duck	0,01	0,01	0,01	0,01	0,01	0,00	0,00
Türkey	0,07	0,08	0,10	0,09	0,27	0,34	0,33
Total	8,97	9,53	11,68	9,68	15,30	22,56	27,60
77% of the total	6,90	7,34	8,99	7,46	11,78	17,37	21,25

By the conclusion of six 10-year periods, commencing from 1961-1970, there was an approximate threefold increase in meat consumption and the protein per capita provided from meat in Türkiye. The statistical data prepared by FAOSTAT for Türkiye indicates that approximately 77% of the protein obtained from meat is allocated to human nutrition and not wasted.

The mean protein intake from total meat consumption per capita for the period 1961-1970, assuming no waste and that all consumption is made by humans, was 8.97 g. This increased to 9.53 g in the 1970s and 11.68 g in the 1980s. However, this was accompanied by a decline in meat production. In the 1990s, there was a concomitant decrease in meat consumption, resulting in a reduction of protein provided from meat to 9.68 g. Following this period, there was an increase to 15.30 g in the 2000s, 22.56 g in the 2010s, and 27.60 g in 2021-2022. If we consider a rate of 77%, the protein provided from meat is 21.25 g. In the 1960s, 47% of the protein from meat came from sheep, 22% from cattle, 15% from chicken, 11% from goat, 4% from buffalo, and 1.5-2% from turkey, goose, and duck. In the 2010s, 45% of protein from meat was derived from chicken, 40% from cattle, 8% from sheep, 2% from goat, 1-1.5% from turkey, and 0.5-1% from goose and duck. In the 2021-2022 period, 53% of protein from meat originated from chicken, 35% from cattle, 10% from sheep, 2% from goat, and approximately 1% from turkey.

The 2022 health survey (TurkStat, 2024) indicates that the mean body weight of the population is approximately 60-65 kg. This is based on the observation that the mean body weight of individuals aged 15 years and above is 73 kg, while 21% of the population is below the age of 15, with an average body weight of 20 kg. In other words, a daily protein intake of 60-65 g per person, with half of this derived from animal sources, is recommended for individuals with a healthy weight. Nevertheless, chicken, one of the animal foods, plays a more prominent role in the fast-food market and is in high demand by consumers due to its economic viability in comparison to red meat. Given that these foods are high in calories, when the proteins consumed are not metabolized, consumers gain weight, resulting in an overall increase in the average body weight of the population over time. In terms of animal food consumption, the following categories are worthy of consideration: meat and meat products, milk and dairy products, eggs and aquaculture products. In Türkiye, meat and meat products are the primary source of animal protein, accounting for the majority of animal food consumption in terms of weight. Prior to 2000, the consumption of animal food was insufficient in terms of protein. However, following this year, it reached an adequate level. Nevertheless, the restriction of movement and the demand for ready-to-eat foods have led to an increase in the prevalence of obesity. In comparison to the data from 2016, the figures from 2022 indicate a decrease in the proportion of the population classified as underweight (from 4.00% to 3.60%), a corresponding increase in the number of individuals with normal weight (from 42.10% to 40.6%), and a rise in the prevalence of the pre-obese group (from 34.3% to 35.6%) and the obese group (from 19.6% to 20.2%). Furthermore, the proportion of males was higher than that of females in groups other than those classified as obese or underweight (TurkStat, 2024).

Conclusion and Recommendations

It is of extreme significance to ensure an adequate intake of quality protein in human nutrition, with meat representing a vital food source in meeting this nutritional requirement. The objective of this study was to calculate the per capita meat consumption and protein intake of bovine, ovine, and poultry, with the exclusion of aquaculture products, in Türkiye for 10-year periods. We conducted the necessary calculations using data on meat production, exports, and imports in Türkiye for the period 1961–2022, sourced from FAOSTAT, and population data for each year in Türkiye to achieve this objective. Consequently, when all meat is not wasted and allocated solely for human consumption, the annual per capita consumption of buffalo meat decreased from 577.17 g for bovine meat, in comparison to the average for the period 1961–1970, to 89.83 g for the period 2021–2022. In contrast, beef consumption increased from 3.20 kg to 14.43 kg over the same period. In terms of ovine meat, there was a notable decline in consumption, with sheep meat decreasing from 7.59 kg to 3.78 kg and goat meat from 1.68 kg to 1.01 kg over the same period. In terms of poultry meat, chicken meat consumption increased from 2.24 kg to 20.12 kg, while turkey meat consumption increased from 113.61 g to 568.16 g. On the other hand, the consumption of goose meat dropped from 42.21 g to 37.01 g, and the consumption of duck meat decreased from 21.43 g to 6.74 g. Furthermore, meat consumption decreased from 21.43 g to 6.74 g. Additionally, in the 1960s, 47% of the protein from meat originated from sheep, 22% from cattle, 15% from chicken, 11% from goat, and 4% from buffalo. Furthermore, turkey, goose, and duck contributed 1.5-2% of the meat protein. During the 2021-2022 period, the protein content of meat was distributed as follows: 53% came from chicken, 35% from cattle, 10% from sheep, 2% from goats, and roughly 1% came from turkey. During the period between 1961 and 2000, per capita protein intake from these meats increased from 8.5 to 12 grams to 15.30 grams in the 2000s, 22.56 grams in the 2010s, and 27.60 grams in 2021–2022. The results indicate that the consumption of animal food was insufficient in terms of protein until 2000. However, after this year, even though the consumption of animal food was sufficient, there was a rise in individuals experiencing weight problems. This was primarily due to an increase in the consumption of ready-to-eat food derived from poultry, as well as limited mobility due to dependence on transportation. Individuals may mitigate the adverse effects of excess weight and associated health complications by limiting their consumption of ready-made food supplements and ensuring that their diet is sufficiently diverse. We also recommend engaging in regular physical activity, such as walking for a minimum of 30 minutes per day.

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Effect of Different Bacterial Strains on the Germination Forage Common Vetch (*Vicia sativa* L.) under Salt Stres

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ABSTRACT: Soil salinity has become an increasingly common global stress by creating a significant impact on agricultural productivity. It negatively affects agricultural productivity and threatens food security. Common vetch (*Vicia sativa*) is widely grown worldwide due to its advantages such as nutritional value and adaptability to climate and soil conditions. It is a very valuable forage plant with different usage areas such as green manure, pasture, silage and straw. The study was carried out in the greenhouses of Atatürk University Plant Production Application and Research Center in 2024. The experiment, which was established according to factorial arrangement in randomized plots, was carried out with 3 replications and one Common vetch (*Vicia sativa*) line was used. In the study, salt applications (%0, 100, 200, 400mM) were made to vetch seeds treated with bacteria (*Pseudomonas chlororaphis*) and the effect of bacteria on germination against salt stress was investigated. As a result of the study, germination percentage (%), germination rate (days), average daily germination (%), peak value (%) and germination value (%) parameters were examined. The results obtained showed that bacteria-applied seeds had higher germination rates in salt applications compared to seeds without bacteria and were found to be statistically significant.

Keywords: Bacteria, Germination, Common Vetch, Salt Stress

INTRODUCTION

Salinity is the phenomenon of soluble salts mixed with groundwater, especially in arid and semiarid regions, rising to the soil surface through capillarity with high groundwater and accumulating on the soil surface as a result of evaporation (Kwiatowsky, 1998). This accumulation can also occur below the surface due to high temperature (Ergene, 1982). When the salt concentration is high enough to reduce the usable water potential (0.5-1.0 bar), the plant experiences stress. This effect is called "salt stress" (Levitt, 1980). Today, soil salinity is considered one of the most severe abiotic stresses in agricultural production (Kesawat et al., 2023). It is estimated that it affects more than 20% of all cultivated land and about half of all irrigated land worldwide (Botella et al., 2007; Shrivastava and Kumar, 2015). It seriously threatens the entire life cycle of plants, especially in the seed germination, seedling formation and reproduction stages, leading to losses in crop yields. In fact, in 2021, the Food and Agriculture Organization of the United Nations estimated that the global annual cost of salt-induced land degradation in irrigated areas was 27.3 billion US dollars in lost crop productivity

(Colin et al., 2023). Therefore, salt tolerance is increasingly recognized as an important agricultural trait for the improvement of modern crops. Germination depends on conditions such as salinity, temperature, light, nutrient, moisture, freedom from pathogens, seed quality (germination capacity and viability), and recovery from dormancy (Otsamo et al., 1996). Salt tolerance is defined as the ability of plants to maintain normal growth and development under saline conditions (Ashraf, 1994). In nature, plants are classified into two groups, halophytes (salt-loving plants) and glycophytes (salt-sensitive plants), considering their salt tolerance capacity (Flowers, 1972). Salinity tolerance during the germination phase should be considered not only as the ability to germinate at high salinities, but also as the ability to germinate and recover after exposure to NaCl (Ungar, 1996).

Common vetch (Vicia sativa L.) is the most cultivated vetch species in our country and in the world (Tan, 2018). It is one of the most economically important annual grain legumes in the world, used as animal feed, roughage (for grain, straw and silage production), a cheap and rich protein, high digestibility and high energy content mineral source (Parissi et al., 2022; Huang, 2017). According to 2023 data in Turkey, it has a production of 38,655 tons (TÜİK, 2024). Since rhizobia interact symbiotically with soil bacteria to fix atmospheric nitrogen, it is ideal for production in sustainable agricultural systems because it uses less fertilizer and emits less pollutants such as pollutant gases (Dalias and Neocleous, 2017). This feature contributes to the improvement of soil properties (Kartal et al., 2020; Chai et al., 2017; Lithourgidis et al., 2011). According to FAO, common vetch production is mostly concentrated in Ethiopia, the Russian Federation and Spain. The annual production of common vetch is more than 934,388 tons and the planting area is 540,761 hectares (FAO, 2024). In this study, the effects of salinity on the germination process of common vetch seeds are examined and the use of bacteria is evaluated as a potential solution to reduce these negative effects. In recent years, soil salinity has become an increasingly serious problem and the use of plant growth-promoting rhizobacteria has become an option to increase the stress resistance of plants (Li et al., 2021). Pseudomonas chlororaphis is a non-pathogenic plant growth promoting rhizobacterium that has the capacity to resist different environmental stresses and synthesize many kinds of bioactive compounds with high yields (Shen et al., 2017). Studies show that some bacterial species colonize the root zones of plants and alleviate the effects of salt stress, thus creating positive effects on seed germination and plant growth. In this context, the identification and use of suitable bacterial species is of great importance for common vetch to be grown more successfully in saline soils and to develop resistance to this environmental stress factor. The aim of this study is to investigate the potential role of bacteria in increasing the germination success of common vetch seeds in saline conditions and to develop new agricultural approaches in this direction.

Material and Method

The study was carried out according to a randomized factorial experimental design with 3 replicates in a controlled environment (25±1°C) in 2024. The study was carried out to determine the effects of irrigating common vetch seeds with different salt concentrations with and without bacteria on germination performance. 'Nilüfer' vetch variety was used as material in the study. The following applications were made with 15 seeds in each petri dish. Eight different applications were made in the study. No salt and bacteria applied (T0B0); no salt applied, bacteria applied (T0B1); no bacteria applied, salt (100 mM) applied (T1B0); bacteria applied, salt (100 mM) applied (T1B1); no bacteria applied, salt (200 mM) applied (T2B0); bacteria applied, salt (200 mM) applied (T2B1); no bacteria applied, salt (400 mM) applied (T3B0); bacteria applied, salt (400 mM) applied (T3B1). In the study, Pseudomonas chlororaphis bacteria (another root bacterium that promotes non-pathogenic plant growth) were used (Liu et al., 2022). Germination counts continued for 7 days in petri dishes in the climate cabinet at 25±1 °C in a completely dark environment. During the study, seeds were counted every day and seeds with a root length of 2 mm were considered to have germinated (Demirkol et al., 2019). Germination percentage (%), germination rate (day), average daily germination (%), peak value (%) and germination value (%) were examined in the study (Czabator, 1962; Ellis and Roberts, 1981; Gairola et al., 2011).

Germination value % : n/Σn x 100 n = Number of germinated seeds Σn= Total number of seeds

Germination rate: n1/t1+ n2/t2 +…… n1, n2,… number of germinated seeds t1, t2, …days

Average daily germination: Total number of germinated seeds/total number of days

Peak value: Highest number of seeds/highest seed yielding day

Germination value: Average daily germination x peak value

Germination Percentage (%)

When the germination percentage was examined, it was seen that the bacteria applications did not affect the germination percentage in the first two applications (control and 100 mM NaCl). In the third application (200 mM NaCl), the germination percentage of the samples without bacteria was 86.66%, while the germination percentage of the seeds with bacteria was determined as 97.77%. The last application, 400 mM NaCl applications, was statistically in the same group, and the seeds with bacteria (T3B1) had a 33% higher germination percentage than the seeds without application (T3B0) (Figure 1). It has been supported in other studies that the germination rate decreases as the salt concentration increases, that bacteria applications increase the resistance to salt stress and that they positively affect the germination parameters examined (Kadıoğlu, 2021; Kadıoğlu, 2024). In a study investigating the effects of different bacterial species on germination in rice and wheat seeds under salinity stress, a significant difference was detected in the germination percentage of bacteria-treated seeds compared to untreated seeds (Damodaran et al., 2019).

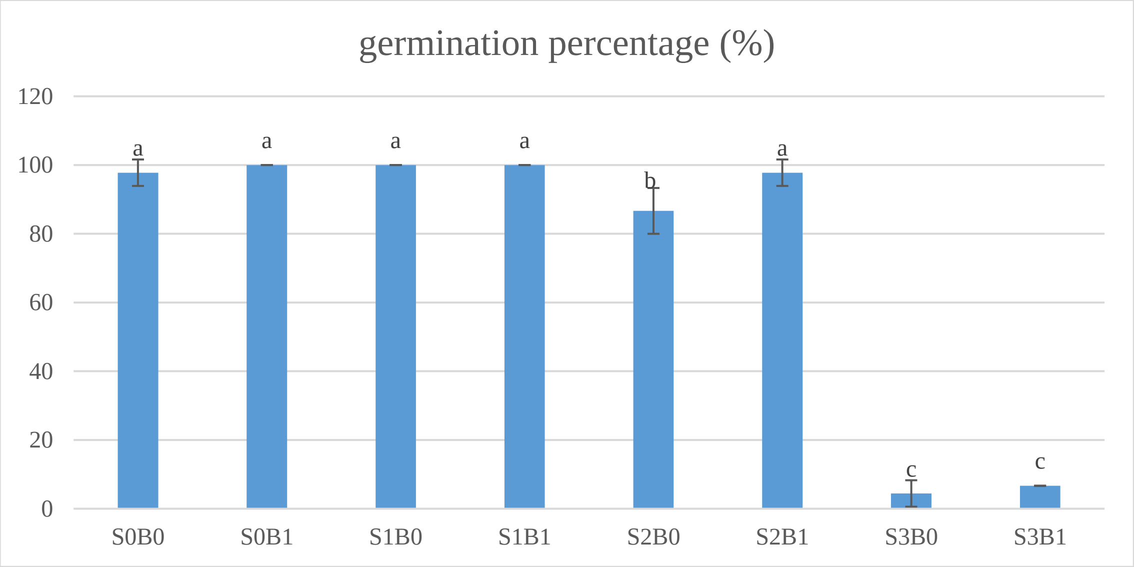

Figure 1. Effect of bacteria applications at different salt doses on germination percentage in common vetch

Germination Rate (days)

In the parameter where the effect of bacterial application on the germination rate of vetch seeds under salt stress is examined, it is observed that the germination rate decreases as the salt concentration increases (Figure 2). Except for the highest salt concentration application (400 mM), bacterial applications in all other applications positively affected the germination rate in seeds compared to seeds without bacteria. The highest germination rate (7.6 days) was obtained from the T1B1 application. The lowest germination rate was obtained from the T3B0 and T3B1 applications (0 days). The T2B0 application is the third lowest application with a value of 4.6 (days) (Figure 2). In a study examining the effects of Bacillus sp. bacteria and different salt concentrations on germination in coriander seeds, it was determined that bacterial applications increased the germination rate (Kadıoğlu, 2022).

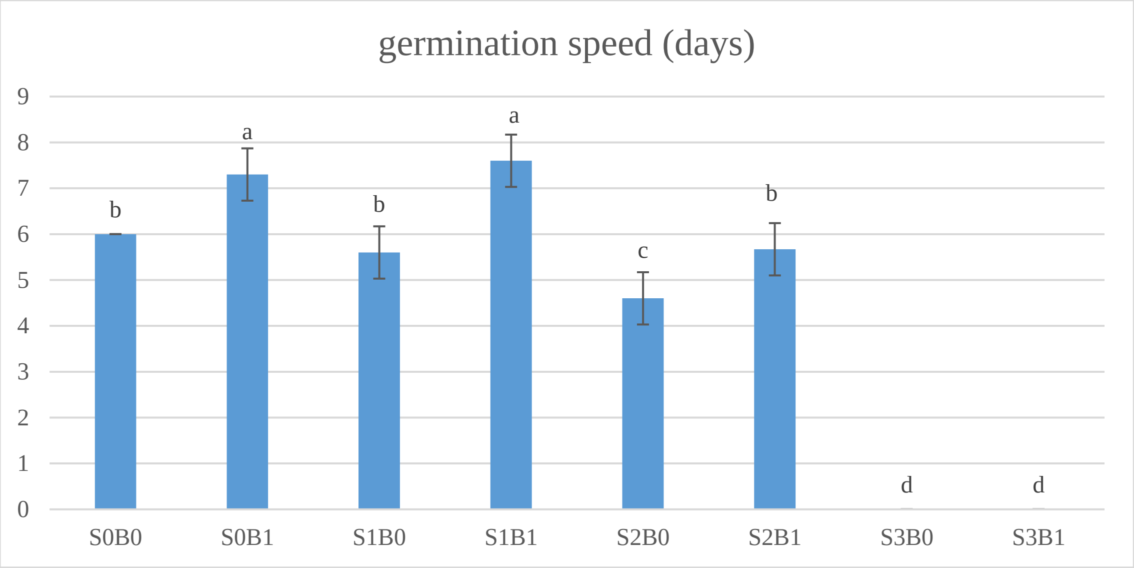

Figure 2. Effect of bacterial applications at different salt doses on germination rate in common vetch

Average Daily Germination (%)

As in the germination percentage, there is no statistical difference between the average daily germination of the seeds treated with and without bacteria in the first two applications (control, 100 mM). In the third application (200 mM NaCl), the seeds treated with bacteria (T2B1) were found to have 33.5% higher daily germination compared to those not treated (T2B0). In a study where bacteria were applied to flax seeds at different salt doses, it was determined that germination parameters decreased as salt doses increased, and bacteria application minimized the negative effects of salt application (Kadioglu, 2022b).

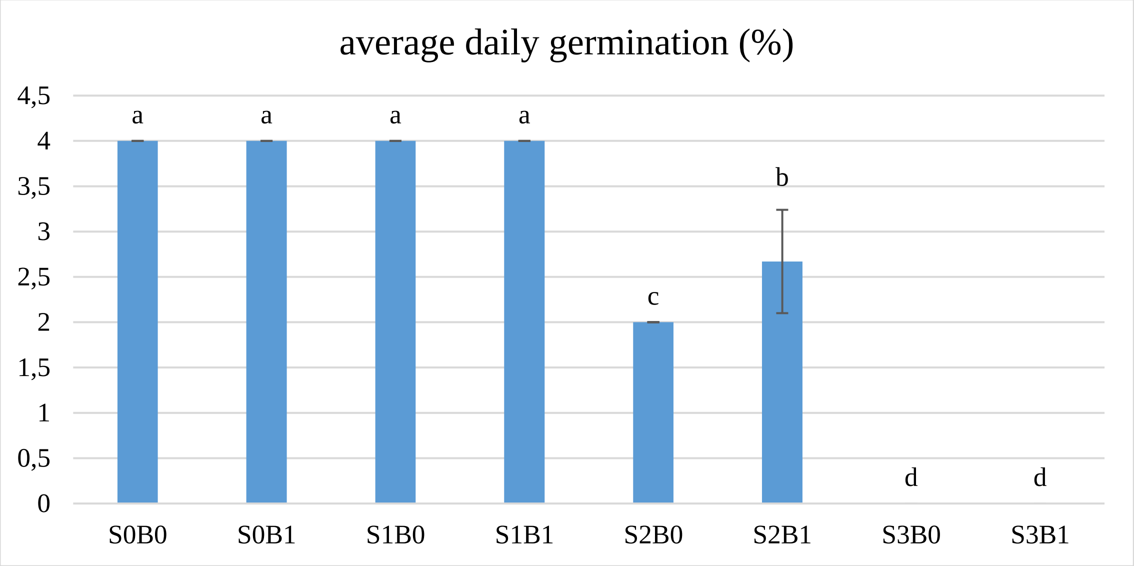

Figure 3. Effect of bacterial applications at different salt doses on average daily germination in common vetch

Peak Value (%)

Depending on the day when the number of germinated seeds was the highest, the peak value obtained varied between 4% (T1B1) and 0% (T3B0, T3B1). T0B1 and T1B1 (3.67%, 4%) were the treatments with the highest peak value percentage (Fig.4). It has been reported that the germination rate, germination index and wheat yield of wheat seeds increased significantly with the application of different bacteria (Pseudomonas putida, Enterobacter cloacae, Serratia ficaria and Pseudomonas fluorescens) in natural saline soils compared to the untreated control (Nadeem et al., 2013).

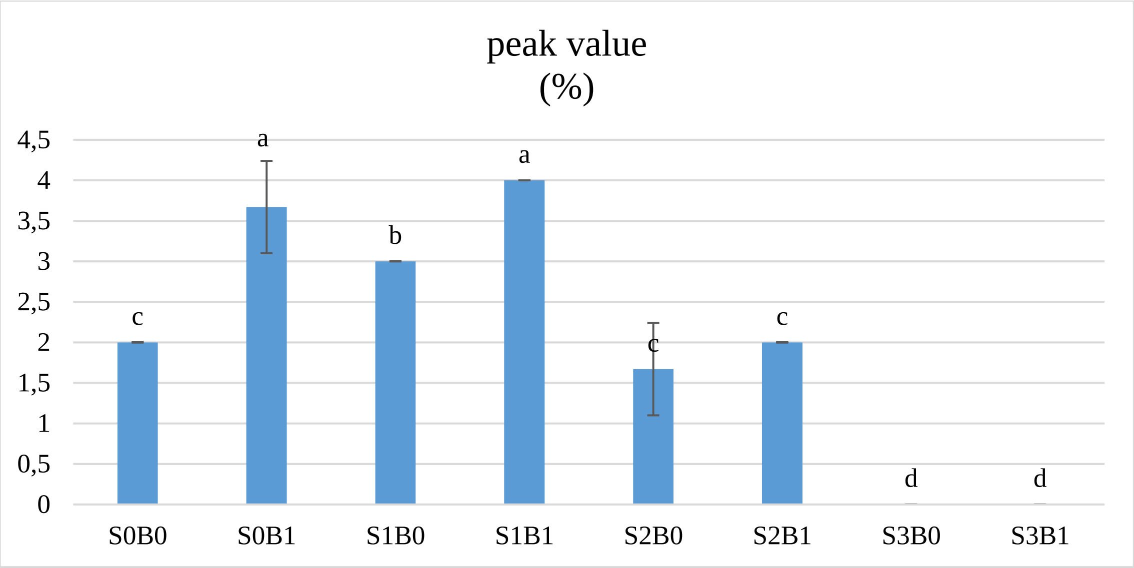

Figure 4. Effect of bacteria applications at different salt doses on the peak value of common vetch

Germination Value (%)

The results of the germination value parameter obtained by multiplying the average daily germination and the peak value are shown in Figure 5. In the first two applications (control, 100 mM NaCl), the germination value percentage of the seeds (T0B1, T1B1) to which bacteria were applied was determined as the highest values with 14.67% and 16%. T2B0 was the application with the lowest germination value in the first three applications with 3.33%. Kaymak et al., (2009), in their study to determine the effect of bacteria applications on the germination of radish (Raphanus sativus L.) seeds in salt concentrations, found that bacteria applications significantly increased seed germination in high salt concentrations.

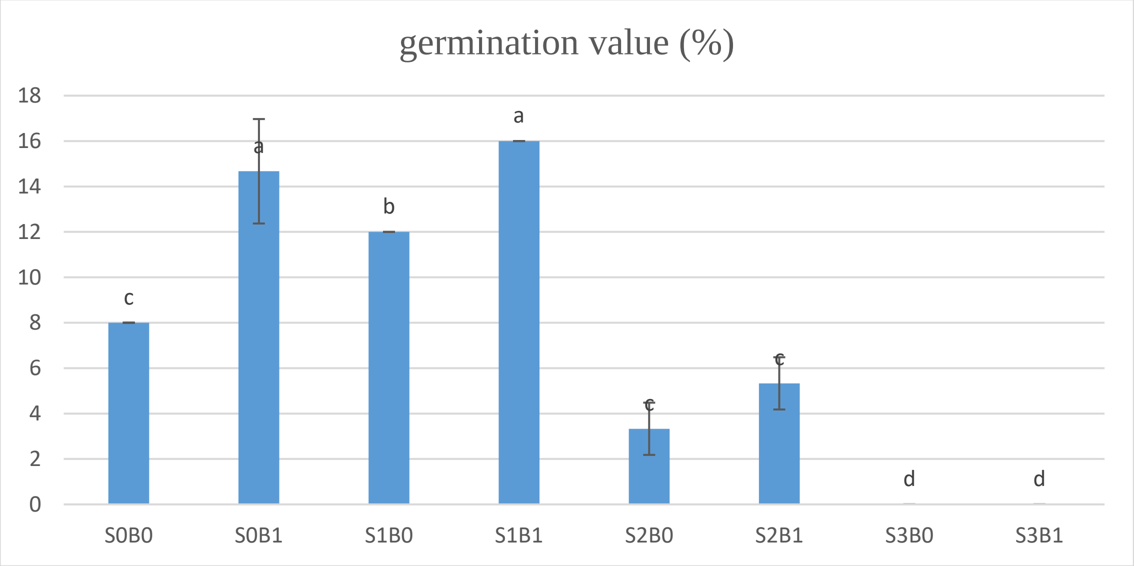

Figure 5. Effect of bacteria applications at different salt doses on germination value of common vetch

Conclusion

In the study; the effect of bacteria (Pseudomonas chlororaphis) applied at different salt doses on germination parameters was investigated, it was determined that bacterial applications were effective compared to the control in all parameters, and the bacteria used could reduce the negative effect of salt stress on germination of vetch seeds. Seed germination and early seedling growth are generally the most sensitive stages affected by salinity (Foolad, 2004) and alleviating the effects of salt at these early stages will increase the probability of successful crop growth under salt stress (Ashraf et al., 2003). Especially in 200 mM NaCl applications, germination parameters of bacteria-applied seeds were found to be higher compared to those not applied. In areas where soil salinity is high, growing plants that can tolerate salt and using soil conditioners such as bio-fertilizers that will alleviate the effects of soil salinity are of great importance in the recovery of lost agricultural lands.

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Investigation of the Effects of Monosodium Glutamate and Tannic Acid on the Glutathione and Thioredoxin Systems in the Liver of Rats*

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ABSTRACT: While there is no conclusive evidence that monosodium glutamate (MSG, a food additive) directly causes liver cancer in humans, certain studies suggest a potential link between MSG-induced hepatotoxicity and cancer development. This study aimed to evaluate the protective effect of tannic acid (TA, a natural polyphenol) against MSG-induced hepatotoxicity through the glutathione and thioredoxin system. Twenty-four rats were randomly divided into control and experimental groups and treated with TA, MSG, and the MSG+TA once daily by oral gavage for 21 days. In addition to major oxidative stress indicators, mRNA expression changes and biological activity responses of components of glutathione and thioredoxin systems were examined in the liver tissues of all animals. The results showed that MGS alone negatively affected both stress indicators (total glutathione; GSH+GSSG and malondialdehyde; MDA) and antioxidant system components (glutathione peroxidase; GPx, glutathione reductase; GR, glutathione-S-transferase; GST, and thioredoxin reductase; TrxR), in terms of mRNA expression and biological activity. However, the combination of MSG and TA demonstrated robust antioxidative effects, surpassing the outcomes of MSG treatment. Our results provide new insights into pivotal molecular targets and protective candidates that should be focused on in future in vivo and in vitro HCC research.

Keywords: Monosodium glutamate, Tannic acid, Glutathione, Thioredoxin, Liver

INTRODUCTION

Liver cancer is highly prevalent and ranks as the third leading cause of cancer-related deaths globally. Several risk factors are linked to hepatocellular carcinoma (HCC), a common type of primary liver cancer in adults (Ceylan, 2021). Along with non-alcoholic steatohepatitis (NASH), hepatitis B and C virus infections (HBV-HCV), and various medical or genetic conditions, lifestyle habits such as smoking, excessive alcohol consumption, and diet are key contributors (Ghouri et al., 2017). While nutrition is a constant environmental factor throughout life, it is also considered a significant modifiable risk factor for HCC (George et al., 2021). Numerous epidemiological studies suggest that certain dietary nutrients or metabolites may trigger mechanisms that contribute to cirrhosis, inflammation, and a higher risk of HCC, potentially through their toxic effects on the liver (Smith, 2013). Beyond influencing the development of HCC, there is a well-established connection between nutrition and the effectiveness of treatments for the disease.

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*This study is a part of the Mohammad Ali Abdulrahem ABUSHIKHA's master thesis accepted by Atatürk University, Graduate School of Natural and Applied Sciences

Over the past thirty years, human dietary habits have undergone significant changes due to the growing global population and shifts in lifestyle (Alt et al., 2022). In addition to social advancements, the rise of multicultural communities driven by globalization has led to cultural changes and shifts in eating patterns (Jacobs et al., 2009). This trend has resulted in a higher demand for convenience and processed foods, particularly toward the end of the 20th century. Nutritional additives, which are chemical substances commonly used in commercial food products today, serve not only to enhance the flavor and aroma but also to extend shelf life (Kouzuki et al., 2019). One such additive, monosodium glutamate (MSG), imparts an umami taste to processed foods (Niaz et al., 2018). Although the Food and Drug Administration (FDA) deems MSG "safe," numerous recent studies have linked it to various forms of toxicity (Park et al., 2000). Moreover, MSG is associated with several health issues, including chronic pulmonary diseases, diabetes, cardiovascular disease, and cancer, all of which are categorized as non-communicable diseases by the World Health Organization (WHO). Several in vivo studies have shown that MSG intake, even below the recommended daily limit for adults (6 g/day), can lead to a range of issues such as kidney toxicity (Koohpeyma et al., 2021), cardiotoxicity (Hazzaa et al., 2020), obesity (Hernandez Bautista et al., 2019), and hepatotoxicity (Omogbiya et al., 2021). Previous research has examined the changes in gene expression within cortical tissue resulting from MSG exposure. Understanding which dietary components negatively affect cellular function and the molecular mechanisms behind these effects in diseases like HCC could help inform the development of more effective diagnostic and therapeutic strategies.

Although chemotherapeutic agents for HCC are theoretically effective, long-term use can lead to clinical challenges due to side effects such as drug resistance and off-target toxicity (Di Costanzo et al., 2015). In recent years, the focus has shifted toward using bioactive natural compounds in the fight against complex diseases like cancer. These naturally occurring compounds are often associated with fewer side effects compared to synthetic pharmaceuticals (Nasim et al., 2022). Recent studies have highlighted that dietary phytochemicals could serve as low-cost, less toxic alternatives to prevent the development or progression of various diseases, including HCC. Tannic acid (TA), a natural polyphenol, is known for its anticarcinogenic, antimutagenic, anti-inflammatory, and antioxidant properties. Due to these diverse benefits, TA has shown promising clinical results in treating conditions such as myocardial infarction, renal failure, and cancer. Additionally, TA has become the subject of numerous studies exploring its potential to counteract HCC tumor progression. Therefore, this study aimed to investigate the effect of MSG exposure as well as TA treatment on the regulation of glutathione and thioredoxin system components in the rat liver.

Material and Method

Animals and Ethics Statement

Twenty-four male Sprague-Dawley rats (*Rattus norvegicus*, male, 180 g ±10 g) were purchased from the Atatürk University Medical Experimental Application and Research Center (Erzurum, Turkiye). Rats were randomly divided into 4 groups as follows: Control, TA, MSG, and MSG+TA groups. The control group rats were treated with a saline-only. TA (50 mg/kg) (Tüzmen et al., 2015) and MSG (2 g/kg) (Beyreuther et al., 2007; Biney et al., 2022) were administered once daily by oral gavage for 21 days. To improve prophylactic effect of the TA, it was administered to the rats in the combined group 1 hour before MSG (Al-Jaouni et al., 2019) All groups were housed in plastic cages under standard conditions (free access to diet and tap water, 22°C ±3°C air condition, 55 % humidity, and 12-12 h lighting). On day 21, all rats were euthanized under ketamine/xylazine (3:1) anesthesia, and liver tissues were removed immediately and kept at −80°C after washing cold phosphate-buffered saline. All of the experimental procedures were performed under the guidelines outlined by the National Research Council's Guide for the Care and Use of Laboratory Animals and were approved by the Atatürk University Local Ethics Council for Animal Experiments (Protocol No: 2021-3/63).

Assessment of Oxidative Stress Indicators

To examine the oxidative stress status after DOX exposure and TA treatment in the liver tissues of untreated and other experimental rat groups, malondialdehyde (MDA; secondary products of lipid peroxidation) levels and total glutathione (GSH+GSSG) contents, which are biomarkers of oxidative stress, were measured. MDA levels in rat liver tissue were measured at wavelengths of 532 nm according to the thiobarbituric acid method described by Suleyman et al(Suleyman et al., 2009), and presented as nanomoles MDA per milligram protein. The reduced glutathione (GSH) quantity in tissue samples was measured at wavelengths of 450 nm as previously described(Kocpinar et al., 2020)

Measurements of the Antioxidant Enzyme Activities

Total protein was determined by the Bradford method (Bradford, 1976). To measure glutathione peroxidase (GPx) enzymatic activity, 100 mg of liver tissue were homogenized (Heidolph Silent Crusher M, Germany) in a buffer containing 1 mM EDTA, 1 mM DDT, 1 mM PMSF, and 50 mM Tris HCl (Hydrochloric acid). To measure glutathione s-transferase (GST) enzymatic activity, the optical density of 10 µL of supernatant of liver tissue homogenate, 20 mM GSH, and 100 mM phosphate buffer contained mixture was measured (Oztay et al., 2020) Thioredoxin reductase (TRXR) enzyme activity was measured by modifying the method by Arner & Holmgren(Arner & Holmgren, 2006) A microplate reader (Multiscan GO, Thermo Scientific, USA) was used for all absorbance measurements.

qPCR analysis

For relative quantification of target genes mRNA expression, total RNA was extracted from rat liver using a commercial extraction kit (Biorad, Hercules, CA, USA) following the manufacturer's instruction. Then, the cDNA library was synthesized using the cDNA synthesis kit (Biorad, Hercules, CA, USA) following the manufacturer's recommendation. Pairs of specific primers (Table 1) were designed using the Primer3 (https://bioinfo.ut.ee/primer3-0.4.0/) online tool (Untergasser et al., 2012) For relative quantification, SYBR Green-based qPCR assay was performed using SsoAdvanced™ Universal SYBR® Green Supermix (Biorad, Hercules, CA, USA). *Gapdh* (NM_017008.3) was used as housekeeping control. The comparative ΔΔCt method (Livak & Schmittgen, 2001) was used for the relative quantification of gene expression.

Table 1. Sequences of primer sets used in quantitative PCR (qPCR). **F**; forward, **R**; reverse, **Tm**; melting temperature.

Gene symbol	Accession number	Sequence	Tm (°C)
Gpx_F	NM_030826.4	$^{5'-}$ TCGGACATCAGGAGAATGG$^{-3'}$	59.57
Gpx _R		$^{5'-}$ AGGTAAAGAGCGGGTGAGC$^{-3'}$	59.44
Gst_F	NM_001010921.1	$^{5'-}$ TTCTGACCCCTTTCCCTCTG$^{-3'}$	59.67
Gst_R		$^{5'-}$ TGGCTGGCTTTCTCTGACTG$^{-3'}$	59.97
Gr_F	NM_053906.2	$^{5'-}$ATTGGCTGCGATGAGATGC$^{-3'}$	60.33
Gr_R		$^{5'-}$ATGAATGGCGACCGTATTGT$^{-3'}$	60.22
Txnrd_F	NM_022584.3	$^{5'-}$AAGCCGTGCAAAACCATGTG$^{-3'}$	59.97
Txnrd_R		$^{5'-}$ACCGTGAACTGTGTGCTCGT$^{-3'}$	60.04
Gapdh_F	NM_017008.3	$^{5'-}$AAACCCATCACCATCTTCCA$^{-3'}$	60.17
Gapdh_R		$^{5'-}$ATACTCAGCACCAGCATCACC$^{-3'}$	60.16

Statistical analysis

Statistical comparison of data obtained from measurements made in triplicate (for each animal and sample) was evaluated with one-way ANOVA and Tukey's post-hoc test using Prism (GraphPad Software, San Diego, CA) software. The statistically significant differences are presented as follows: $^{ns}p > 0.05$ (not significant compared to the control group); *$p<0.05$

(significant); **$p<0.01$ (very significant); *** or **** $p<0.001$ or .0001 (extremely significant).

Results and Discussion

Effects of MSG and TA administration on liver MDA and total GSH content

To investigate the impact of MSG and TA on rat liver redox balance, lipid peroxidation and total total glutathione contents were examined. Initially, the MDA concentration was measured in the livers of rats subjected to MSG treatment, both solely and in conjunction with TA. As depicted in Figure 1A, a notable elevation in MDA levels was observed in the livers of rats within the MSG-only group, relative to the control group. Conversely, TA administration by itself did not lead to a marked rise in MDA levels. Furthermore, TA effectively mitigated the rise in lipid peroxidation prompted by MSG. Upon examining GSH levels, it was noted that MSG treatment alone significantly diminished the total GSH content, whereas TA on its own had no impact on GSH levels (Figure 1B). Additionally, the concurrent administration of TA with MSG reversed the reduction in GSH levels caused by MSG.

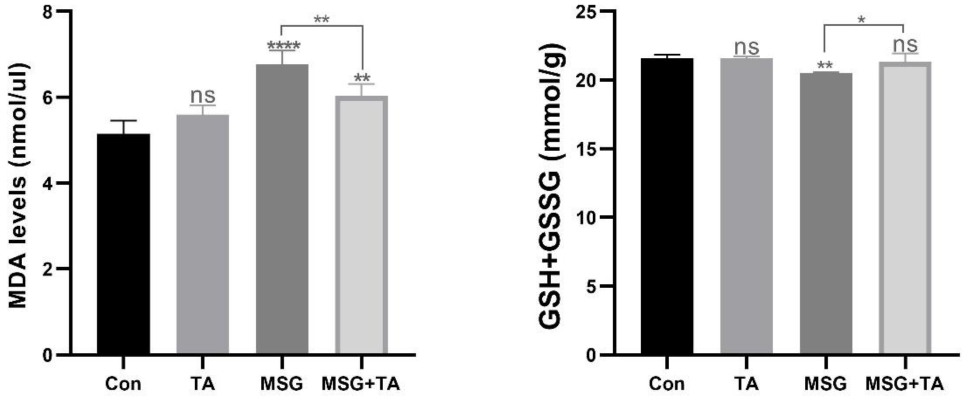

Figure 1. Malondialdehyde (MDA) levels and total glutathione (GSH+GSSG) content in the rat liver tissues. MDA levels in liver tissues **(A)** and comparison of total GSH content **(B)**. ^{ns}represents $p>0.05$, *represents $p<0.05$, **represents $p<0.01$, ***represents $p<0.001$, and ****represents $p<0.0001$ vs control group. The data are shown as mean ± SEM (n=5).

Glutathione system status of liver tissue after MSG and TA administration

The impact of MSG and TA on antioxidant system components was examined at both gene and protein levels. As depicted in Figure 2A and 2B, the notable reduction in *Gpx* mRNA expression induced by MSG was counteracted with TA treatment. A similar trend was observed in GPx enzyme activity. The MSG-induced loss of enzyme activity was significantly recovered by TA, reaching the control group's level. *Gst* mRNA expression was significantly diminished by MSG exposure, but TA administration did not affect it. Furthermore, the combination of

MSG+TA significantly prevented the severe reduction in gene expression compared to MSG administration alone (Figure 2C). It was also noted that GST enzymatic activity significantly decreased after MSG administration (Figure 2D). Comparable outcome was found for glutathione reductase. *Gr* mRNA expression, which was suppressed by MSG exposure alone, rebounded with TA supplementation (Figure 2E). It was noted that GR enzyme activity was significantly reduced after MSG. However, TA supplementation steadily increased enzyme activity (Figure 2F).

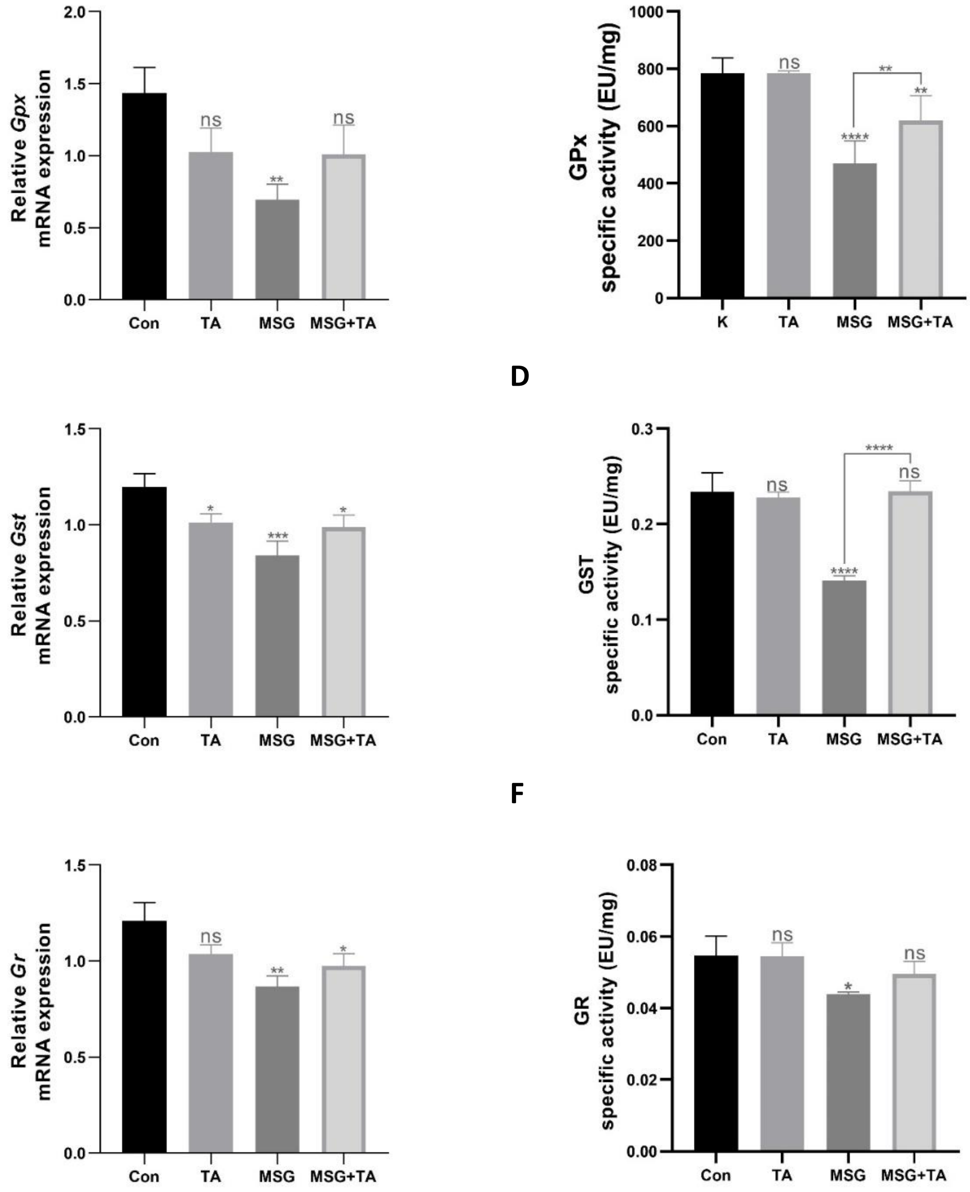

Figure 2. Effects of MSG and TA on the mRNA expression and specific activities of glutathione metabolism members in the rat liver tissues. The relative mRNA expressions of *Gpx*; glutathione peroxidase **(A)**, *Gst*; glutathione s-transferase **(C)**, *Gr*; glutathione reductase **(E)**. The enzymatic activities of GPx **(B)**, GST **(D)**, GR **(F) a**fter saline, TA, MSG, and MSG+TA treatment. ^{ns}represents $p>0.05$, *represents $p<0.05$, **represents $p<0.01$, ***represents $p<0.001$, and ****represents $p<0.0001$ vs control group. The data are shown as mean ± SEM (n=5).

Thioredoxin system status of liver tissue after MSG and TA administration

Lastly, the quantification of thioredoxin reductase mRNA and enzyme activity were evaluated. mRNA expression of *Txnrd* was significantly suppressed after MSG exposure. However, the simultaneous administration of TA with MSG reversed the MSG-induced reduction in gene expression (Figure 3A). Similar outcomes were found for thioredoxin reductase activity. It was noted that the enzyme activity, which was significantly suppressed by MSG application, rebounded with TA treatment (Figure 3B). These findings suggest that TA may protect liver tissue from MSG-induced oxidative stress by enhancing the liver's antioxidant capacity.

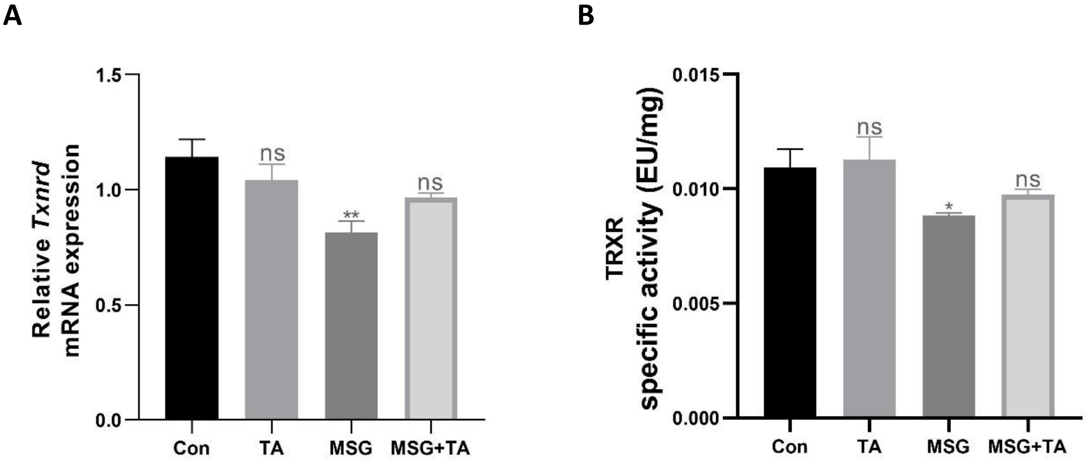

Figure 3. Effects of MSG and TA on the mRNA expression and specific activities of thioredoxin metabolism members in the rat liver tissues. The relative mRNA expressions of *Txnrd*; thioredoxin reductase **(A).** The enzymatic activities of TRXR **(B) a**fter saline, TA, MSG, and MSG+TA treatment. ^{ns}represents p>0.05, *represents p<0.05, **represents p<0.01, ***represents p<0.001, and ****represents p<0.0001 vs control group. The data are shown as mean ± SEM (n=5).

CONCLUSION

While the mechanisms behind monosodium glutamate-induced liver injury are becoming better understood, addressing and mitigating its harmful effects remains a significant challenge in the field of nutrition-related toxicity, and much still needs to be discovered. This study offers a comprehensive overview of the current knowledge on MSG-induced hepatotoxicity, along with potential preventive and therapeutic approaches. However, additional in-depth research, interdisciplinary collaboration, and human studies are essential to enhance the quality of life.

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Statement of Conflict of Interest

The author(s) should declare that they are no conflict of interest.

Authors' Contributions

HC; Conceptualization and design, Data curation, Formal analysis, Writing-original draft. MA; Data curation, Formal analysis, Animal care, and experiments. All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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ONLINE

ABSTRACT

ORAL PRESENTATIONS

Ethnobotanical Survey of Plant Used for The Treatment of Sexual Hormonal Disorder in Two South Localities in Algeria

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ABSTRACT: For centuries, plant resources have played an important role in human life. Some have nourished him, others have cured him of his deseases. Through time and experience, we have acquired knowledge about plants, discovered the medicinal ones among them, and developed practices and skills to preserve our health. Medicinal plants still have an important place in humanity's therapeutic arsenal. They are an important source of bioactive molecules that are generally part of secondary metabolites, which are molecules essential to plant life and their interaction with the environment, and are also important sources for pharmaceutical products. In this context, an ethnobotanical survey was carried out among 100 people in the South of Algeria between November 2022 and March 2023, has recorded the use of 55 plants for treatment of the reproduction disorder both in males and females. The maily used species were *Origanum majorana* and *Glycyrrhiza glabra*. Leaves and flowers were the most parts used with 44,9% and 15,09 respectively, decoction was the prefered method to prepare remedies. This study constitutes a source and scientific basis for chemists and biologists in algeria in the development of new drugs.

Keywords: Ethnobotanical Survey, Medicinal Plants, Infertility, South Algeria

Biofortification of Tomatoes with Iodine under Conditions of Closed Artificial Agroecosystems

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ABSTRACT: The palatability and balanced nutrient composition of plant products are important for both field and vertical farming. In recent decades, much of the research on biofortification has focused on specific compounds such as vitamins and amino acids, while minerals have remained less studied. The aim of the research is to increase the iodine content of tomato fruits to improve the nutritional value of the product and to provide the human body with the required amount of iodine. This research aims to develop effective methods to increase iodine concentration in tomatoes without compromising their flavor and yield, which is especially important for iodine deficient regions. Iodine bio-enrichment of tomatoes was carried out by introducing potassium iodate (KI) into the nutrient solution at concentrations from 0 to 13.0 mg/L. The results of the study showed a clear relationship between the dose of KI application and iodine accumulation in tomato leaves and fruits.

When KI was added to the nutrient solution in the range of 0.5-1.0 mg/L, an initial detection of iodine in leaves with a concentration of 0.04 µg/100 g was recorded. Subsequent increase in KI dose resulted in a significant increase in iodine levels in leaves, reaching a maximum of 35.96 µg/100 g when KI was used in the range of 11.0-13.0 mg/L.A similar trend was observed in tomato fruits. The first traces of iodine appeared in fruits at KI dosage of 2.0-3.0 mg/L, amounting to 0.39 µg/100 g. As the KI concentration increased from 2.0 to 13.0 mg/L, a consistent linear accumulation of iodine in fruits was observed.

Thus, the results of this study confirm the efficiency of tomato bio-enrichment with iodine by adding potassium iodate to the nutrient solution. The obtained data can serve as a basis for the creation of optimized methods of tomato biofortification aimed at increasing iodine content in plant products.

Keywords: *Solanum lycopersicum* L., Biofortification, Iodine

Inventory of Foraging insect and Role of Bees in the Pollination of two Market Garden Crops (Coriander and Zucchini) in the Constantine Region

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ABSTRACT: The pollinating insects of market garden crops, coriander and zucchini were determined during the flowerings of 2021 and 2023 in the locality of Hamma Bouziane (north of Constantine) and in private agricultural farms. Three orders of insects were recorded on these two plants: Hymenoptera, Diptera and Coleoptera. Hymenoptera are the most abundant visitors and are represented mainly by the super family of Apoidea. Diptera only frequented coriander and are represented mainly by Syrphidae with species such as Eristalis arbustorum (L, 1758) and Eupeodes luniger (Meigne, 1822). The honeybee, Apis mellifera, is the most frequent insect on these plants. On coriander, its visitation rates were 6.5±2.17 inf/min and 31.6±6.61 flr/min. On zucchini, the honeybee visited staminate flowers much more but spent significantly more time on pistillate than staminate flowers. Its pollinating efficiency estimated from the number of fruits obtained from one visit and two visits on the flower showed that both types of flowers produced fruits and that those obtained from flowers that received 2 visits were larger and contained significantly more seeds. The percentages of fruits obtained in the presence of insects are higher than those obtained in their absence (18% and 100% in zucchini; 39% and 61% in coriander).

Keywords: Honeybee, Pollinating Efficiency, Yield, Coriander, Zucchini

Effects of Natural Bioactive Compound Mixture on Broiler Growth Performance, Physiological Health, and Meat Quality

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ABSTRACT: The increasing demand for sustainable poultry production has driven heightened interest in the utilisation of natural feed additives as alternatives to antibiotics, particularly considering the European Union's prohibition on the subtherapeutic use of such pharmacological agents. Thus, the aim of this study was to investigate the impact of a mixture of natural bioactive compounds, including organic acids, plant extracts, and essential oils, on broiler health and meat quality. A feeding trial was conducted with Ross 308 broiler chickens, divided into two groups, each containing one hundred three thousand birds. The control group received a standard diet, while the experimental group was supplemented with the bioactive mixture at one kilogram per tonne of feed. During the 41-day trial, growth performance, physiological health, and carcass quality were analysed. While growth rates did not differ significantly, the experimental group showed marked improvements in blood parameters such as total protein, aspartate aminotransferase (AST), and alanine aminotransferase (ALT) levels ($p < 0.05$). Enhanced nutrient absorption was indicated by an increased *villus* height-to-crypt depth ratio in the *ileum*. Carcass quality was also improved, with higher yields, greater breast muscle mass, and a more intense breast muscle colour ($p < 0.05$). Moreover, adding natural bioactive compounds to broiler diets significantly improved physiological health and meat quality, highlighting their potential in sustainable poultry production.

Keywords: Sustainable Poultry, Bioactive Compounds, Organic Acids, Plant Extracts, Broiler Health, Meat Quality

Exploring The Antifungal Activities of Lignosus Rhinocerus-Based Silver Nanoparticles

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ABSTRACT: *Fusarium solani* and *Aspergillus ochraceus* are pathogenic fungi responsible for significant agricultural and health-related challenges, causing crop losses and mycotoxin contamination. Conventional management strategies include synthetic fungicides but their prolonged use has led to resistance and environmental concerns. Nanotechnology offers an innovative alternative, leveraging nanoparticles for enhanced antifungal efficacy. In this study, silver nanoparticles (AgNPs) were synthesized using the aqueous extract of *Lignosus rhinocerus*. Nanoparticles characterization revealed a peak at 317 nm via UV-visible spectroscopy, particle sizes ranging from 50 to 70 nm through SEM, and elemental composition (P, S, Cl, N, O) confirmed by EDX analysis. Five concentrations of AgNPs (100–500 ppm) and fluconazole were tested for antifungal activity against *Fusarium solani* and *Aspergillus ochraceus* using well diffusion method. Results showed that 500 ppm AgNPs produced an inhibition zone diameter of 33.67 mm against *Fusarium solani* and 16 mm against *Aspergillus ochraceus*. Comparatively, fluconazole at 500 ppm formed diameters of 38 mm and 18 mm, respectively. Similarly, the best concentrations from treatment and drug were selected to further evaluate the antifungal activities using radial growth method. The results revealed that LR-AgNPs inhibited *F. solani* 77% and *A. ochraceus* 75.3%. The antifungal drug controlled 80% *F. solani* and 60% *A. ochraceus.* Therefore, potential of *Lignosus rhinocerus*-based AgNPs as an eco-friendly, effective alternative to conventional antifungal agents. Future research should explore the mechanism of action, optimize nanoparticle synthesis, and evaluate field applications to establish these nanoparticles as a sustainable solution for managing fungal pathogens.

Keywords: Nanotechnology, Bioassay, Mushroom, Mycosynthesis, Eco-Friendly Approach

Assessing the Effects of Salt Stress on Growth and Physiological Traits of Different Okra (*Abelmoschus esculentus* L.) Cultivars

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ABSTRACT: The saline of the underground water supply is a main problem that adds to setting agricultural productivity. The salt-stressed plants have shown inhibited growth patterns with a slight lifespan of leaves and remaining productivity. By looking at these landscapes, an experiment was led to calculate the salt stress results of selected okra cultivars on seedling traits i.e., shoot and root length, shoot and root weight, number of leaves, flowers and chlorophylls 'a' and 'b' contents. The okra cultivars Green Star, Sabaz Pari, and Pahuja Seed improved Bhindi, and White Radish was used for this study. Sodium chloride (100 mM) was used to create the salinity while distilled water was used as the control. Salt stress expressively shorter the shoot and root length of all the tested okra cultivars. The lowest Shoot length 6 cm and root length 10.6 cm was found in 'Sabaz pari cultivar in salt stress conditions while White Radish showed the highest shoot and rot lengths 7.5 and 12.4 cm respectively. The weight of roots and shoots decreased under salt stress for controlled conditions. White Radish also showed the highest weight under salt stress. Salt stress also expressively reduced the quantities of chlorophylls 'a' and 'b' contents of okra cultivars. From these clarifications, it was arrived that the 'White Reddish' cultivar of okra could sustain the physiological attributes moderately better than the other tested cultivars under salinity situations. White Radish, therefore, could be selected as the most salt-tolerant okra cultivar which could boom and make it successful in the salt-affected areas of the sandy region.

Keywords: Salt, Seedling Parameters, White Reddish, Okra

Genetic Profiling of Wheat Aleurone Layer: Investigating Phenotypic Diversity in Mutant Lines

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ABSTRACT: In wheat, starch and protein accumulate in the endosperm, whereas most phytonutrients are found in the Aleurone layer (AL). The AL is the outermost layer of the endosperm and is removed with the bran during conventional milling. This study investigates the genetic diversity of wheat Aleurone layers through the analysis of thousands of mutant lines. Studying genetic diversity is crucial for breeding programs, especially in elucidating the genetic variability available to breeders. We systematically cut grains from diverse mutant populations and examine the resulting seeds under a high-resolution microscope. Targeted mutagenesis and molecular screening are employed to identify genetic mutations responsible for phenotypic variations. Our approach aims to identify and characterize mutant seeds exhibiting alterations in the Aleurone layer, shedding light on the genetic factors influencing its development. We aim to identify novel genetic markers associated with Aleurone layer development and provide a comprehensive catalog of mutant lines exhibiting diverse Aleurone phenotypes. By elucidating the genetic basis of Aleurone layer variability, this research not only expands our understanding of wheat biology but also offers valuable insights for crop improvement strategies. These findings will be used in future breeding programs, contributing to the development of wheat varieties with enhanced nutritional content, stress tolerance, and overall yield.

Keywords: Aleurone Layer, Phenotype, Mutant Screening, Molecular Markers, Crop Improvement

Enhancing Drought Resistance in Maize (*Zea mays.* L) to Meet the Demand for Sustainable Crop Production

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ABSTRACT: Drought is a critical challenge to global maize production, particularly semi-arid regions worlwide. The increasing demand for the sustainable crop production has emphasized the necessity of developing drought tolerant maize genotypes, especially for the regions facing water scarcity. The present study evaluated the genetic diversity of 50 maize genotypes by using molecular and phenotypic approaches to identify potential candidates for drought tolerance. Field trails were conducted under drought stressed and well-watered conditions and key traits such as green fodder yield, plant height, number of leaves, chlorophyll and stomatal conductance were assessed. Molecular analysis using SSR markers identified genetic clusters and alleles linked to drought tolerance. Among the studied genotypes three genotypes 17, 29 and 35 exhibited 22%, 27% and 30% higher green fodder yield under stressed conditions, alongside superior physiological traits including good water use efficiency and delayed leaf senescence. The genotypes identified in this study will serve as the foundation for the development of drought tolerant maize verities. These findings underscore the potential of combining traditional breeding with molecular techniques to enhance the development of maize accessions capable of thriving under drought stress.

Keywords: Maize, Drought Tolerance, Fodder, Genotypes, Genetic Diversity, SSR Markers, Breeding

Assessing the Influence of Rhizosphere-Derived Bacterial Strains on Phosphate Solubilization and Growth Promotion in Quinoa (*Chenopodium quinoa* Willd.)

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ABSTRACT: Quinoa (*Chenopodium quinoa*) is a gluten-free, nutrient-dense crop with a unique protein profile, making it an important food source. This study investigates the impact of different rhizosphere bacterial strains from quinoa on phosphorus (P) solubilization, organic acid production, and plant growth promotion. A total of five plant growth-promoting rhizobacteria (PGPR) were isolated from the quinoa rhizosphere, including *Azospirillum zeae* Cq-10, *Azospirillum lipoferum* Cq-11, *Azospirillum brasilense* Cq-12, *Azotobacter chroococcum* Cq-13, and *Azotobacter vinelandii* Cq-14, identified via 16S rRNA gene sequencing. These strains exhibited phosphate solubilization, bacterial growth, and the production of organic acids such as malic and citric acid in TCP-amended culture media. Additionally, the strains synthesized indole-3-acetic acid (IAA) in both the presence and absence of L-tryptophan. These bacterial strains promoted quinoa growth in pot trials, enhancing shoot biomass and grain yield. These PGPR isolates' multifaceted traits and plant growth-promoting properties suggest their potential for developing biofertilizers to improve quinoa growth and productivity. These findings provide valuable insights into sustainable agricultural practices for quinoa cultivation.

Keywords: Quinoa, Plant Growth-Promoting Rhizobacteria, Phosphorus Solubilization, Organic Acids, Biofertilizers, Sustainable Agriculture

Breeding Strategies in Sesame to Combat Charcoal Rot (*Macrophomina phaseolina*) with Special Reference to GWAS

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ABSTRACT: Sesame (*Sesamum indicum* L.) is a globally cultivated important oilseed crop. Presently, the sesame plants are threatened by several phytopathogens, but the soilborne fungus, charcoal rot caused by *Macrophomina phaseolina*, has become a major threat in sesame fields, and it causes severe yield loss, which is recorded at 10-70% in susceptible fields. Developing the resistant cultivars is essential for sustainable sesame production and reducing economic losses. Progress in genomics and molecular breeding has transformed the identification of resistance loci and expedited the development of resistant cultivars. Genome-wide association studies (GWAS) have become an effective method for analyzing the genetic structure of complex traits such as disease resistance. GWAS facilitate the identification of single nucleotide polymorphisms (SNPs) and quantitative trait loci (QTLs) associated with charcoal rot resistance in sesame germplasm. It utilizes natural genetic variation to develop critical resistance loci and genes. GWAS methodology has opened new direction for marker-assisted selection (MAS) and genomic selection (GS), allowing breeders to incorporate resistance gene into susceptible cultivars effectively. The amalgamation of phenomics and genomics for improved accuracy in resistance breeding is also examined. However, challenges remain in translating genomic insights into practical breeding outcomes. A multidisciplinary approach combining traditional and modern breeding techniques is needed to combat charcoal rot in sesame.

Keywords: Charcoal Rot, Genome-Wide Association Studies (GWAS), Resistance Breeding, Marker-Assisted Selection (MAS), Genomic Selection (GS), Quantitative Trait Loci (QTL)

Influence of Different Selenium Forms on Productive Performance and Pork Chemical Composition in Fattening Pigs

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ABSTRACT: Selenium is an essential trace element fundamental to the nutritional physiology of both humans and animals. Its metabolism in swine is markedly influenced by the bioavailability and physiological effects of various organic and inorganic forms. A comprehensive understanding of these selenium sources is imperative for optimising swine productivity and enhancing meat quality traits. So, the objective of this study was to evaluate the effects of different selenium forms on productivity and meat quality in fattening pigs. A total of sixty 62-day-old pigs (Landrace × Yorkshire as the maternal line and Pietrain × Duroc as the paternal line) were individually weighed and randomly assigned to two dietary treatments (n = 30 pigs per group) across four replicate stalls. Over a period of 13 weeks, the pigs were fed ad libitum with a standard compound diet composed of wheat, barley, and soybean meal, which was supplemented with either 0.3 mg/kg of Na2SeO3 and 0.2 mg/kg of Se-methionine (SeI group) or 0.5 mg/kg of Se-methionine (SeII group). During the feeding trial, the following productivity traits were recorded: individual body weight, average daily gain (ADG), and feed conversion ratio (FCR). Muscle and fat characteristics in live pigs were measured using ultrasonic equipment (Piglog 105). After slaughter, samples were taken from the M. longissimus dorsi, between the 12th and last rib, for further analysis of selenium accumulation and chemical composition of the pork. Throughout the entire trial period, the weight, ADG, and FCR of the fattening pigs did not differ significantly between groups. However, the fattening pigs in the SeII group exhibited thicker fat thickness, while the SeI group had thicker muscles (mm) and a higher muscularity (%). When comparing selenium accumulation in the muscles, the SeII group showed higher concentration by 0.799 μg/g dry matter (DM) when organic selenium was used, compared to the SeI group, which used a mixture of organic and inorganic selenium. Analysis of the chemical composition revealed that the SeII group's muscles had higher levels of DM, proteins, and ash, while the SeI group contained more fat. In conclusion, the recent study indicates that while the choice of selenium form significantly affects some meat quality traits and fat thickness in fattening pigs, it does not have a significant impact on overall productivity.

Keywords: Organic Selenium, Inorganic Selenium, Chemical Composition, Growth Performance, Se Accumulation

International Conference on
Food, Agriculture and Animal Sciences
19-22 December 2024, Erzurum, TÜRKİYE

Utilization of 3D Printing Technology to Valorize Food Waste

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ABSTRACT: Global food waste amounts to 2.3 billion tons annually, underscoring the urgent need for advanced recycling technologies. As mass customization grows, 3D printing offers transformative potential in food production by integrating food waste into circular economy models. Direct Ink Writing (DIW) is the leading method in food waste-based 3D printing due to its effectiveness with viscous gels and pastes. Examples include the development of food inks from spinach and kale stems, okara (soybean by-product), and orange peels, showcasing excellent printability and nutritional value. Okara-based cookies have demonstrated enhanced dietary fiber content and superior sensory qualities compared to commercial alternatives. Research has also highlighted orange peel inks' antioxidant properties and their use in creating decorative foods and functional products, with customization enabled by blending with other ingredients. Despite these advancements, challenges remain, particularly regarding safety concerns and consumer acceptance of waste-derived food products. Innovations such as using DIW to create biodegradable food packaging from sugarcane bagasse further illustrate the potential of 3D printing to drive sustainability in food production, paving the way for environmentally friendly solutions in waste management and product development.

Keywords: 3D Printing, Food Waste, Direct in Writing (DIW), Circular Economy, Sustainable Food Production

Functional Analysis of ErLAC12 Reveals that β-glucosidase Plays an Important Role in the Lactose Permease Activity of *Exserohilum rostratum* against L. *chinensis*

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ABSTRACT: Bioherbicidal agents like *E. rostratum*, a soil-borne pathogen, provide a valuable chemical alternative against the noxious weed *L. chinensis*. In this study, a stable *Agrobacterium tumefaciens*-mediated transformation system for *E. rostratum* was developed to verify the role of lactose permease (LAC) in the pathogenic mechanism of *ErLAC12* overexpressing transformants. The pCAMBIA overexpression vectors and localization vectors were constructed for the ATMT of *E. rostratum*. The maximum number of transformants was achieved using a conidial concentration of 10^5, with 200 µM acetosyringone, after 5 days of co-culture at 28 °C and subsequent selection with 50 µg/mL acetosyringone. Successful genomic integration of the T-DNA in *E. rostratum* was confirmed via PCR, sequencing, and fluorescence microscopy. *ErLAC12* overexpressing strains exhibited significant morphological and microscopic variations. The pathogenicity of X050-$\text{OX}_{\textit{ErLAC12}\text{-X050}}$ and Y9511-$\text{OX}_{\textit{ErLAC12}\text{-Y9511}}$, was associated with a 4.5-fold and 3-fold increase in β-glucosidase activity, respectively, and a 4-fold and 2.5-fold increase in cellulase activity compared to the wild-type Y9511 strain. This leads to significant accumulations of malondialdehyde (50.3% and 80.4%) and hydrogen peroxide (24.4% and 40.2%) in *L. chinensis* leaves, resulting in growth inhibition of 79% and 87% at the 4-leaf stage due to cellular damage, thereby underscore the potential for effective weed management.

Keywords: *Agrobacterium tumefaciens*-Mediated Gene Transformation, Enhanced Green Fluorescent Protein (eGFP), Bioherbicidal Activity, CWDE Activity, Oxidative Stress and Cell Cytology

Screening of In Vitro Antidiabetic and Antioxidant Activities of Young Leaves and Flowers of Selected Sri Lankan Medicinal Plants*

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ABSTRACT: Sri Lanka uses medicinal plants for diabetes and oxidative stress. This study investigated the antidiabetic and antioxidant properties of five Sri Lankan plants: young leaves of *Artocarpus heterophyllus*, *Andrographis paniculata*, *Coccinia grandis*, *Ficus racemose* and flowers of *Aloe barbadensis* aiming to provide a natural, affordable alternative to synthetic drugs. Antioxidant assays (TPC, TFC, DPPH, FRAP) and enzyme inhibition assays (alpha-amylase, alpha-glucosidase) were conducted to assess their potential. *Artocarpus heterophyllus* exhibited the highest TPC (54.225±0.754 mg GAE/g) and TFC (18.3402±0.1384 mg QE/g). *Ficus racemose* displayed the highest FRAP value (23.836±1.133 mg TE/g). Jack young leaves showed a lower IC50 value (236.636±0.44 ppm) in the DPPH assay compared to Ivy gourd (337.649±1.456 ppm). Conversely, Ivy gourd displayed the strongest alpha-amylase inhibition (IC50 = 9.145±0.0485 ppm), while Jack leaves exhibited the strongest alpha-glucosidase inhibition (IC50 = 1.49367±0.00379 ppm). *Aloe barbadensis* showed antioxidant activity with TPC, TFC, and FRAP values of 38.119 ± 0.391 mg GAE/g, 11.5822 ± 0.0342 mg QE/g, and 9.118 ± 0.826 mg TE/g, respectively. At 500 ppm the DPPH, alpha-amylase and alpha-glucosidase inhibition values were 15.837± 0.1718%, 40.817± 0.616%, and 34.04± 3.09 %. Further research using in vivo models is required to validate the potential use of these medicinal plants.

Keywords: Antioxidant, Anti-Diabetic, Herbal, Inhibition, Oxidative Stress

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*This study is a part of Jinangi Isurandi Bentharavithana's undergraduate thesis accepted by the Industrial Technology Institute, Sri Lanka and the University of Peradeniya, Sri Lanka.

Comparative Nutritional Analysis of Rabbit Meat from Intensive and Extensive Rearing Systems

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ABSTRACT: The nutritional quality of meat is determined by a variety of factors, including the method of rearing employed, which can have a considerable impact on the morphological, chemical, and sensory aspects of the final product. Intensive and extensive rearing methods are two separate approaches to animal husbandry, with each having ramifications for meat quality, animal welfare, and customer choice. So, this study was designed as a comparative analysis of the rabbit meat nutritional value from intensive and extensive rearing systems, focusing on morphological composition, chemical and physical indicators, as well as sensory and emotional responses of consumers. The research was carried out on industrially chilled carcasses of rabbits from intensive rearing, purchased from a supermarket, and extensively reared California rabbits from a local rabbit farm, representing extensive rearing (n = 10 rabbits per rearing system). Key indicators analysed included the morphological composition of the carcasses, physical and chemical properties of the meat, sensory evaluation by consumers, and associated facial emotional expressions. Results indicated that, with the exception of leg and back muscle yields, all morphological indicators were statistically higher in extensively reared rabbits ($p < 0.05$). However, the analysis of chemical composition, sensory properties, and facial emotional expressions did not reveal any statistically significant differences between the two rearing methods ($p > 0.05$). Moreover, the physical assessment of fresh loin samples demonstrated a significantly higher intensity of yellowness and redness of the rabbits from the extensively reared system compared to those raised intensively ($p < 0.05$). In general, recent study concludes that while extensively reared rabbits exhibited superior morphological indicators and distinct colour characteristics compared to those reared intensively, no significant differences were found in chemical composition, sensory properties, or consumer emotional responses between the two systems.

Keywords: Intensive Rearing, Extensive Rearing, Rabbit Production, Meat Quality, Sensory Analysis

Green Fertilization In Land Cultivation for the Sake of the Green World

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ABSTRACT: Currently, the modern world is faced with problems caused by a number of different natural crises. The Conference of the parties to the 2024 UN Framework Convention on climate change, or COP 29 for short-the UN climate change conferences will be held in Baku on November 11-22, 2024, is of great importance. The goal of the COP 29 - measure is to reduce the amount of carbon dioxide (CO2) in the world by 1,5% by 2050, up to 40 degrees Celsius, as in the pre-industrialization period. Azerbaijan understands the Supreme purpose of the convention, the importance of joint efforts to combat climate change and constantly declares its partnership to the whole world to prevent all human-threatening interventions in the climate system. The Prevention of this secular crisis depends on us. For the sake of the" green world", the rational use of nature and its resources and the preservation of land and vegetation for future generations should be the supreme goal of every person The golden rule of organic farming says - the soil cannot be kept without cover. In order to implement this rule, by applying organic farming, in the 2022-2023 Research year, soybean seeds were sown to obtain green fertilizer or sideration as soon as the grain harvest was completed at the Agstafa subsidiary practice farm of the Research Institute of Agriculture, and the green mass was mixed into the soil during the flowering phase of the plants. In the Research year, the winter durum wheat variety "fertile 95" was studied and it was determined that the plant density was 290-273 units in the control variant, 20 t of black cattle manure was 308-300 units, 5T of bird Zili was 310-302 units, 6T of bird Zili was 340-322 units, and 345-328 units in the soybean variant. The results of the study also show that the best plant density was obtained in the variant green manure-siderate of the soybean plant.

Keywords: Soil, Organic Farming, Legume, Siderate, Green Fertilizer

International Conference on
Food, Agriculture and Animal Sciences
19-22 December 2024, Erzurum, TÜRKİYE

Plant-Based Meat Alternatives: Extraction Methods and Applications in the Food Industry

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ABSTRACT: Plant-based meat alternatives have gained significant attention in the global food industry due to increasing interest in environmental sustainability, mitigating the negative impacts of animal-based food production, and promoting healthy eating. Ethical concerns and the high environmental costs of animal protein production have encouraged broader adoption of plant-based alternatives, with a particularly rapid rise in demand in developed countries. Legumes, oilseeds, and cereals are prominent sources for these alternatives, offering high-quality proteins, balanced amino acid profiles, low fat content, and potential health benefits. Protein extraction is a crucial step in determining the nutritional value and functional properties of plant-based meat products. Traditional extraction methods, such as alkaline extraction, isoelectric precipitation, and enzyme-assisted extraction, remain widely used. However, innovative and eco-friendly techniques like natural deep eutectic solvents and microwave-assisted extraction have emerged, improving protein yield and product quality while reducing energy consumption and environmental impact. These methods help lower the environmental footprint of food production. This study examines the components of plant-based meat alternatives, protein extraction methods, and their applications in the food industry. It also highlights the environmental sustainability advantages of plant-based proteins and their positive health impacts, emphasizing their growing importance in sustainable food production.

Keywords: Meat Alternatives, Protein Extraction, Sustainability, Healthy Diet

Structure and Regulation of Rice Transcription Factors

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ABSTRACT: Transcription factor regulates gene expression in crop plants at the transcription level. Usually, transcription factor contains some domain that helps in regulation activities including the transcription regulatory region, DNA binding region, oligomerization site, and nuclear localization signal region. All domain decides the functional activities of genes such as gene function, characteristics, nuclear localization, and regulation of transcription factors. Transcription factors inhibit or activate the expression of genes through binding functional domain to promoter cis-acting element or their interaction with other proteins. However, Transcription factor function and structure have become crucial roles in plant molecular biology in the upcoming breeding research era.

Keywords: Transcription Factor, DNA Binding Region, Cis-Acting Element

Investigation of the Total Phenolic and Total Flavonoid Contents in Lyophilized Infusion Extracts of the Rosemary (*Salvia rosmarinus* Spenn.)

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ABSTRACT: Rosemary plant (*Salvia rosmarinus* Spenn.) (SR) belongs to Lamiaceae family. Rosemary has rosmarinic acid, flavonoids, some vitamins (A, C, B1, B6, B9), some minerals (magnesium, cupper, calcium, manganese and iron) and some essential oils (cineole, alpha pinene and camphor). It benefits the digestive system; with its anti-inflammatory properties, it is traditionally consumed as a natural remedy for stomach ulcers, indigestion and intestinal disorders. In addition, rosemary has a protective role against some cancer types (breast, liver, ovarian, pancreatic and prostate). The aim of this study was to investigate total phenolic and flavonoid contents in lyophilized rosemary extracts prepared at different concentrations of rosemary (weight/volume); 2.5% (SR-2.5), 5% (SR-5), 10% (SR-10), and 20% (SR-20). Rosemary plant purchased from a local market was cut into small pieces using a blender. Boiling water was added into a flask including plant material. Rosemary infusions were obtained and filtrated. Lyophilization was performed to get powdered extracts. Extract yield was calculated. Total phenolic and total flavonoid contents were determined using an UV-Vis spectrophotometer. The highest extract yield (23.2%) was found in SR-2.5 and yield decreased depending on concentrations. The highest total phenolic content was determined in SR-2.5 group (250 mg gallic acid equivalent/mg extract). Total phenolic contents of the SR-2.5 and SR-5 groups were statistically significant than SR-10 and SR-20. On the other hand, the highest total phenolic content was measured in SR-10 (74.3 mg quercetin equivalent/mg extract) and it was statistically significant than other groups.

Keywords: Yerba mate tea, *Ilex paraguariensis*, Infusion extract, Total phenolics, Total flavonoids

The Influence of Different Cultivation Methods on the Number of *Virginia tobacco* Weeds in Open Ground in the Sheki-Zagatala Economic Region

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ABSTRACT: Tobacco production occupies a special place in Azerbaijan's agriculture. The development of tobacco farming in the republic on scientific basis and the creation of high industrial potential in this field coincided with the 60-70 years of the last century. In those years, fertile conditions were created for the rapid development of tobacco farming in Azerbaijan and the strengthening of the industrial potential of this field. In the 1970s and 1980s, the cultivated area of tobacco was 17,000 hectares, and the volume of production was more than 60,000 tons. Due to its economic importance, tobacco is considered the second technical crop in Azerbaijan after cotton.

The highly profitable tobacco field is cultivated in 21 districts of our Republic, mainly in Sheki-Zagatala region.At the end of the study, it was determined that 122 before the 1st cultivation, 45 before the 2nd cultivation, 45 before the 3rd cultivation in the 90×40 cm nutrient field on the background of $N_{45}P_{120}$+20 tons of manure at the irrigation rate of 70-80-50% units 17 units before the 3 rd cultivation, 70-80-60% irrigation norm, 119 units before the 1st cultivation, 48 units before the 2nd cultivation, 16 units before the 3rd cultivation, 70-70-60% irrigation norm There were 121 weeds before the 1st cultivation, 47 weeds before the 2 nd cultivation, and 16 weeds before the 3 rd cultivation.

Key words: Virginia, Tobacco, Cultivation, Yield, Weeds, Food Area, Irrigation Rate

Chemical Composition of Camel Meat: A Meta-Analysis and Meta-Regression Study

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ABSTRACT: Compared to ruminants, camels are a promising protein resource in arid and semiarid areas. However, the results published in the literature vary according to several factors. This study aimed to evaluate the physicochemical quality of camel meat using a meta-analysis and meta-regression approach. Four search databases and bibliographies were used from January 1991 to August 2024, and the parameters were analyzed using a random-effects meta-analysis model. The live body weight (LBW) of fattened camels averaged 379.79 kg. After slaughtering, the chemical composition was 5.77 for meat pH, 32.52% for dry matter, 70.06% for moisture, 4.75% for intramuscular fat, 20.30% for protein, and 1.39% for ash. Concerning physical quality, the expressed juice, cooking loss, and shear force averaged 36.09%, 34.50%, and 7.75 kg/cm², respectively. Meta-regression and subgroup analysis showed that the moderators employed (species, breeding system, and age), affected some parameters. Indeed, for crossbreeds, there was a significant decrease in LBW and an increase in protein, ash, fat, and cooking loss. Camels subjected to the extensive system were characterized by higher LBW, but lower fat, expressed juice, and lightness (*L**). Concerning the age of camels, animals aged > 6 years were characterized by high FBW, ash, fat, low *L**, and expressed juice. Future studies should consider these results and continue to evaluate these factors in detail to determine production practices and to improve the quality of camel meat on a global scale.

Keywords: Camel Meat, Physicochemical, Meta-Analysis, Subgroup

Molecular Insights into Begomovirus Infections in Tunnel-Grown Peppers

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ABSTRACT Begomoviruses pose a serious threat to pepper (*Capsicum* spp.) production, especially in tunnel farming systems where the microclimate creates an ideal setting for the virus's growth and its vector, the whitefly (*Bemisia tabaci*). Although tunnel farming can increase yields and lengthen growing seasons, it also unintentionally fosters an environment that is more vulnerable to disease. Increased virus transmission results from warm temperatures, high humidity, and restricted air circulation inside tunnels, which speed up vector movement and reproduction. The purpose of this study was to discover and describe the begomoviruses that infect peppers that are grown in tunnels. The presence of begomoviruses was verified by polymerase chain reaction (PCR) analysis using degenerate primers that target conserved sections of the viral genome. Infected samples produced a diagnostic 550bp amplicon. The extensive occurrence of begomoviruses in peppers cultivated in tunnels is supported by molecular evidence, which implies that the conditions there increase the frequency and intensity of disease. In order to lessen the impact of viruses in tunnel farming, the results highlight the urgent need for integrated disease management techniques, which include vector control, resistant cultivars, and optimum cultural practices. Vector population management may be aided by the implementation of sustainable techniques like biological controls and the sparing application of pesticides. It is essential to comprehend how disease epidemiology, vector dynamics, and tunnel microclimates interact in order to protect pepper production in protected growing systems.

Keywords: Disease Management, Geminiviruses, Microclimate Effects, Virus Prevalence, Whitefly Vector

Impact of Maturity Stage at Harvesting Point on Physicochemical Quality of Ceylon Black Pepper, *Piper nigrum*

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ABSTRACT: Ceylon black pepper, *Piper nigrum* contains a range of bioactive compounds with antioxidant and antimicrobial properties, making it a valuable spice in both culinary and medicinal applications. The aim of the study was to identify the impact of harvesting maturity stage on physicochemical quality of pepper cones to ensure better quality product. Moisture content, essential oil content, bio active composition, oleoresins percentage and piperine yield of matured berry and medium berry dried black pepper were qualitatively and quantitively analyzed to comparatively assess the changes with maturity. Moisture content was measured using Dean and Stark method. Hydro distillation was used to extract pepper essential oil from each sample and their bio active profiles were analyzed through GC-MS analysis. Oleoresin from each mature berry and medium berry sample was extracted using Soxhlet extraction with 99.99% acetone and the piperine percentage of each oleoresin sample was analyzed with HPLC analysis. The values of moisture content are 11.1±0.11% and 10.6±0.13% respectively for medium and mature black berry. The highest essential oil content (3.3±0.07%) was recorded from medium berry dried black pepper sample and the lowest (2.2±0.07%) was recorded from the matured berry dried black pepper sample. As important bio active compounds β-caryophellene, D-Limonene, α-myrcene and copaene were detected from both essential oil samples. The highest oleoresins percentage (10.7215±0.0237%) and piperine content (8.6936±0.0120%) was detected from medium berry dried black pepper sample and the lowest oleoresins percentage (9.6850±0.0318%) and piperine content (7.4154±0.0236%) was recorded from the matured berry dried black pepper sample confirming that there is a direct impact of maturity stage at harvesting time on quality.

Keywords: Essential Oil, Oleoresins, Piperine, Maturity, Mature Berry, Medium Berry

First Record of *Fusarim equiseti* and *Fusarium solani* as Pathogens of Lettuce (*Lactuca sativa* L.) in Türkiye

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ABSTRACT: In order to determine the fungal diseases in the growing areas of Ankara province, which is an important lettuce producer, surveys were carried out in July and August 2022 and a total of 66 isolates were obtained from diseased leaf and root tissues. Three of these isolates were identified as Fusarium equiseti and four of these isolates were identified as Fusarium solani based on their morphological and cultural characteristics. The identification of Fusarium equiseti isolates was also confirmed by molecular methods. The TEF-1α (translation elongation factor 1-alpha) gene region of the isolates was sequenced using primers EF1 (ATGGGTAAGGAGGACAAGAC) and EF2 (GGAAGTACCAGTGATCATGTT). The isolates were then submitted to GenBank and confirmed as F. equiseti (accession numbers: PQ463291, PQ463292, PQ463293) and showed %100 similarity to the sequences of F. equiseti (KM025421), (MT158484), (MK361175) in GenBank. The pathogenicity tests of the isolates belonging to both species were carried out as seed hypocotyl test; while the disease severity of one of the F. equiseti isolates was lower than the other two isolates (%22.6), the disease severity values caused by the other two isolates were determined to be %62.5 and %86.0. The virulence of the F. solani isolates varied between %28.3 and %90. The pathogenicity of F. equiseti isolates was also confirmed by plant tests on susceptible lettuce cultivars at the 4-5 leaf stage. For this purpose, seedlings were inoculated with spore suspensions of F. equiseti isolates at a concentration of 1 x10^6 conidia/ml and kept in an acclimation chamber at an average temperature of 23±2°C. Koch's postulates were fulfilled by reisolating the leaves of symptomatic lettuce plants 10-14 days after inoculation from the typical small, circular, grey-brown spots on the leaves of symptomatic lettuce plants and from the parts where these spots had developed into necrotic lesions and from the leaves of lettuce plants kept as control plants without any symptoms. Fusarium equiseti and Fusarium solani were found to be pathogens of lettuce in Turkey for the first time in this study and these data are the first records for our country.

Key words: Lettuce, *Lactuca sativa, Fusarium equiseti, Fusarium solani*

A Holistic Approach to Cinnamon Extraction: Optimizing Extraction Processes, Profiling Compounds, and Assessing Antioxidant Activity of Essential Oil and Oleoresin Extraction from Ceylon Cinnamon Bark*

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ABSTRACT: Ceylon cinnamon, renowned for its flavor and health benefits, is a valuable commodity. This study aimed to optimize extraction methods for essential oil and oleoresin from various cinnamon grades defined by the Department of Cinnamon Development, Sri Lanka. Cinnamon offcuts, a byproduct of the grading process, emerged as the most economically viable grade for large-scale processing due to their high sieved percentage (95.39±0.29%) and essential oil yield (1.38±0.01 ml/g) at 100°C and 4h extraction. While H2, H3, and Special grades had higher oil contents, offcuts offered the lowest raw material cost. Chemical analysis revealed variations in key components, mainly H3 had the highest cinnamaldehyde (72.31±0.30%) and eugenol (5.27±0.02%), offcuts had the highest linalool (2.63±0.002%), and C4, C5, and M4 had the highest safrole (0.61-0.62%). Special grade had the highest cinnamyl acetate (3.37±0.02%). Offcuts also demonstrated the highest DPPH radical scavenging activity (3.53±0.01 TE mg/g) compared to H3 and other grades. This study underscores the potential of cinnamon offcuts for sustainable and cost-effective essential oil production, promoting the availability of this valuable spice.

Keywords: Cinnamon, Oleoresin, Yield, Antioxidant, Extraction

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*This study is a part of Madhawa J.K.R.’s undergraduate thesis accepted by the Stay Natural Pvt Ltd Matale, Sri Lanka and the University of Peradeniya, Sri Lanka

International Conference on
Food, Agriculture and Animal Sciences
19-22 December 2024, Erzurum, TÜRKİYE

Assessment of Wheat Production Systems in the Moscow Region: Evaluating Essential Economic Parameters of Spring Wheat Varieties

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ABSTRACT: The global wheat demand is projected to increase by 60% by 2050, highlighting the need for advanced production systems. This study evaluated the economic performance of spring wheat production systems and three varieties (Agros, Belyana, and Radmira) in a field experiment conducted in 2022 and 2023. The study used a split block design with three replications to compare low, moderate, and high production systems. Results showed that production systems and varieties significantly ($p < 0.05$) influenced grain yields, partial factor productivity (PFP) of potassium and phosphorus, and agronomic efficiencies. Agronomic efficiencies increased with improved production systems, with basic and intensive cultivation technologies exhibiting the lowest and highest results. Low production systems yielded 3.6 t/ha, while high production systems reached 4.9 tha-1. Belyana achieved the highest yield (4.6 t ha-1) under high production, followed by Radmira (4.5 t-ha-1). The economic analysis highlighted the substantial benefits of improved systems. Belyana recorded the highest gross income (40952.3 Rub.ha-1) and grain yield value (60060.0 Rub. ha-1), while Radmira achieved the highest marginal returns (0.624), net return (14985.0 Rub.ha-1), and variable cost ratio (1.61). The study concluded that high-production systems maximize yield and profitability, particularly for Belyana and Radmira, making them viable options to meet rising wheat demand.

Keywords: Wheat, Production Systems, Net Returns, Variety, Partial Factor Productivity, Agronomic Efficiency

Eco-friendly Remediation of Pollutant Load from Wastewater Using *Dracaena sandriana* and *Bacillus atrophaeus* (B16)

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ABSTRACT: Wastewater, if discharged untreated into the environment, can cause significant pollution. This study aims to assess the levels of nitrate, nitrite, and ammonium pollution in Oued K'sob (Bordj Bou Arreridj region, Algeria) over the course of one year, measuring concentrations at five locations spaced 2 km apart. Additionally, it proposes the use of *Dracaena sandriana* as a potential solution for removing the total pollutant load from wastewater over a 40-day contact period. The results indicate dangerously high ammonium levels, well above the FAO standard of 6.5 mg/L, while nitrate and nitrite levels remain low. Phytoremediation using *Dracaena sandriana* leads to a significant reduction in total nitrogen, achieving a maximum removal rate of 66.5%, compared to an unplanted control tank. Furthermore, the ability of *Bacillus atrophaeus* (B16) to remove zinc and copper was evaluated using the murexide-Zn/Cu reduction assay, where the color intensity of the murexide-ion complex was measured spectrophotometrically. The B16 strain showed exceptional uptake, with a maximum removal of 93% for ZnCl2 at 25 µl of bacterial suspension and 91% for CuSO4 at 100 µl, outperforming the EDTA standard.

KEYWORDS: *Dracaena sandriana*, *Bacillus atrophaeus*, Water Pollution, Bioremediation, Phytoremediation, Nitrogen Pollution.

Recovery of Organic Waste for Degraded Soils Rehabilitation and Agricultural Product Quality Improvement

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ABSTRACT: Nowadays, anthropogenic activities and high human consumption cause serious problems such as pollution, and household and industrial waste management difficulties. In addition, intensive agriculture using chemical fertilizers and phytosanitary products cause soil depletion. Composting has become an essential solution for recycling household, agricultural and food industry waste. While compost production may initially appear straightforward, the quality of the resulting compost and its suitability as a soil fertilizer are determined by several factors, including the composition of the materials to be composted, the chosen composting method, rhizospheric activity, and the specific composting conditions employed.In this work, we propose a comparison between different compositions and different methods of composting and soil fertilization and industrial interest plantgrowth improvement in a compost-soil mixture.

Keywords: Compost, Soilfertilization, İntensive Agriculture, Waste Management

Spondylarthrite, Symptoms, Mechanism of Action and Treatment

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ABSTRACT: Spondylarthritis is classified as a chronic inflammatory rheumatic disorder that primarily affects the axial skeleton, especially the sacroiliac joints and the spine. Characteristic symptoms include inflammatory back pain, stiffness, and limited spinal mobility, frequently associated with peripheral arthritis, enthesitis, and extra-articular manifestations such as uveitis and psoriasis, this disease can also cause rheumatic disorders, Axial involvement or pelvic-spinal syndrome, pelvic and spinal symptoms are characterized by axial enthesopathy affecting the pelvis, the spine and the chest wall. This pain reflects inflammation of the sacroiliac joint and may radiate to the posterior aspect of the thigh as far as the knee. The pathophysiology of the disease is influenced by a multifaceted interaction of genetic, immunological, and environmental elements, with the HLA-B27 antigen being a key factor. This antigen provokes an abnormal immune response, which leads to inflammation, bone erosion, and the development of new bone. Standard treatment approaches typically involve the use of non-steroidal anti-inflammatory drugs (NSAIDs), disease-modifying antirheumatic drugs (DMARDs), and biologic agents that target specific inflammatory pathways, such as TNF inhibitors. Furthermore, physical therapy and exercise are essential components in managing symptoms and improving the quality of life for affected individuals.

Keywords: Spondylarthritis, Inflammatory, HLA-B27, Anti-inflammatory

Exploring the Impact of Water Stress and PGPR Inoculation on Morphological, Physiological, and Biochemical Parameters in Tomato Plants

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ABSTRACT: This study investigates the effects of varying water stress levels, from mild to severe, on the growth and physiology of tomato plants (Campbell 33 variety), alongside the influence of soil inoculation with Plant Growth-Promoting Rhizobacteria (PGPR). Three bacterial strains *Bacillus amyloliquefaciens* (SF14), *Alcaligenes faecalis* (ACBC1), and *Bacillus aryabhattai* (B11)—were tested for their potential to mitigate stress impacts. Morphological, physiological, and biochemical parameters, including root growth, stem diameter, leaf and flower count, water content, biomass (fresh and dry weights), chlorophyll, anthocyanin, and flavonoid levels, were measured. Severe water stress significantly reduced plant growth and physiological performance. However, PGPR inoculation improved most parameters, highlighting its potential to enhance plant resilience. Interestingly, under severe stress, bacterial inoculation was associated with reduced anthocyanin levels, suggesting complex interactions between bacterial activity and plant stress responses. These findings contribute to understanding the role of PGPR in sustainable agriculture by elucidating the interplay between soil microbiomes, environmental stressors, and plant physiology.

Keywords: Flavonoids, Biochemical Parameters, Inoculation, Bacterial Strains, Anthocyanins, Flavonoids, Biochemical Parameters

Advancing Sustainable Strategies and Research Priorities for Mosquito-Borne Disease Control

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ABSTRACT: Mosquitoes have long been recognized as vectors of complex and devastating diseases. However, the widespread use of chemical insecticides has driven the evolution of resistance in both mosquitoes and the pathogens they transmit, posing significant challenges to control efforts. This review synthesizes current research on mosquitoes, mosquito-borne diseases, and associated management strategies, highlighting critical knowledge gaps and priority areas for future investigation. To promote sustainable and effective control measures, we emphasize the importance of natural and integrated management approaches. Key research priorities include understanding the effects of climate change on vector dynamics, addressing insecticide resistance, and advancing innovative genetic strategies such as RNA interference (RNAi), the Sterile Insect Technique (SIT), and biocontrol methods utilizing plants and other natural products. Additionally, we advocate for the development of a global, long-term monitoring framework that leverages advanced technologies to enhance surveillance and management capabilities. This holistic approach aims to guide research and implementation efforts, fostering a sustainable and globally coordinated framework for the control of mosquito-borne diseases.

Keywords: Mosquitos**,** Sustainable Management, Implementation, Technologies

Studying The Impact of Water Supply on Productivity and Yield Components in Wheat Plants

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In the article, the effect of drought on productivity and structural elements of the crop was studied in wheat varieties that differ in terms of spike duration (early, medium and late spike) in different irrigation regimes. The morphophysiological characteristics of the genotypes studied in different irrigation regimes were different. Depending on the variant, the difference between them was observed more in the late- maturing varieties, and the least in the group of early- maturing varieties. The studied yield elements of wheat plant also depend on water supply as well as the biological characteristics of the variety. İn these indicators the difference between the variants is higher in late maturity.

Depending on the water supply, the yield was higher in early-stemming varieties in the initial drought variant compared to the control (drought), and in the complete drought variant compared to the irrigation variant, the difference was sharper, and it was higher in late-stemming varieties. The difference between yield elements was higher in late-stemming varieties compared to drought in the initial irrigation variant.

As a result of the study, it is recommended to select genotypes with less depressed morphophysiological traits in the creation of new productive varieties for drought-prone regions and use them as initial material in the hybridization.

Keywords: Wheat, Plant, Breeding, Drought, Productivity

In Vitro Antioxidant Activities of Methanolic and Aqueous Extracts of Nettle

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ABSTRACT: This study explored the *in vitro* antioxidant properties of methanol and aqueous extracts derived from nettle leaves, a plant renowned for its medicinal and pharmacological uses. The research aimed to evaluate the radical scavenging activities of these extracts and determine their total phenolic and flavonoid contents. The results indicated that both extracts exhibited antioxidant activity, as assessed by the 1,1′-diphenyl-2-picryl-hydrazil (DPPH) assay at a concentration of 1 mg/mL. The methanol extract demonstrated a significantly higher percentage of inhibition (95.91%) compared to the aqueous extract (56.86%). Furthermore, the methanol extract outperformed the aqueous extract in ferrous ion chelating activity, with percentage inhibitions of 70.68% and 56.79%, respectively. Analysis of the total phenolic content revealed that the methanol extract contained a substantially higher amount (60.861 ± 1.111 µg GAE/mgE) than the aqueous extract (42.972 ± 1.667 µg GAE/mgE). Similarly, the methanol extract showed a greater flavonoid content (3.01 ± 0.17 µg R/mgE) in comparison to the aqueous extract (1.2 ± 0.05 µg R/mgE). These findings underscore the superior antioxidant potential of the methanol extract, suggesting its valuable pharmacological applications.

Keywords: Nettle, Antioxidant, Medicinal Plant, Phenolic, Flavoniod

Amino acid profile of shrimp species; *Penaeus kerathurus, Penaeus semisulcatus, Parapenaeus longirostris,* and *Aristaeomorpha foliacea*

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ABSTRACT: Shrimp is a highly nutritious seafood, containing a well-balanced essential amino acid profile. The determination and comparison of the amino acid profile of four shrimp species *(Penaeus kerathurus, Penaeus semisulcatus, Parapenaeus longirostris, and Aristaeomorpha foliacea)* in the Northeastern Mediterranean were revealed. The highest total essential (EAA) and non-essential (nEAA) amino acid content was observed in *Parapenaeus longirostris.* Arginine (1.23-1.77g/100g), lysine (1.40-1.89g/100g), and leucine (1.36-1.79 g/100g) were identified as the most abundant EAAs across shrimp species. Furthermore, glutamic acid (3.03-3.44g/100g) and aspartic acid (1.54-2.03g/100g) were also found major nEAAs. It was determined that the mass fractions of EAA and nEAA in all shrimp species were within the recommended ranges. The branched-chain amino acids (BCAAs) values of the *Penaeus kerathurus*, *Penaeus semisulcatus*, *Parapenaeus longirostris*, and *Aristaeomorpha foliacea* were found to be 3, 3.29, 3.65, and 2.57g/100g respectively. The cholesterolemic index (CI) values of *Parapenaeus longirostris* (0.94g/100g) and *Aristaeomorpha foliacea* (1.01g/100g) species were higher than those of the species. The data indicated that all shrimp samples contained amino acids, with levels that align with the recommended daily intake values in terms of an adequate and balanced diet. Moreover, the mass fractions and BCAA results demonstrated that *Parapenaeus longirostris* exhibited the most well-balanced amino acids for health, in comparison to other shrimp species.

Keywords: Amino Acid Profile, Cholesterolemic Index, Shrimp

Antidiabetic effect of several varieties of cheese

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ABSTRACT: Cheese is a highly nutritious fermented milk product with diverse flavor and texture. As a functional food it has gained a lot of attention in recent times because of their health benefitting properties. In the present study, four varieties of cheese (Gouda, Gruyere, Edam and Emmental) are tested for their antidiabetic effect. In fact, an aqueous extract is prepared by maceration of cheese pieces in phosphate buffer. Inhibitory effect against α-amylase of extract, pH and proteins content are investigated. Results show pH value between 5.2 and 5.9 with protein content between 4.5 and 9.14%. Inhibitory effect against α-amylase is moderate with IC50 values of 49.29±4.02, 38.5±6.05, 70.66±12.52 and 25.9±6.82 mg.mL-1 for Goud, Gruyere, Edam and Emmental respectively.

In fact, we can conclude that Emmental cheese has the best inhibitory effect on porcine pancreatic α-amylase compared to Gouda, Gruyere and Edam cheeses. Investigation of active ingredient in cheese especially in Emmental may be interesting.

Keywords: Cheese, Emmental, α-amylase Inhibition, Diabetes Mellitus

Clinical Investigation of Mastitis in Camels (Camelus dromedarius) in the Oued Souf Province, Algeria

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ABSTRACT: This study investigated the types and incidence of mastitis in 240 camels from nine herds in Southeastern Algeria over three seasons (autumn, winter, and spring) between October 2023 and May 2024. Data were gathered using a questionnaire addressing factors such as season, age, lactation stage, calving number, anti-suckling device use, and udder lesions. Clinical mastitis prevalence was 8.75%, with chronic mastitis being more common (6.25%) than acute mastitis (2.5%).The study revealed that 71.42% of mastitis cases were linked to the use of anti-suckling devices, while 28.53% occurred without their use. Tick infestation and anti-suckling devices showed a significant association ($p < 0.05$) with mastitis prevalence. Mastitis prevalence varied across lactation stages, being highest during the initial stage (20%), followed by the middle stage (5.45%) and the late stage (4.16%). Pathological lesions included chronic mastitis in 71.42% of cases and acute mastitis in 28.57%.The findings highlight the influence of anti-suckling devices, lactation stages, and other risk factors on mastitis in camels, emphasizing the need for targeted preventive measures and management practices to mitigate the condition in this region.

Keywords: Acute Mastitis, Camel, Chronic Mastitis, Clinical Study, Udder

Clinical Investigation of Mastitis in Dromedary Camels (*Camelus dromedarius*) in Oued Souf Province, Algeria

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ABSTRACT: This study assessed the incidence and types of mastitis in camels in Southeastern Algeria. Data were collected from nine herds in the Beni Guecha area, covering 240 camels over three seasons (autumn, winter, spring) from October 2023 to May 2024. Factors such as season, age, lactation stage, calving number, use of anti-suckling devices, and udder lesions were considered. The overall prevalence of clinical mastitis was 8.75%, with chronic mastitis (6.25%) being more common than acute mastitis (2.5%). Notably, 71.42% of mastitis cases involved the use of anti-suckling devices, while 28.57% did not. Tick infestation and the use of anti-suckling devices were significantly associated ($p < 0.05$) with mastitis prevalence. The highest mastitis prevalence occurred during the initial lactation stage (20%), followed by the middle (5.45%) and late stages (4.16%). Pathological lesions observed included chronic mastitis in 71.42% of affected udders and acute mastitis in 28.57%. These findings highlight the importance of managing risk factors, such as anti-suckling devices and tick infestations, to reduce the incidence of mastitis in camels.

Keywords: Acute mastitis, Camel, Chronic mastitis, Clinical study, Udder

Prevalence and Risk Factors of Camel Mastitis in Oued Souf Province, Southeastern Algeria

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ABSTRACT: A cross-sectional study conducted between November 2023 and April 2024 in the Oued Souf province reported a mastitis prevalence of 31.10% in lactating camels, with 3.88% clinical cases and 27.22% subclinical cases. Among 670 teats examined, the right hind quarter showed the highest infection rate (15.47%), followed by the left hind quarter (11.97%), right front quarter (9.58%), and left front quarter (8.38%). The highest prevalence (5.41%) occurred during early lactation. Hygiene practices were notably poor, with 93.33% of owners not washing udders or teats before milking, 90% not washing hands, and none using disinfectants. Additionally, 10% of owners milked infected camels first, 43.33% milked them last, and 46.66% had no specific milking order. Isolated bacteria included Staphylococcus spp and Streptococcus spp. Factors like parity, lactation stage, age, and tick infestation contributed to mastitis. Antibiotic susceptibility testing revealed 37.97% of isolates were susceptible to all tested drugs, while resistance was highest for tetracycline (27.14%), oxacillin (24.28%), and streptomycin (22.85%). The study underscored the significant role of poor milking hygiene in exacerbating mastitis prevalence ($P < 0.05$), emphasizing the need for improved management practices.

Keywords: Clinical Mastitis, Lactating Camel, Quarter Level, Subclinical Mastitis

In Vitro Antioxidant Potential of Methanolic and Aqueous Extracts from a Plant of the Genus Atriplex

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ABSTRACT: This study investigated the in vitro antioxidant activities of the methanolic and aqueous extracts of the leaves of a Xero-halophyte species belonging to the *Chenopodiaceae* family, with a particular focus on the Atriplex genus. This plant is widely distributed in both non-saline and saline areas, ranging from subhumid to arid regions of Southern Europe, the Eastern Mediterranean, and North Africa, including the Sahara in Algeria. The objectives of the research were to assess the radical scavenging activity of the extracts and determine the total phenolic and flavonoid contents. The results revealed that both methanol and aqueous extracts exhibited radical scavenging activity, as evidenced by the reducing power assay at a concentration of 1 mg/mL. The methanol extract exhibited a percentage inhibition of 68.47%, whereas the aqueous extract exhibited no significant effect. Additionally, the methanol extract demonstrated superior hydroxyl radical scavenging, with a percentage inhibition of 66.24%, compared to 55.79% for the aqueous extract at the same concentration. The methanol extract showed a total phenolic content (40,749 ± 1,375 µgGAE/mg) and a total flavonoid content (16,462 ± 0,649 µgQE/mg), the aqueous extract showed a total phenolic content (15,83 ± 1,632 µgGAE/mg) and a total flavonoid content (8,149 ± 0,144 µgQE/mg).

Keywords: Chenopodiaceae, Atriplex, Total Phenolic, Flavonoids, Reducing power, Hydroxyl radical scavenging

Chemistry, Anti-Inflammatory and Anti-Ulcer Activities of *Anastatica* Hierochuntica hydromethanolic Extract

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ABSTRACT: Plants have phenolic compounds with important biological activities. This work aims to examine the phytochemical, anti-inflammatory and anti-ulcer activities of *Anastatica Hierochuntica* (AH). Total polyphenol contents were determined using Folin-Ciocalteu's reagent. Total flavonoid contents were estimated using aluminum chloride. Anti-inflammatory activity was measured using carrageenan-induced rat paw edema assay. The anti-ulcer activity was evaluated using ethanol-induced gastric ulcer model in rats. The results showed that the hydromethanolic extract of AH (AHHME) contained good total polyphenol content (501.351±5.63 ug gallic acid equivalents/mg of dry weight). As well AHHME contained strong flavonoid contents (378.51±5.51 ug quercetin equivalent/ mg dry weight). The results revealed that AHHME (400 mg/kg) exhibited a significant anti-inflammatory activity (93%). Also, the AHHME extract (400 mg/kg) dose showed a good anti-ulcer effect (92%). These results indicate that *Anastatica Hierochuntica* has a potent anti-ulcer and anti-inflammatory effects and may use in the treatment of gastric ulcer and inflammation as an alternative to synthetic drugs with unwanted side effects.

Keywords: *Anastatica Hierochuntica*, Polyphenols, Flavonoids, Anti-Ulcer Effect, Anti-Inflammatory Activity

Comparative and Correlational Evaluation of The Phytochemical and Anti-Ulcer Activity of *Atriplex Halimus* Aqueux and Methanolic Extracts

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ABSTRACT: Phytochemicals are important compounds found in medicinal plants that are active and exert beneficial effects on health or in amelioration of diseases. According to a report by the World Health Organization, 80 % of the population in developing countries depend on traditional medicine for their primary health care, and 85 % of traditional medicine is derived from plant extracts. Several studies reported a significant correlation between the biological activity of herbs and the phytochemical content. Phenolic substances are considered to be the most bioactive phytochemicals present in medicinal plants. The objective of this study is to evaluate and compare total polyphenols and flavonoids contents and anti-ulcer activity of aqueux extracts (AHAE) and methanolic (AHME) from aerial part of *Atriplex halimus*. The anti-ulcer activity was evaluated using ethanol-induced gastric ulcer model in rats. Indeed, results showed that AHAE (2mg/ml) is rich in polyphenols (555.31±9.68 ug gallic acid equivalents/mg of dry weight) and flavonoids (209.87±8.58 ug quercetin equivalent/ mg dry weight), in comparison with ASME (336.34±9.60 ug gallic acid equivalents/mg of dry weight) and flavonoids (158.72±6.87 ug quercetin equivalent/ mg dry weight). Also, the AHAE extract (400 mg/kg) dose showed a better anti-ulcer effect with a significant reduction in ulcer (90%) compared to ASME (72%, $P \leq 0.001$). AHAE exhibited a better reduction of ulcer gastric than the positive control; ranitidine (81% ; $P \leq 0.05$). The results showed a good correlation entre the gastro-protective activity and phenolic contents from *Atriplex halimus* extracts. This gastro-protective activity could be attributed to phenolic contents. These results indicate that *Atriplex halimus* may use in the treatment of gastric ulcer as an alternative to synthetic drugs with unwanted side effects.

Keywords: Polyphenol, Flavonoids, *Atriplex halimus*, Ethanol-Induced Gastric Ulcer, *in vivo* Anti-Ulcer Activity

Phytochemical Characterization and Antioxidant and Anti-Inflammatory Activity of *Prunus persica* L, Leaves from the Tlemcen Region, Algeria

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ABSTRACT: Today, medicinal plants represent an essential source for the discovery of new therapeutic molecules, highly effective against many diseases. This study is part of a project to evaluate the antioxidant activity of the leaves of the peach tree *Prunus persica* L, which belongs to the Rosaceae family. This tree is widely used in traditional Algerian medicine for its numerous therapeutic virtues. The aim of this study was to determine the phenolic compounds and evaluate the antioxidant activity of *Prunus persica* L peach leaf extract, The leaves were extracted by maceration in hexane. Total polyphenol content was determined using the Folin-Ciocalteu reagent, Flavonoids were evaluated using the Aluminium trichloride (AlCl3) method, Tannins were evaluated using the vanillin method, Antioxidant activity was determined, in vitro, using the DPPH free radical scavenging method, Anti-inflammatory activity was evaluated using the method described by Gambhire et al. The extract yield was 16.90%. Total polyphenol content was 26.15 ± 0.60 mg GAE/g MS. Flavonoid content was 40.38 ± 0.20 mg CE/g DM. Tannin content was 8.36 ± 0.24 mg CE/g MS. The result of the antioxidant activity IC50 is equal to 1.96 mg/ml, and the percentage of inhibition of protein denaturation is equal to 60%. This study confirmed that *Prunus persica* L. leaves have significant antioxidant and anti-inflammatory properties.

Keywords: *Prunus persica* L, Phenolic Compounds, Antioxidant Activity, Anti-Inflammatory Activity

Agronomic Characteristics of Acclimatized In Vitro Plants of Two Potato Varieties (*Spunta* and *Désirée*) Developed on a Saline Environment

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ABSTRACT: The objective of this project is to evaluate the effect of saline stress on G0 seedlings of two varieties (*Spunta* and Désirée) of potato (Solanum tuberosum, L.), grown on a saline medium. The in vitro plants of the two varieties studied were developed in MS medium (C0) and another MS medium modified with different concentrations of Na Cl (0.1g/l- 0.15g/l- 0.20g/l), for 35 days of micropropagation and 21 days of acclimatization in greenhouse until harvest with ten repetitions, following agronomic characters concerning the number and weight of mini-tubers produced per size. The results obtained depend on the intra-varietal response and the concentration for the first parameter, where *Spunta* and *Désirée* produce almost the same number of tubers (295 vs 287) without being influenced by the environment, while recording a non-significant effect. While the weight and size of the tubers depend on the variety only, where *Désirée* shows a significant effect compared to *Spunta*. It appears that the presence of Na Cl in low concentrations has no significant influence on the different characteristics of the vitro plants studied. The *Désirée* variety seems more tolerant to saline environments.

Key words: Potato, Salt Stress, Agronomic Characteristics, Mini-Tubers

Water Treatment: Effect of *Opuntia ficus indica* Mucilage on the Removal of Suspended Particles, Copper, and *Saccharomyces cerevisiae.*

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ABSTRACT: Prickly pear (*Opuntia ficus indica*; OFI) is a plant native to Mexico, known for its many benefits for human health, its agro-food applications, and for its growing interest in wastewater treatment processes. Our objective is to valorize the OFI cladodes mucilage in order to improve the efficiency of a water treatment process: electrocoagulation-electroflotation (EC-EF), for the removal of silica gel, copper and *Saccharomyces cerevisiae* yeast cells. The mucilage of the cladodes was extracted by ultrasound-assisted extraction and by microwave-assisted extraction, for silica gel and copper and yeast, respectively. The addition of 10 mg of mucilage to the EC-EF process improved the turbidity removal efficiency of silica gel by 30 % compared to the mucilage-free process. For copper removal, the results showed that the copper removal efficiency reached 100 % in less than 5 min with 30 mg/L mucilage at pH 7.8. It was also observed that 10 mg of mucilage allowed the removal of yeast after 10 min of treatment with a final cell concentration of 4.88×10^6 compared to 5.51×10^7 using mucilage-free process. These results promote sustainable development and encourage the use of mucilage as a natural flocculant to substitute EC-EF chemicals and to enhance its efficiency.

Keywords: *Opuntia ficus indica*, Cladode, Mucilage, Electrocoagulation-Electroflotation

Application of Plant Growth-Promoting Rhizobacteria to Promote Durum Wheat Growth through Stimulation of Beneficial Rhizobacterial Community

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ABSTRACT: Plant growth promoting rhizobacteria (PGPR) plays an important role in agricultural systems, especially as biofertilizer. However, there are still concerns and limited data on their effects on endemic rhizosphere communities, which can significantly influence plant health, yield quantity, and quality. Therefore, this study demonstrate the effects of two PGPR, Pantoea agglomerans strain Pa and Bacillus thuringiensis strain B25 on the plant growth of two durum wheat varieties, Bousselam and Boutaleb; Additionally, it investigated their influence on the frequency of the cultivable beneficial indigenous bacterial communities in the rhizosphere. The bacterial strains were applied as seed primers (individually or in consortia) by coating them with carboxymethyl cellulose (CMC 1%). The different inoculation treatments in natural soil (after 114 days) significantly improved all morphological parameters in both wheat varieties. Bacterial densities of the rhizosphere cultivable communities did not differ significantly. However, the number of cultivable beneficial bacteria isolated from rhizosphere with multiple PGP traits was significantly increased. These results demonstrate that the modulation of the rhizomicrobiome for the plant's benefit may be another mechanism, through which, PGPR enhance plant growth. We might think more about the bio-inoculants as biotechnological tools to recuperate degraded agricultural soils, or only to keep them fertile.

Keywords: PGPR, Durum Wheat, Rhizobacterial Community, Biofertilizers, Sustainable Agriculture

Study of the Antioxidant, Anti-Inflammatory and Antimicrobial and Activity Extract of the Aerial Parts of *Inula viscosa* L.

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ABSRACT: The genus *Inula* has been used in traditional medicine because of its antiphlogistic, antiseptic, diuretic, and anti-inflammatory qualities. The aim of the present research is to investigate the methanolic exract of the aerial parts *Inula viscosa* L. from Algeria and assess its in vitro antioxidant, anti-inflammatory and antimicrobial properties. The antioxidant activity was evaluated with DPPH and β-carotene tests, and the anti-inflammatory activity with inhibition of HRBC membrane stabilization methods. The results showed that *Inula viscosa* extract is rich in phenolic compounds with a total phenol and flavonoid contents of 41.63 ±0.394 mg GAE/gE and 13.97 ±0.33 mg EQ/gE, respectively. In the DPPH assay methanolic extract showed the higher scavenging capacity (IC_{50} = 0. 35 ± 0.01 mg/ml). In the test of β-carotene /linoleic acid, the percentage of inhibition was 67.954 ± 1.64% of methanolic extract. For the anti-inflammatory activity, the highest tested concentration (100 µg/mL) gave 56.61% of membrane stabilization. With regards to antimicrobial results, *Staphylococcus aureus* was the most sensitive bacteria with an inhibition.

Keywords: *Inula viscosa*, Anttioxidant Activity, Anti-Inflammatory Activity, Antimicrobial Activity.

A New Danger is at the Door for Türkiye Honey Bee (*Apis mellifera*) Breeding: *Tropilaelaps mercedesae*

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ABSTRACT: Honeybees (*Apis mellifera*), which are indispensable creatures for human life due to the bee products they produce and the pollination they perform, are under the threat of many damaging factors. *Tropilaelaps mercedesae* is increasingly becoming a focus of global concern due to its severe impacts on western honeybee colonies (*Apis mellifera*) and its recent geographic spread. *Tropilaelaps mercedesae* was recently detected in honey bee colonies in Georgia, a neighbouring country of Türkiye. While no effective control method has been developed for *Varroa desructor*, the most important honey bee parasitic pest in Türkiye, the presence of a new ectoparasite and the risk of its spread is considered as a great danger for honey bee breeding. It is inevitable for Türkiye to recognise the danger that this *Tropilaelaps mercedesae* mite may pose in honey bee (*Apis mellifera*) breeding, to give due importance to this issue and to take necessary measures to prevent possible significant economic losses in the near future. Therefore, in order to prevent a possible *Tropilaelaps mercedesae* infestation in Türkiye, it is recommended to carry out regular hive controls and to establish an urgent action plan for early detection and effective control of this mite.

Keywords: Western Honey Bee (*Apis mellifera*), *Tropilaelaps mercedesae*, Ectoparasite, Mite

International Conference on
Food, Agriculture and Animal Sciences
19-22 December 2024, Erzurum, TÜRKİYE

Nutritional Composition of Bitter Vetch Ecotypes in Northern Morocco

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ABSTRACT: Bitter vetch (*Vicia ervilia* (L.) Willd) is an underused drought-tolerant crop legume used as animal feed. Recently, efforts have been made to introduce alternative eco-friendly fodder plants. This study aimed to assess the biodiversity of bitter vetch ecotypes in relation to their nutritional status. Seeds of 17 ecotypes from Northern Morocco were cultivated using a randomized complete block design with three replicates during 2019 and 2020. At the maturity stage, plants were harvested to determine the grain yield. The grains were separated from the straw, and their nutritional composition was analyzed. The results highlight that in terms of the nutritive value of the grains, the ecotypes had lower crude protein (CP, 22.9% vs. 26.6 - 28.0% DM) and digestibility (30.0 vs. 52.3%) compared to ecotypes from the Mediterranean area, whereas for straw, the CP content was higher (10.7 vs. 9.1% DM). The results indicated a decrease in fiber content, an increase in CP and EE content, and digestibility for grains in the second year. These findings could be related to increased rainfall, which promoted carbohydrate accumulation instead of fiber accumulation. Opposite results were reported for straw, with an increase in NDF, ADF, and ADL, and a decrease in CP content. These results provide valuable insights into the potential nutritive value of bitter vetch as an alternative feed resource for sustaining animal productivity.

Keywords: Bitter vetch; Ecotypes, Nutritive Value, Morocco

Effect of Bitter Vetch and Sorghum Grains Incorporation on Goat Kids' Fatty Acid Profile

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ABSTRACT: Generally, ruminant meat in extensive and semi-extensive systems is characterized by an improved fatty acid (FA) profile. However, owing to environmental constraints, the exploration of underused feed crops, such as bitter vetch and sorghum, is needed. This study aimed to assess the effects of incorporating these grains into the diet of local goats on meat FA profile. Twenty-four kids were divided into three groups. The control group received a conventional diet consisting of oat hay, barley, and fava beans. The experimental groups were fed modified diets: one with bitter vetch substituting fava beans (BV) and the other with sorghum replacing barley (SRG). After 90 days, the animals were slaughtered, and the fatty acid profile of the *longissimus dorsi* (LD) was determined. The SRG diet was associated with lower PUFA, PUFA/SFA, and C18:2 n-6 values than the Co diet. The lower PUFA/SFA ratios are in line with the lower amounts of C18:3 n-3 measured in the corresponding diet and because of the biohydrogenation that reduced C18:2 n-6 despite its higher concentration in the SRG diet. Conversely, the BV diet increased the C18:3 n-3 content. The lower levels of C15:0 in SRG diet are attributed to the slower fermentability of sorghum starch. Sorghum and bitter vetch grains can be used without negatively affecting the FA profile.

Keywords: Bitter vetch, Sorghum, Meat, Fatty Acid Profile

International Conference on
Food, Agriculture and Animal Sciences
19-22 December 2024, Erzurum, TÜRKİYE

Study of Anti-Inflammatory and Immunomodulatry Properties of *Ammodaucus leucotrichus*

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ABSTRACT: This comprehensive study investigated the potential of Ammodaucus leucotrichus seed extracts as a therapeutic agent for rheumatoid arthritis and joint inflammation. Methanol and n-hexane extracts were tested for their anti-inflammatory and anti-arthritic properties. The methanol extract demonstrated a significant ability to inhibit trypsin, an enzyme involved in inflammation, by 85% at a concentration of 125 µg/mL. This was notably superior to the n-hexane extract and the commonly used anti-inflammatory drug, diclofenac. On the other hand, the n-hexane extract showed a remarkable ability to prevent the denaturation of bovine serum albumin, a model protein, by 90.4% at a concentration of 62.5 µg/mL. Rheumatoid arthritis was induced in rat models using two methods: immunization with Freund's complete adjuvant and a solution of type II collagen derived from chicken cartilage. The therapeutic efficacy of the extracts was evaluated at varying doses and compared with methotrexate, a standard treatment for rheumatoid arthritis in humans. Both the extracts and methotrexate improved the mobility of the rats, as evidenced by increased walking distance, stride length, intra-step distance, and footprint area. They also positively influenced biochemical markers of inflammation, increasing the serum concentration of the antioxidant glutathione and reducing that of complement C3, malondialdehyde, and myeloperoxidase. Further analysis using gas chromatography-mass spectrometry revealed the presence of several secondary metabolites in the extracts. In silico docking studies identified several compounds with potential trypsin inhibitory activity: 2-hydroxyaceto hydrazide showing superior inhibitory effects compared to diclofenac. In conclusion, this study provides compelling evidence that suggests the potential of Ammodaucus leucotrichus seed extracts as a promising alternative therapy for rheumatoid arthritis and joint inflammation. The findings pave the way for further research and development in this area, potentially leading to new therapeutic options for patients suffering from these debilitating conditions.

Keywords: Reproductive Management, Dairy, Profitability

POSTER PRESENTATIONS

Polyphenols Content and Antioxidant Activity of *Atractylis humils* L. Roots Extracts

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ABSTRACT: Considering the urgent need of developing new therapeutic alternatives, the present study aimed to investigate the chemical composition and assess the antimicrobial as well as the antioxidant activity of the essential oils (EOs) obtained from *Atractylis humilis* L. growing in Algeria. EOs were extracted by hydrodistillation, and identified by gas chromatography (GC) and gas chromatography/mass spectroscopy (GC/MS) analyses. Aerial part EOs were characterized by sesquiterpene hydrocarbons and non terpenic compounds while root EOs were dominated by sesquiterpenes where the main components were β-elemene, α-selinene, and β-selinene. Evaluation of the antibacterial activity of the EOs against seven bacteria was performed by disc diffusion method and determination of minimum inhibitory concentration (MIC). The root EOs produced the best antibacterial activity mainly against *Bacillus subtilis, Bacillus cereus* and *Staphylococcus aureus*. Also, antifungal activity of *A. humilis* EOs was assessed by contact and fumigation methods against three fungi: *Penicillium e*xpansum, *Fusarium graminearum*and *Zymoseptoriatritici*. Above aerial part EOs appears to be as effective in inhibiting mycelial growth of target strains as root EOs, with an exception of *Z. tritici*.

The results showed that the essential oils obtained from root *A. humilis* exhibited generally a moderate antimicrobial activity against gram-positive-bacteria.

Keywords: *Atractylis humilis* L., Essential Oil, GC, GC/MS, Antimicrobial

International Conference on
Food, Agriculture and Animal Sciences
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Ethnobotanical Survey of a Plant Used in the Treatment of Metabolic Diseases

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ABSTRACT: Ethnobotanical studies provide an effective approach to understanding, within a given region, the uses and socio-cultural and economic perceptions of plant resources by local populations. Fieldwork was undertaken to conduct an ethnobotanical survey on a medicinal plant in the Tlemcen region, with the objective of identifying its therapeutic uses and the habits of local populations. The survey allowed us to collect information about the individuals as well as on the parts of the plant used and their methods of preparation. Data gathered from 80 people showed that rural populations predominantly rely on plants for health care, often following recipes suggested by traditional healers. The results indicate that older individuals possess more knowledge of medicinal plants compared to other age groups. Additionally, a significant portion of the medicinal plant users in the study area are illiterate. Thus, plant-based treatment appears to be inversely related to the individual's level of education.

The survey highlighted the moderate use of various parts of the D. gnidium species and documented its limited usage. It was found that all parts of the plant are utilized to treat various ailments. Traditional practitioners specifically use the aerial parts to treat sinusitis and water retention.

Keywords: Ethnobotanical Survey, *Daphne gnidium* L., GC, Traditional Medicine

Green Synthesis of Silver Nanoparticles Using *Agave Americana* L. Root Extract, Caracterization and Evaluation of their Antioxidant Activity

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ABSTRACT: Green synthesis offers an eco-friendly alternative for producing metal nanoparticles without harmful by-products. This study explores the synthesis of silver nanoparticles (AgNPs) using the aqueous root extract of *Agave americana*. AgNP formation, indicated by a color shift from yellow to dark brown, occurred at room temperature within 24 hours. Characterization techniques, including UV–Vis spectroscopy, particle size analysis, X-ray diffraction (XRD), and Fourier-transform infrared spectroscopy (FTIR), confirmed a clean crystalline structure, homogeneous distribution, and the presence of stabilizing biomolecules. The synthesized AgNPs displayed a plasmonic peak and an average size of 106.9 nm. Antioxidant activities were evaluated using DPPH and FRAP assays, showing notable efficacy. IC_{50} values for the DPPH assay were 5.68 ± 0,11 mg/mL for the extract and 6.93 ± 0,13 mg/mL for AgNPs. For FRAP, values were 0.97 ± 0,09 mg/mL and 1.28 ± 0.13 mg/mL, respectively. This green synthesis method provides an innovative and sustainable way to produce AgNPs with potential applications in medicine, food safety, and environmental fields, emphasizing its role as a versatile and environmentally responsible technology.

Keywords: Green Synthesis, Silver Nanoparticles, Agave americana, Characterization, Antioxidant Activity

Sensorial and Organoleptiques Characteristics of Pomegranate Skin Grown in Ghardaïa (Algeria)

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ABSTRACT: The fruits of the pomegranate punica granatum as well as its flowers, seeds and bark are used by various ancient civilizations. According to modern research following a diet is the most obvious way to keep our body healthy and prevent various diseases. Pomegranate skin (Punica granatum L.) is an inedible part obtained during the processing of pomegranate juice. Pomegranate skin is a rich source of tannins, flavonoids and other phenolic compounds. Antioxidant and antibacterial properties of pomegranate peel in in vitro model systems have been reported. Our work is in the context of a contribution to the valorization of pomegranate skin, relatively low market value, by its transformation into flour. This flour is an excellent food with a high nutritional and energetic value, due to the high content of sugars that give them a high energy value. Moreover, les fruits of the pomegranate are rich in minerals and particularly in potassium. This mineral is necessary for the regulation of blood pressure and the transmission of nerve impulses. Because of the level of iron they contain, are recommended for people who suffer from anemia. The vitamin profile of pomegranate skin is characterized by significant levels of B vitamins. They are immediate precursors of coenzymes essential to almost all living cells. Pomegranate skin are very rich in fiber, which facilitates intestinal transit and prevents constipation.

Keywords: Pomegranate, Skin, Nutritional Value

Evaluation of the Physicochemical and Microbiological Quality of Raw Cow's Milk and Detection of Antibiotic Residues

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ABSTRACT: The present study investigates the quality of raw cow's milk by evaluating its physicochemical and microbiological parameters, along with the identification of antibiotic residues. The overarching aim is to assess potential risks to food safety and to evaluate the effectiveness of good hygiene practices during the research process. The study is based on two raw milk samples collected from a dairy farm located in the El-Eulma region, a site chosen to represent common veterinary treatment practices. Physicochemical analysis of the raw milk samples revealed the following parameters: a pH of 6.7, an acidity of 18°D, a density of 1030 g/L, a fat content of 39 g/L, a protein content of 35 g/L, a lactose content of 52 g/L, and a salt content of 0.8 g/L. Additionally, the freezing point was recorded at -0.613°C, with no detectable addition of water. Microbiological analysis evaluated key indicators of microbial contamination. The total aerobic mesophilic bacteria count (TAMC) exceeded 300 colony-forming units (CFU), indicating a high microbial load. Thermotolerant coliforms (TTC) were also present at levels exceeding 300 CFU, raising concerns about fecal contamination. Furthermore, tests for pathogenic bacteria, including *Staphylococcus aureus* and *Salmonella spp.*, were conducted, although neither pathogen was detected in the samples. In terms of antibiotic residue detection, the presence of beta-lactam antibiotics was confirmed in the raw milk samples. This finding underscores the risks associated with veterinary drug residues in milk and their potential implications for public health.

Keywords: Raw milk, Physicochemical parameters, Microbiological analysis, Antibiotic residues, Food safety

Pollution Prevention in The Dairy Industry

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ABSTRACT: In Algeria, the cheese industry rejects 6,000 liters of whey per day, or 12 kg for 1 kg of cheese produced. Whey can be used in pharmacy, for dietetics or for human food. These extremes are economically possible and frame a whole series of technologically feasible possibilities. The valorization of whey must make it possible to recover, then to use at little cost this product often very interesting on the economic level; which makes it possible to reduce the dreadful pollution. The objective of our work is to valorize the whey, by mixing it in the reconstitution of the milk intended for the manufacture of a yoghurt to drink, in order to avoid their rejection. In this work, we tried to valorize the sweet (raw) whey obtained from the draining of mozzarella cheese, by mixing it with milk powder in well-defined proportions in order to have a powder/whey ratio equal to that of cow milk. The next step is to make a comparative study of the evolution of the physicochemical parameters during fermentation between a drinking yogurt based on whey and a drinking yogurt based on dairy milk. Organoleptic analyzes were carried out, relating to taste, smell and color, on the yogurt tests. We carried out physicochemical and sensory analyses in order to determine product quality finished. The made report is that this product has an unremarkable acidity given the origin of the whey used. The test of tasting realized almost identical evaluation results as yogurt prepared from cow's milk.

Keywords: POLLUTION PREVENTION, DAIRY INDUSTRY, Whey, Recovery, VALUATION

Determination of the Total Phenolics and Flavonoids in Lyophilized Infusion Extracts Prepared from Yerba Mate Tree (*Ilex paraguariensis*) Leaves

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ABSTRACT: Yerba mate (YM) tree (*Ilex paraguariensis* A.St.-Hil.) is a plant belonging to the Aquifoliaceae family, which grows naturally and is cultivated only in South America, between the 10th and 30th parallels, in the north of Argentina, in the southern parts of Brazil and in the east of Paraguay. The tea prepared from its leaves is called as 'Mate Tea'. Mate has anti-inflammatory, antimicrobial, antihyperglycemic, antioxidant, cardioprotective, anticancer, protective effects against obesity and bone health. This study aimed to determine total phenolic and flavonoid contents in lyophilized leaf infusion extract prepared as different concentrations (weight/volume); 2.5% (YM-2.5), 5% (YM-5), 10% (YM-10), and 20% (YM-20). Commercially available mate leaves were purchased from local market. Leaves were ground using a blender. Water at 100°C were poured onto ground leaves to prepare infusion. After 10 minutes incubation, infusions were filtrated and were frozen in an ultra-freezer. Water was removed by using a freeze dryer. Lyophilized extracts were stored and used for analysis. Extract yield, total phenolic and flavonoid contents were calculated. The highest extract yield (17.2%) was in YM-2.5. The highest total phenolic content was determined in YM-2.5 and it was significantly higher than YM-10. There were no significant differences between applications for total flavonoid content.

Keywords: Yerba Mate Tea, *Ilex paraguariensis*, Infusion Extract, Total Phenolics, Total Flavonoids

Antioxidant Activity of the Extract of *Cupressus lusitanica* Leaves from Cameroun

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ABSTRACT: Oxidative stress is a key factor in the development of several diseases. The search for new sources of antioxidants is essential. In this context, Cupressus lusitanica, a plant native to Cameroon, is recognized for its medicinal properties and potential as a source of antioxidants. The aim of this research is to extract and quantify the polyphenols present in the leaves of Cupressus lusitanica and to evaluate their antioxidant activities in order to determine their potential in combating oxidative stress. In this study, a hydroalcoholic extraction of Cupressus lusitanica leaves will be carried out to extract polyphenols. The quantification of polyphenols will be performed using the Folin-Ciocalteu method. Meanwhile, the antioxidant activity of this extract has been evaluated using methods such as FRAP, and DPPH, to understand its potential as a source of antioxidants.

The results show that the extract of Cupressus lusitanica leaves contains a significant concentration of polyphenols and exhibits notable antioxidant activity, indicating their potential as protective agents against oxidative stress.

In conclusion, this study highlights the importance of Cupressus lusitanica leaves as a potential source of natural antioxidants. The results encourage further research to explore the applications of this plant in nutrition and health, emphasizing its medicinal properties and its role in combating oxidative stress.

Keywords: Cupressus lusitanica, Oxidative Stress, Polyphenols, Antioxidant Activity

Harnessing Osmotolerant Plant Growth-Promoting Rhizobacteria to Enhance Durum Wheat Growth and Photosynthetic Pigments under Drought Stress

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ABSTRACT: Drought is a major constraint for global wheat production and constitutes a significant abiotic factor affecting plant growth. This study aimed to characterize the effect of osmotolerant plant growth-promoting bacteria (PGPB) on durum wheat (Triticum durum L.) under water stress conditions.

This study evaluated 24 PGPB strains from arid and semi-arid soils for tolerance to abiotic stresses, including salinity, pH, temperature, and drought. Strains were cultivated in LB broth under stress conditions: PEG-6000 (0%, 10%, 20%, 30%), NaCl (up to 1200 mM), pH (4, 7, 9, 11), and temperature (4 to 50°C). Four highly tolerant strains—*Providencia vermicola* ME1, *Pantoea agglomerans* Pa, *Pseudomonas knackmussi* MR6, and *Bacillus* sp. D13—were selected for further testing of plant growth-promoting (PGP) activities such as siderophore production, phosphate solubilization, and indole-3-acetic acid (IAA) synthesis under osmotic stress (0-30% PEG). These strains maintained robust PGP activities even under stress.

The impact of these strains on wheat (*Triticum durum* L.) under drought conditions was assessed in pots under three water regimes: well-watered (100% field capacity), moderate stress (50% FC), and severe stress (25% FC). Drought stress significantly reduced growth parameters (shoot and root length, fresh and dry weights of shoots and roots) in uninoculated plants, as well as chlorophyll pigment content. However, bacterial inoculation markedly mitigated these effects, enhancing growth parameters and chlorophyll content under stress. Notably, strains D13 and MR6 were particularly effective under moderate stress, promoting shoot and root biomass. Under drought, all bacterial inoculations significantly increased chlorophyll content compared to the non-inoculated control.

These results demonstrate the potential of osmotolerant PGPB strains to support wheat growth under drought stress, highlighting their potential for sustainable agriculture in drought-prone regions.

Keywords: PGPB, Durum Wheat (*Triticum durum* L.), Drought Stress, PGP Activities

Evaluation of *Raphanus Sativus* L. Behavior under Water and Salt Stress Effects at the Germination Stage

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ABSTRACT: The present study was conducted to evaluate the behavior of a medicinal plant (*Raphanus sativus* L) under water and salt stress effects at the germination stage. The effects of drought stress induced by different osmotic potential levels [0(control), 0,03, - 0,7 -, -1, -1,6 MPa] of polyethylene glycol 6000 (PEG 6000). Our results show that the highest percentage of germination (Pg) is obtained in the control seeds (83,3%) %). At the osmotic pressure of -1,6 MPa, the germinative capacity is reduced by 18% compared to the control and reached 65%. Like Pg, the MGT required for *R. sativus* increases with osmotic pressure. Salt stress was simulated with increasing concentration NaCl solutions (0, 10, 15, 20 and 25 *mmol*). Results show that Pg variation as a function of NaCl concentrations is highly. Seed Pg decreases in response to increased NaCl concentration in the imbibition's substrate. The MGT factor of *R. sativus* is increases significantly with elevated environmental salinity. The effect of salinity on germination kinetics is manifested by the germination retardation caused by the increasing concentrations of NaCl and PEG substrate (first phase of germination). The germination is practically inhibited at the highest concentration tested (15 *mmol*). The obtained results showed that this species is more sensitive to salt for the science of seed germination in high levels of sodium chloride.

Keywords: Water Stress, Salt Stress, Germination, Sodium Chloride, Polyethylene glycol 6000, *Raphanus sativus*

Acute Toxicity Evaluation of Aqueous Extract from *Hertia cheirifolia* in Swiss Albino Mice

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ABSTRACT: *Hertia cheirifolia* L. is a medicinal plant belonging to Asteraceae family. It is traditionally used to treat gastrointestinal ailments, infections, and spasms. The aim of this study is to evaluate the oral acute toxicity of aqueous extract from *Hertia cheirifolia* on female Albino wistar mice. Animals were divided into three groups, the first group received distilled water and was used as control; Mice of the second and third groups received the plant extract at doses of 2g/kg and 5g/kg body weight of animals, respectively. The mice were monitored for 14 days for their general behavior, adverse effects and mortality. The results showed that no death or toxic signs were observed, no changes were seen in food consumption, body weight and organ weight in the treated animals compared to the controls. However, an increase in AST and ALT levels was recorded in mice treated with the extract.

Keywords: *Hertia cheirifolia* L., Acute Toxicity, Biochemical Analysis, Body Weight

Evaluation of Acute Toxicity of *Helıchrysum Arenarium* Aqueous Extract in Swiss Albino Mice

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ABSTRACT: *Helichrysum arenarium* is a medicinal plant from the *Astéraceae* family, used as an antimicrobial and for the treatment of digestive diseases such as indigestion and anorexia. The aim of this study is to evaluate the acute toxicity of *Helichrysum arenarium*aqueous extract. The mice were divided into three groups each with 3 mice, the first group received distilled water, the second and third groups were administered orally at single dose of 2000 mg/kg and 5000 mg/kg respectively, and then observed individually for the first four hours, then over a period of 24 hours and at least once daily for 14 days. The results showed that a single administration of the aqueous extract of *Helichrysum arenarium* up to a dose of 5000 mg/kg did not cause any mortality or signs of toxicity, an increase in food consumption and body weight of treated mice compared to control, No change in organs weights. The biochemical study also showed a slight increase in ALT in rats treated with 5g/kg, a slight decrease in the levels of AST in rats treated with 2g/kg and a slight decrease in the levels of Créa in rats treated with 2g/kg and 5g/kg in comparison to the control rats.

Keywords: *Helichrysum arenarium,* Acute Toxicity, Aqueous Extract, Biochemical Parameters

Lethal dose 50, Sex Sensitivity in Mice to Evaluate Toxicity (case of *Ruta Montana*)

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ABSTRACT: The lethal dose 50 value is presently the basis for toxicological classification of substances and is thus required by government bodies in various situations. In this study, treated animals are examined hourly for the first 24 hours then daily for two weeks, and changes in appearance and behavior are reported. A variety of clinical symptoms can be used to characterize and describe acute systemic toxicity. The results indicate that as the dose of total alkaloids of *Ruta montana* increases, so does the mortality rate of male or female mice. This made it possible to deduce a dose-response effect of the alkaloid extract of *Ruta montana* on mice. The methods (Leichtfeld and Wilcoxon (1949), Miller and Tainter (1944), Trevan (1927), and the least squares method) allowed for an LD50 in male mice of 372.6±13.7 mg/kg and 217± 8.3 mg/kg in female mice, and according to the classification of Hodge and Sterner (1949), the total alkaloids of *Ruta montana* aerial parts are considered a moderately toxic product, and very toxic product according to Gosselin *et al.* The results indicate that female mice are sensitive to *Ruta montana* alkaloids. The sensitivity of sex allowed us to calculate the risk factor K using the DL84, DL50, DL16, and S and which was less than 0.1, indicating that the total alkaloids of *Ruta montana* classed among the chemicals less harmful to the animal as a highly toxic substance to humans. The determination of the SR and PR values, as well as these FSR and FPR parameters, show a considerable variation in terms of biological impact between male and female mice. After that, male mice received doses ranging from 0 to 200 mg/kg, whereas female mice received doses ranging from 0 to 100 mg/kg. These levels, which appear to be body-tolerable, could therefore be applied experimentally in an acute and subacute toxicity research. This study is crowned by the evaluation of the cumulative index in male and female mice, which is between 1 and 3 indicating that the alkaloids of the *Ruta montana* species had a cumulative impact.

Keywords: Lethal Dose 50, Sex Sensitivity, *Ruta montana*, Total Alkaloids, Toxicity

A review of the role of lectins in the reproductive system

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ABSTRACT: Lectins are carbohydrate binding proteins present in most of the plants and in some animals. Sperm glycocalyx modifications are known to occur during capacitation and the acrosome reaction. These changes are very important for gamete recognition and fertilization in mammals but are not fully understood. Both spermatozoa and egg chorion of Ciona have binding sites for fluorescein-conjugated Con A and APL. Despite a decrease in fertilization following lectin treatment of eggs, the outcomes were inconsistent. The mitogenicity of lectins is strongly associated with the stimulation of germinal vesicle breakdown as well as cumulus expansion. The dosage of lectin concentration and maturation rate of the COCs are directly proportional to each other up to some level. Therefore, lectin seems to have different effects on the reproductive system of animals. This article discusses the role of lectin in the reproductive system including sperm and embryo in animals.

Keywords: Lectin, Sperm, Reproductive, Oocyte, Spermatozoa, Embryogenesis

Antimicrobial Activity of *Arbutus unedo* Fruits Rich with Phenolic Compounds

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ABSTRACT: The *Arbutus unedo* is a shrub that grows in regions with a mild climate, belongs to the Ericaceae family, also it is used in traditional medicine to treat several diseases such as urinary infections. The fruits of the plant have been traditionally used as antiseptics, diuretics and laxatives in folk medicine.The aim of this study was to evaluate the antibacterial activity of the water-acetone extract, n-butanol and aqueous fractions obtained from the fruits of *Arbutus unedo*. Phytochemical compounds were evaluated. After harvest, the fruits were macerated in a water-acetone, followed by a liquid-liquid extraction with n-butanol. The antibacterial activity was tested by the diffusion method which results in a zone of inhibition more or less important depending on the sensitivity of the bacteria studied: *Staphylococcus aureus, Escherichia coli, Pseudomonas aeroginosa, Enterococcus feacalis*. Phytochemical analysis shows that *Arbutus unedo* contains flavonoids, tannins, Alkaloids and free quinones, The results of the antibacterial activity showed that the n-butanol fraction has the best activity against *Staphylococcus aureus* with inhibition zones of 19 mm compared to the aqueous fraction, while no effect of the extract water-acetone against all strains tested. In conclusion, the results obtained in this study show that this plant has an interesting antibacterial activity.

Keywords: *Arbutus unedo*, Antibacterial Activity, N-butanol, Phytochemical Compounds, Water-Acetone

FULLTEXT

ORAL PRESENTATIONS

Postbiotics in Aquaculture

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ABSTRACT: One of the most important alternatives to the increasing food demand parallel to the rapid population growth in the world is aquaculture**.** Due to the protein and mineral substances it contains, seafood is one of the most important and healthiest alternatives to meet the increasing food demand**.** Although seafood is a valuable source of food, it is quite sensitive to spoilage. In this context, various preservatives are used to reduce food losses and produce safe and quality foods. The increasing tendency of consumers to prefer fresh, minimally processed and preservative-free foods has brought about the necessity of developing natural antimicrobial substances as innovative additives in food safety assurance, and natural food preservation, where biological preservatives are used to increase food safety and extend shelf life, also has positive effects on improving consumer health. Postbiotics are known as antioxidant and antimicrobial agents suitable for food preservation, which have positive properties such as non-toxicity, long shelf life, standardization and ease of transportation. In this review, information about postbiotics will be given and their usage areas in aquaculture will be discussed.

Keywords: Postbiotic, Aquaculture, Preservation, Health

INTRODUCTION

While the total aquaculture production in the world is 182 million tons, aquaculture production is approximately 91 million tons (IZKA, 2024). If we look at aquaculture production in Turkey; In 2021, it increased by 1.8% compared to the previous year and reached 799 thousand 851 tons. 335 thousand 644 tons of this amount was in the seas and 136 thousand 042 tons in inland waters (TUİK, 2022).

One of the most important alternatives to the increasing nutritional needs in parallel with the rapid population growth in the world is seafood due to the protein and mineral substances it contains (Korkut et al., 2003; Özlüer-Hunt et al., 2015).

Aquaculture has been around for a very long time, and high-intensity aquaculture and globalization of seafood trade have enabled significant developments in the aquaculture industry. Unfortunately, disease is a major problem in aquaculture, which has suppressed both economic and social development in many countries, leading to farmers using more chemicals and drugs. Feed availability for aquaculture is another major challenge in the concentration of the aquaculture sector. Therefore, natural feed additives have become increasingly popular and have gained much attention over the last three decades as an alternative to antibiotics and other chemical treatments in aquaculture. Probiotics, prebiotics and synbiotics have long been considered promising feed additives for the treatment of bacterial, viral and parasitic diseases in fish and shellfish (Tuan et al., 2013).

Although seafood is a valuable source of nutrition, it is quite sensitive to spoilage. In this context, various preservatives are used in order to reduce food losses and produce safe and high-quality foods. The increasing tendency of consumers to prefer fresh, minimally processed and preservative-free foods has brought about the necessity of developing natural antimicrobial substances as innovative additives in food safety assurance, and natural food preservation, in which biological preservatives are used to increase food safety and extend shelf life, also has positive effects on improving consumer health. Postbiotics are known as antioxidant and antimicrobial agents suitable for food preservation, which have positive properties such as non-toxicity, long shelf life, standardization and ease of transportation (Küley and Sakarya 2024).

Definition and Classification of Postbiotics

The term "biotic" refers to dietary interventions used to alter the gut bacterial composition in a way that benefits the host's health. The word "biotic" is derived from the Greek term *biōtikós*, meaning "related to life," and encompasses ecosystems consisting of living organisms and their surrounding environment. Prebiotics, probiotics, and synbiotics contribute to the reorganization of the gut microbiota composition, influence its activity, and directly affect immune responses. The latest addition to this biotic family is postbiotics, which are bioactive compounds naturally produced through a fermentation process by beneficial microorganisms (Figure 1) (Kantal et al., 2024).

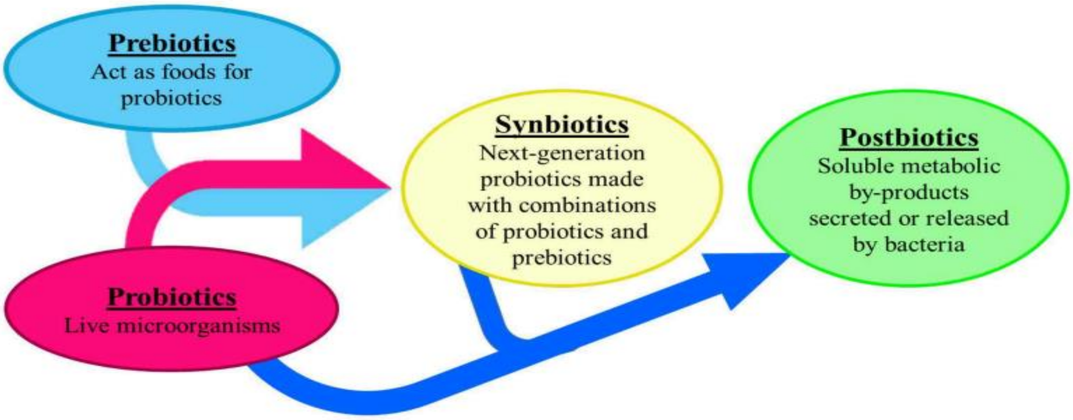

Figure 1. Concept of biotics (Kantal et al., 2024).

The term "postbiotic" is derived from the Latin word "post," meaning "after," and the Greek word "bios," meaning "life" (Szydłowska and Sionek, 2022).

Postbiotics are defined as bioactive soluble factors (products or metabolic by-products) produced by live probiotic microorganisms or that provide any physiological benefit to the host after cell rupture. Postbiotics, which are soluble, non-living bacterial products with a molecular weight of 50 to 100 kDa, are known to have biological activities on the host (Uğur et al., 2021).

Postbiotics are generally defined as non-living bacteria or by-products produced by living microorganisms, such as probiotics, that have positive effects on host health during fermentation (Sak and Soykut, 2021).

Postbiotics generally include short-chain fatty acids, teichoic acids, peptides, enzymes, peptidoglycan-derived muropeptides, endo and exopolysaccharides, vitamins, cell surface proteins, plasmalogens and organic acids, of which the important postbiotics are organic acids, short-chain fatty acids and bacteriocins. Postbiotics can be classified into different categories according to the various physiological benefits they provide or according to their compositions, which can be derived from bacterial cell compounds and microbial action (Aydın, 2024).

Studies have shown that postbiotics have antimicrobial, antioxidant, anti-inflammatory, antihypertensive, immunomodulatory, antiobesity, antidiabetic, antiproliferative, antitumor, and hypocholesterolemic properties and have beneficial effects on health (Aşit and Saka, 2023).

Postbiotics are also widely used in the food industry. They are used in food application areas such as food packaging, biofilm control, and biodegradation of contaminants (Hastaoğlu, 2024).

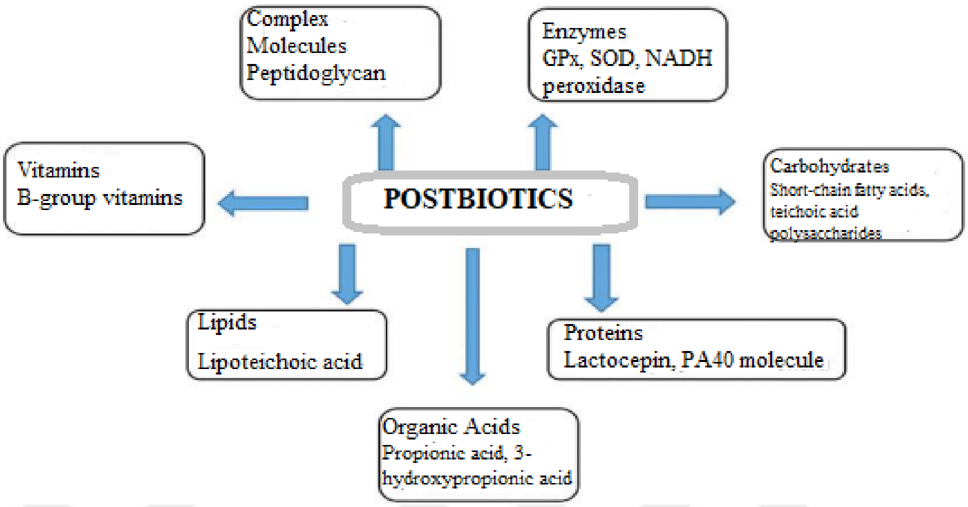

Figure 2. Postbiotic Types (Açar and Kaya, 2021)

Postbiotics in Aquaculture

Postbiotics have proven their potential in aquaculture applications as growth enhancers, stress relievers, viral disease reducing agents and promoters of general animal health (Kantal et al., 2024).

The continuous expansion of aquaculture is creating widespread infectious disease outbreaks that can result from the movement of hatchery-produced stocks, the introduction of new culture species, and trade liberalization. Control measures such as chemotherapeutic treatment and vaccination have been widely used to reduce disease outbreaks. However, the use of chemotherapeutic agents such as antibiotics has led to the development of antibiotic-resistant microbiological infections, and vaccination has been used primarily as a preventive measure and has been limited to organisms with weakened immune systems. Therefore, alternative disease control methods using prebiotics, probiotics, and postbiotics are currently being studied. Since an imbalance in the intestinal microbiota may contribute to the development of various diseases, the use of prebiotics, probiotics, and postbiotics to alter the intestinal microbiome has recently attracted attention. The use of postbiotics in pharmaceutical products, commercial food-based products, and terrestrial agriculture is currently being studied (Debroy et al., 2023).

Studies conducted with different fish species show that postbiotics have the potential to be used as natural antimicrobials and inhibitors of biogenic amine formation in aquatic products (Hastaoğlu, 2024).

Postbiotics, a new class of non-living probiotic feed additives, hold promise for improving the quality and productivity of aquaculture. Postbiotics derived from probiotic microorganisms include inactive probiotic cells, bacterial cell components, and microbial metabolites, thus potentially providing health benefits to aquaculture (Tao et al., 2024).

Seafood products are highly sensitive to spoilage. The use of preservatives to reduce food losses, especially in fish, and to produce safe and high-quality foods has become the focus of researchers and industry, and this has led to an increase in the tendency to prefer preservative-free foods and the necessity to develop natural antimicrobial substances as innovative additives in food safety assurance. Natural food preservation, where biological preservatives are used to increase food safety and extend shelf life, also has a positive effect on improving consumer health. Postbiotics, which have positive properties such as non-toxicity, long shelf life, standardization and ease of transportation, are known as suitable antioxidant and antimicrobial agents for food preservation. For this reason, antioxidant and antimicrobial active films containing postbiotics are being developed to delay spoilage and increase the shelf life of perishable foods without changing their sensory properties (Küley and Sakarya, 2024).

Funding

No financial support was received in conducting this study.

Statement of Conflict of Interest

The authors declare that there is no conflict of interest for this article.

Authors' Contributions

POY designed the study. POY, GA; Literature review; POY, GA; Article writing. Both authors read and approved the final version of the article

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Biocontrol of Post-Harvest Fungal Rotting of *Citrus* Caused by *Penicillium digitatum* and *Penicillium italicum*

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ABSTRACT: Citrus fruits are susceptible to post-harvest decay caused by *Penicillium digitatum* (green mold) and *Penicillium italicum* (blue mold). Biological control, employing antagonistic fungi, represents a promising approach to mitigate these pathogens and reduce losses in the citrus industry. Fungal species were isolated from orange peel and evaluated for their antagonistic activity against target organisms in *in vitro* bioassays. In a 7-day *in vitro* experiment, four fungal isolates (*Trichoderma* spp. and *Metarhizium* sp.) demonstrated significant inhibitory effects against the phytopathogens *P. digitatum* and *P. italicum*. All isolates achieved inhibition rates exceeding 57%, with *Trichoderma* spp. exhibiting the most potent antifungal activity. Mycelial growth of both *P. digitatum* and *P. italicum* was suppressed by over 90% when treated with *Trichoderma* spp. The findings indicate that *Trichoderma* species may be a viable biological control agent for green and blue mold diseases in citrus fruits. This research offers valuable information for the citrus industry in developing sustainable and environmentally friendly post-harvest diseases management strategies.

Keywords: Biocontrol, Blue Mold, Green Mold, Mycelial Growth Inhibition, Post-Harvest Disease, *Trichoderma* spp.

INTRODUCTION

Citrus fruits, encompassing a diverse range of species including oranges, mandarins, grapefruit, lemons, and limes, constitute a cornerstone of global fruit production. Cultivated globally, these fruits play a pivotal role in the fruit industry, with annual production exceeding 98 million tons. Among these, oranges dominate production, followed by mandarins, lemons/limes, and grapefruits. China, Brazil, the European Union, and the United States emerge as the leading producers (Li et al., 2019; Wang et al., 2018; Bhatta, 2022). While the United States holds a significant position in global citrus exports, its market share has been gradually declining, primarily attributed to reduced orange exports (Parafati et al., 2016). The global citrus trade encompasses two primary markets: fresh fruit and processed products, with oranges constituting the predominant source for both. Beyond the substantial production of fruit juice, citrus processing generates a range of valuable byproducts, including essential oils, pectin, molasses, and dried pulp (Yun et al., 2013; Trabelsi et al., 2016).

The postharvest handling and distribution of citrus fruits present significant challenges, particularly in mitigating the impact of fungal pathogens (Wang et al., 2018). Post-harvest operations, encompassing activities such as harvesting, packaging, storage, transportation, and marketing, can predispose fruits to mechanical injuries (Li et al., 2019). These wounds serve as entry points for a variety of fruit-rotting microorganisms, leading to accelerated spoilage, reduced shelf life, and substantial economic losses (Wisniewski and Wilson, 1992). The incidence of fruit rot in citrus can vary significantly, ranging from 10-30% under typical conditions and escalating to 50% or more under adverse circumstances (Velásquez et al., 2014; Sui et al., 2016). In untreated fruits, losses due to fungal decay can be particularly severe, reaching as high as 90% during post-harvest handling and marketing (Yun et al., 2013; Lin et al., 2019).

Among the numerous postharvest diseases affecting citrus, green mold and blue mold pose the most significant threats to the industry. Green mold, caused by *Penicillium digitatum* Sacc., and blue mold, caused by *P. italicum* Wehmer, are responsible for substantial economic losses worldwide. These fungal pathogens exhibit rapid growth and reproduction, with disease cycles typically ranging from 3 to 5 days at optimal temperatures. *P. digitatum*, a necrotrophic fungus, primarily infects citrus fruits through mechanical wounds. It rapidly colonizes the wounded tissue, producing a characteristic greenish-colored conidia. The fungus penetrates the fruit's pericarp, spreading to the mesocarp and causing tissue breakdown. This leads to the formation of sunken, mummified lesions and ultimately, fruit rot. *P. italicum*, a nesting-type pathogen, exhibits rapid spread within packed containers, even under cold storage conditions. It infects adjacent fruits, forming a dense network of white mycelium and producing blue-green conidia (Parafati et al., 2016; Trabelsi et al., 2016; Wang et al., 2018; Papoutsis et al., 2019).

The reliance on synthetic fungicides to control these pathogens has raised significant concerns. The widespread use of these chemicals has contributed to the emergence of fungicide-resistant strains of *P. digitatum* and *P. italicum*, diminishing the effectiveness of chemical control measures. Furthermore, the environmental impact of synthetic fungicides, including potential risks to human health and soil quality, necessitates a shift towards more sustainable and environmentally friendly control strategies. Biological control approaches, utilizing antagonistic microorganisms such as yeasts, bacteria, and fungi, offer a promising alternative to synthetic fungicides. These biological control agents can effectively suppress the growth and development of *P. digitatum* and *P. italicum*, while minimizing environmental impact and enhancing the overall sustainability of citrus fruit production and distribution (Montesinos-Herrero et al., 2016; Usall et al., 2016; Liu et al., 2017; Liu et al., 2019; Moraes Bazioli et al., 2019).

This study aimed to evaluate the efficacy of *Trichoderma* spp. (Tr1, Tr2, and Tr3) and *Metarhizium* sp. in controlling blue mold and green mold diseases under laboratory conditions.

Material and Method

The antagonistic potential of three *Trichoderma* spp. (Tr1, Tr2, and Tr3) and *Metarhizium* sp. against *P. digitatum*, and *P. italicum* was investigated. A dual culture assay on potato dextrose agar (PDA) plates was employed. Agar plugs containing four-day-old cultures of each antagonistic fungi and the respective phytopathogen were placed on opposing sides of the plates, maintaining a 2 cm distance from the plate edge for the antagonistic fungi plug and a 5 cm distance between the plugs. Control plates included only a PDA plug in place of the *Trichoderma* and *Metarhizium* isolates. Each treatment was replicated three times with five plates per replicate. All plates were incubated at 28°C for seven days (Rhouma et al., 2024). Subsequently, the percent inhibition of radial growth of the phytopathogens in the presence of *Trichoderma* spp. and *Metarhizium* sp. was calculated using the formula: $I (\%) = (1 - Cn/C0) \times 100$, where Cn represents the radial growth of the pathogen in the presence of the antagonist, and C0 represents the radial growth of the pathogen in the control (Figure 1) (Matrood and Rhouma, 2021).

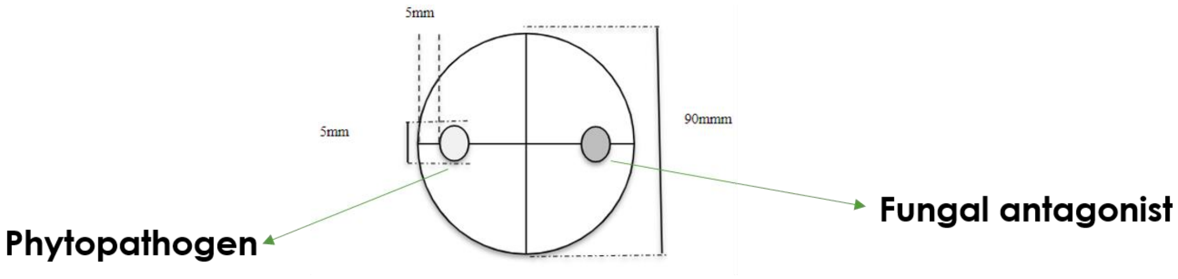

Figure 1. Evaluation of antagonistic fungi against phytopathogens using a dual culture assay.

Results and Discussion

Table 1 demonstrated the significant inhibitory effects of *Trichoderma* spp. and *Metarhizium* sp. on the mycelial growth of *P. digitatum* under *in vitro* conditions. *Trichoderma* sp. (Tr1) exhibited the highest inhibition (95.32%), followed closely by Tr3 (94.69%), while Tr2 showed slightly lower inhibition (90.15%). In contrast, *Metarhizium* sp. demonstrated significantly lower inhibition (56.99%). Statistical analysis using Duncan's multiple range test confirmed these differences, indicating that *Trichoderma* spp. (Tr1 and Tr3) exhibited comparable activity, while Tr2 and *Metarhizium* sp. differed significantly from all *Trichoderma* species. These findings suggest that *Trichoderma* species, particularly Tr1 and Tr3, possess strong antifungal potential against *P. digitatum* and could be valuable biocontrol agents for managing this pathogen (Table 1).

Table 2 showed the significant inhibitory effects of *Trichoderma* spp. on the mycelial growth of *P. italicum*, surpassing the inhibitory activity of *Metarhizium* sp. under *in vitro* conditions. *Trichoderma* sp. (Tr3) exhibited the highest inhibition (97.66%), followed closely by Tr1 (95.39%), while Tr2 showed slightly lower inhibition (90.46%). In contrast, *Metarhizium* sp. demonstrated significantly lower inhibition (57.91%). Statistical analysis using Duncan's multiple range test confirmed these differences, indicating that *Trichoderma* spp. (Tr3 and Tr1) exhibited comparable activity, while Tr2 and *Metarhizium* sp. differed significantly from all *Trichoderma* species. These findings strongly suggest that *Trichoderma* species, particularly Tr3 and Tr1, possess potent antifungal potential against *P. italicum* and could serve as effective biocontrol agents for managing this pathogen (Table 2).

Green and blue molds, caused by *P. digitatum* and *P. italicum* respectively, pose significant threats to citrus fruit quality and cause substantial economic losses. These fungal pathogens can rapidly decay fruits, rendering them unmarketable. To combat these diseases, researchers have explored the use of biological control agents, particularly *Trichoderma* species, as an environmentally friendly alternative to synthetic fungicides (Parafati et al., 2016; Trabelsi et al., 2016; Wang et al., 2018; Papoutsis et al., 2019).

Trichoderma fungi exhibit a multifaceted approach to suppressing green and blue molds. They exhibit mycoparasitism, directly attacking and parasitizing the *Penicillium* hyphae. Additionally, *Trichoderma* produces a range of antifungal compounds, including gliotoxin and viridin, that inhibit *Penicillium* growth. Furthermore, *Trichoderma* competes with *Penicillium* for essential resources such as nutrients and space. Beyond direct antagonism, *Trichoderma* can also induce systemic resistance in the host plant. This involves activating the plant's natural defense mechanisms, making it more resistant to fungal infections. Moreover, *Trichoderma* produces enzymes that can degrade plant cell walls, enabling it to colonize the fruit more effectively and outcompete *Penicillium*. *Trichoderma* species offer a promising and sustainable alternative to synthetic fungicides for controlling green and blue molds in citrus fruits. Their multifaceted mechanisms of action provide a robust defense against these pathogens. However, optimizing *Trichoderma* application requires careful consideration of strain selection, environmental conditions, and application methods to ensure effective and consistent disease control (Singh et al., 2013; Ruiz-Cisneros et al., 2018; Oszust et al., 2020; El-Katatny and Emam, 2021; Vukelić et al., 2021; Hajji-Hedfi et al., 2023).

Table 1. Effect of *Trichoderma* spp. (Tr1. Tr2 and Tr3) and *Metarhizium* sp. on mycelial growth inhibition of *Penicillium digitatum* after 7 days of incubation at 25 ± 2 °C under *in vitro* conditions.

Treatments	**Mycelial growth inhibition (%)**
Trichoderma sp. (Tr1)	95.32a[a]
Trichoderma sp. (Tr2)	90.15b
Trichoderma sp. (Tr3)	94.69a
Metarhizium sp.	56.99c
P-value [b]	**<0.01**

[a] Duncan's multiple range test; the values followed by the various superscripts differ significantly at $P \leq 0.05$.
[b] Probabilities associated with individual F tests.

Table 2. Effect of *Trichoderma* spp. (Tr1. Tr2 and Tr3) and *Metarhizium* sp. on mycelial growth inhibition of *Penicillium italicum* after 7 days of incubation at 25 ± 2 °C under *in vitro* conditions.

Treatments	**Mycelial growth inhibition (%)**
Trichoderma sp. (Tr1)	95.39a[a]
Trichoderma sp. (Tr2)	90.46b
Trichoderma sp. (Tr3)	97.66a
Metarhizium sp.	57.91c
P-value [b]	**<0.01**

[a] Duncan's multiple range test; the values followed by the various superscripts differ significantly at $P \leq 0.05$.
[b] Probabilities associated with individual F tests.

Conclusion

This study investigated the *in vitro* inhibitory effects of *Trichoderma* spp. and *Metarhizium* sp. against P*enicillium digitatum* (green mold) and *Penicillium italicum* (blue mold), major postharvest pathogens of citrus fruits. Results demonstrated that *Trichoderma* spp., particularly strains Tr1 and Tr3, exhibited significantly higher inhibition rates compared to *Metarhizium* sp. against both pathogens. While these *in vitro* results are promising, further research is crucial to translate these findings into effective in vivo control strategies. This includes conducting *in vivo* trials to evaluate the efficacy of *Trichoderma* strains under real-world postharvest conditions, assessing their practicality and economic feasibility in commercial citrus orchards, and optimizing strain selection and application methods.

Acknowledgement

Authors are thankful to the review editor and anonymous reviewers for their invaluable comments and suggestions for improving the clarity of the research paper.

Funding

The authors received no external funding for this article.

Statement of Conflict of Interest

The authors should declare that they are no conflict of interest. The authors report no known financial or personal relationships that could have influenced the work presented in this article.

Authors' Contributions

All authors contributed equally to this work.

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Control of Post-harvest Gray Mold Caused by *Botrytis cinerea* through Aqueous Extracts of *Ocimum sanctum*

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ABSTRACT: *Botrytis cinerea* is causal agent of post-harvest gray mold of tomato. This phytopathogen is airborne and responsible for significant losses annually. Fungicides are commonly used to control gray mold, but their prolonged use can pose health risks to humans and contribute to environmental pollution. Aqueous extracts of *Ocimum sanctum*, prepared at concentrations of 5%, 10%, 20%, and 30%, were assessed for their ability to inhibit the growth of mycelia on potato dextrose agar medium under laboratory conditions. Among the tested aqueous extracts, *O. sanctum* extract at 30% concentration proved to be the most potent, achieving an inhibition rate exceeding 95% under *in vitro* conditions. Conversely, the concentrations 5% exhibited minimal inhibitory effects (below 10%). *O. sanctum* extracts at a concentration of 30% demonstrated efficacy in inhibiting the growth of B. cinerea, suggesting their potential as a sustainable alternative to synthetic fungicides. This finding highlights the potential of O. sanctum extracts for environmentally friendly plant disease management.

Keywords: Aqueous Plant Extracts, Biocontrol, Mycelial Growth Inhibition, Post-Harvest Disease, *Solanum lycopersicum*

INTRODUCTION

Tomato is a globally significant crop due to its high vitamin C and lycopene content (Zheng et al., 2021). However, gray mold, caused by the fungal pathogen *B. cinerea*, poses a significant threat to tomato production, leading to substantial economic losses during cultivation, storage, and transportation (Hajji-Hedfi et al., 2023). *B. cinerea* is a versatile pathogen capable of infecting various plant species and surviving in diverse environmental conditions. Its pathogenesis involves reactive oxygen species and extracellular proteins, influencing its growth, development, and virulence. The fungus's ability to infect multiple plant parts at various stages of the plant life cycle further complicates its control (Hajji-Hedfi et al., 2023).

Traditionally, chemical fungicides have been the primary method for managing *B. cinerea*. However, the increasing prevalence of fungicide resistance in the pathogen and concerns about environmental pollution and human health risks associated with chemical residues have prompted a shift towards more sustainable approaches (Adnan et al., 2018). Several strategies have been proposed to control the phytopathogen *B. cinerea*, including those inhibiting spore germination and appressorium formation. Aqueous plant extracts, such as those derived from *Ocimum sanctum*, offer a promising eco-friendly alternative to chemical fungicides. *O. sanctum* extracts have demonstrated efficacy against *B. cinerea* in both *in vitro* and *in vivo* studies, inhibiting fungal growth and inducing systemic resistance in plants (Matrood and Rhouma, 2021; Hajji-Hedfi et al., 2023).

The antifungal activity of *O. sanctum* extracts is attributed to their diverse chemical composition, including vitamins, minerals, proteins, and a variety of phytochemicals. These compounds, such as phenolic acids and antioxidants, have been shown to possess antimicrobial and antifungal properties. The specific efficacy of an extract can vary depending on its chemical composition (Hussain et al., 2017). *O. sanctum* is a rich source of bioactive compounds, including sesquiterpenes, monoterpenes, and phenylpropanoids, which contribute to its strong antifungal activity. The plant's aqueous extract and essential oils have been shown to effectively inhibit the growth and development of *B. cinerea* under laboratory and field conditions. The antioxidant properties of O. sanctum extracts, particularly those associated with compounds like carotene, rosmarinic acid, and tocopherol, further enhance their antifungal potential (Cohen 2014; Akladious et al. 2015; Hussain et al. 2017).

The pervasive nature of tomato gray mold, caused by *B. cinerea*, coupled with the adverse environmental and economic consequences of fungicide use, necessitates further research for the development of sustainable management strategies. This study aimed to evaluate the efficacy of aqueous extracts of *O. sanctum* at concentrations of 5%, 10%, 20%, and 30% in controlling gray mold under laboratory conditions.

Material and Method

Ocimum sanctum leaves were subjected to thorough washing with tap water followed by air drying to achieve a 50% reduction in initial weight. Subsequently, leaf extracts were prepared by macerating a known weight of semi-dried plant material in distilled water at a 1:1 (w/v) ratio. The resulting macerate was then filtered through four layers of fine cloth and subsequently centrifuged at 3000 rpm for 20 min. The supernatant was further filtered using Whatman filter paper and collected in 250 mL Erlenmeyer flasks (Matrood and Rhouma, 2021; Hajji-Hedfi et al., 2024).

In vitro studies were conducted to assess the inhibitory effects of aqueous plant extracts on the mycelial growth of *B. cinerea* using the poisoned food technique. Varying concentrations (5%, 10%, 20%, and 30%) of each plant extract filtrate were incorporated into potato dextrose agar (PDA) medium under aseptic conditions. Fifteen milliliters of the resulting 'poisoned' medium was dispensed into sterile Petri dishes, with appropriate controls included. A 0.5 cm diameter disc of a 4-day-old *B. cinerea* culture was inoculated onto the center of each plate. Control treatments consisted of pathogen discs grown on PDA without any plant extract. The experiment was conducted in triplicate with five replicates per treatment. All plates were incubated at 25 ± 2 °C for 7 days (Matrood and Rhouma, 2021; Slathia et al., 2021).

The percentage of mycelial growth inhibition (I) was subsequently calculated using the formula of Rhouma et al. (2024): $I (\%) = (1 - Cn/C0) \times 100$, where Cn represents the radial growth diameter of the pathogen in the presence of the plant extract treatment, and C0 represents the radial growth diameter of the pathogen in the control treatment.

Data analysis was conducted using mean values calculated from replicate measurements. Statistical analysis was performed using ANOVA implemented within SPSS version 26.0 (IBM Corp., Armonk, NY, USA). Prior to ANOVA, homogeneity of variances and normality of data distribution were assessed. Duncan's Multiple Range Test was employed to determine significant differences among treatment groups. All statistical analyses were conducted at a significance level of 0.05 ($P \leq 0.05$).

Results and Discussion

Figure 1 presented the results of an in vitro study investigating the antifungal activity of aqueous extracts of *O. sanctum* leaves against *B. cinerea*. The study employed four different concentrations of the extract (C1: 5%, C2: 10%, C3: 20%, and C4: 30%) and assessed their impact on mycelial growth inhibition after 7 days of incubation at 25±2°C. The data reveals a clear trend: increasing extract concentration correlated with a significant increase in mycelial growth inhibition. At the lowest concentration (C1, 5%), inhibition was modest (9.59%), while at the highest concentration (C4, 30%), it reached a remarkable 95.93%. This substantial inhibition at higher concentrations strongly suggests a potent antifungal property of the *O. sanctum* leaf extract against *B. cinerea*. Statistical analysis using Duncan's multiple range test further supports these findings. The test revealed significant differences ($P \leq 0.05$) in mycelial growth inhibition between all treatment groups, confirming the concentration-dependent nature of the observed antifungal activity. These results indicate that the aqueous extract of *O. sanctum* leaves exhibits promising antifungal potential against *B. cinerea*, with the potency of the activity increasing with increasing extract concentration (Figure 1).

Plant extracts have emerged as promising agents for the management of phytopathogens. Numerous studies have demonstrated the antifungal activity of extracts derived from various plant parts, including bulbs, leaves, roots, and seeds (Derbalah et al., 2011). *In vitro* experiments have consistently shown that foliar application of these extracts can effectively inhibit fungal growth (Dheeba et al., 2015; Roy et al., 2019). Aqueous leaf extracts of *O. sanctum* have been shown to inhibit the growth of *B. cinerea* and other phytopathogens *in vitro* (Nashwa and Abo-Elyousr, 2012; Sharma et al., 2017; Roy et al., 2019). Furthermore, both greenhouse and field trials have demonstrated the efficacy of *O. sanctum* extracts in reducing the severity of gray mold disease (Prasad et al., 1986). Aqueous leaf extracts of *A. sativum* have exhibited strong antibacterial activity against *Ralstonia solanacearum* in laboratory conditions (Abo-Elyousr and Asran, 2009). Additionally, foliar applications of *O. sanctum* extracts have been shown to significantly reduce disease incidence when applied at higher concentrations (Khalil, 2000).

The antifungal mechanisms of these plant extracts likely involve the inhibition of key fungal processes. Studies have demonstrated that plant extracts can effectively inhibit spore germination and block the formation of appressoria, essential structures for fungal penetration (Iram et al., 2018). The antifungal activity of *O. sanctum* extracts can be attributed to the presence of various secondary metabolites, including flavonoids, saponins, terpenoids, steroids, tannins, coumarins, alkaloids, phenols, and others. Previous research has indicated that coumarins and their derivatives possess significant antimicrobial activity against a wide range of plant pathogens (Chohan et al., 2019).

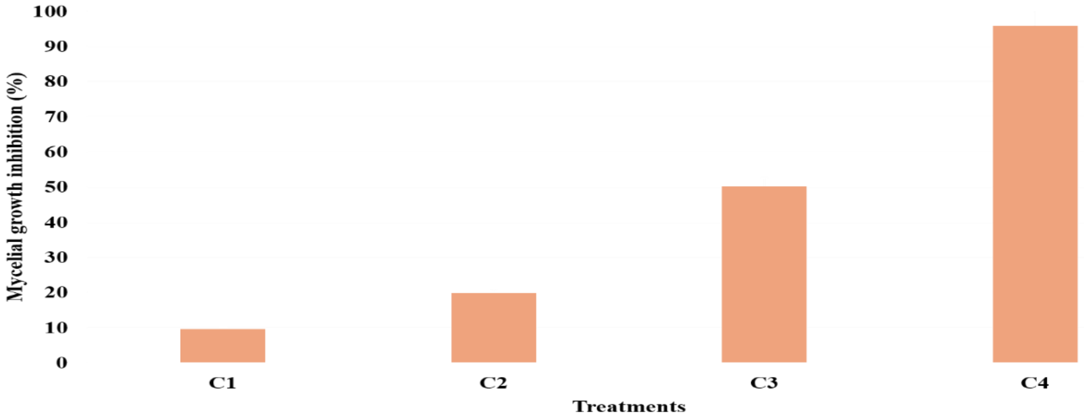

Figure 1. Effect of aqueous leaves extracts (*Ocimum sanctum*) at different concentrations (5, 10, 20, and 30%; C1, C2, C3, and C4, respectively) on mycelial growth inhibition of *Botrytis cinerea* after 7 days of incubation at 25 ± 2 °C under in vitro condition. Different letters above bars indicate statistically significant differences between treatments within the experiments ($P \leq 0.5$) according to the Duncan's multiple range tests.

Conclusion

This *in vitro* study demonstrated the potent antifungal activity of aqueous extracts of *O. sanctum* leaves against *B. cinerea*, the causal agent of gray mold disease. The results clearly showed a concentration-dependent effect, with higher extract concentrations exhibiting significantly greater mycelial growth inhibition. These findings strongly suggested that *O. sanctum* leaf extracts possess promising potential as a natural and eco-friendly alternative to synthetic fungicides for the management of gray mold and other fungal diseases in agricultural settings. This study contributed to the growing body of evidence supporting the use of plant-derived natural products as effective and sustainable alternatives to synthetic agrochemicals. The observed antifungal activity of *O. sanctum* leaf extracts aligned with previous research demonstrating the antimicrobial properties of various plant species.

Further research is needed to elucidate the specific mechanisms underlying the antifungal activity of *O. sanctum* extracts against *B. cinerea*. Identifying the key bioactive compounds responsible for the observed effects and understanding their mode of action will provide valuable insights for optimizing the use of these extracts. While this study provides valuable *in vitro* data, further research is necessary to evaluate the efficacy of *O. sanctum* leaf extracts in controlling gray mold disease under field conditions. *In vivo* studies on various plant species are crucial to assess the impact of these extracts on disease incidence, yield, and fruit quality. Research should focus on developing effective and practical formulations for the application of *O. sanctum* leaf extracts in agricultural settings. This may involve optimizing extraction methods, developing stable formulations, and exploring suitable application techniques.

Acknowledgement

Authors are thankful to the review editor and anonymous reviewers for their invaluable comments and suggestions for improving the clarity of the research paper.

Funding

The authors received no external funding for this article.

Statement of Conflict of Interest

The authors should declare that they are no conflict of interest. The authors report no known financial or personal relationships that could have influenced the work presented in this article.

Authors' Contributions

All authors contributed equally to this work.

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Post-harvest Management of *Alternaria alternata* in Tomato Fruits with *Trichoderma harzianum*

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ABSTRACT: Alternaria fruit rot is a significant disease caused by *Alternaria alternata*. Among the post-harvest diseases affecting tomatoes, *A. alternata*-induced fruit rot is the most detrimental. While fungicides are commonly used to control this disease, their potential negative health impacts due to residues in fruits and vegetables cannot be ignored. The development of eco-friendly methods for managing Alternaria rot in tomato fruits offers a promising alternative approach. The present study investigates the potential of *Trichoderma harzianum* filtrates as a biological control agent for tomato fruit rot. Three species of *T. harzianum* were evaluated for their efficacy in reducing disease incidence under laboratory conditions. The results showed that the area of the tomato fruits covered by *A. alternata* (FAA) and the disease severity index (DSI) were significantly lower compared to untreated tomato fruits. All species of *T. harzianum* induced the best results with a decrease in FAA to less than 0.70 cm (positive controls= 7.53 cm) and DSI to less than 20% (positive controls= 100%). The culture filtrates of *T. harzianum* demonstrate efficacy in suppressing Alternaria fruit rot during storage. This microbial biofungicide offers a potential alternative to chemical fungicides, providing a sustainable and environmentally friendly approach to managing post-harvest diseases.

Keywords: Alternaria Fruit Rot, Biocontrol, Post-Harvest Disease, *Solanum lycopersicum*, *Trichoderma harzianum* Filtrates

INTRODUCTION

Fruits and vegetables serve as essential sources of vitamins, fats, minerals, oils, and dietary fibers, contributing significantly to human nutrition and health. However, their limited shelf life poses a significant economic challenge (Etana et al., 2019). During storage and transportation, fruits and vegetables become susceptible to fungal pathogens, which can cause decay and render them unfit for market, resulting in substantial post-harvest losses (Ahmad et al., 2020). In industrialized countries, it is estimated that more than 20-25% of harvested fruits and vegetables succumb to decay during post-harvest handling. This issue is even more pronounced in developing countries, where post-harvest losses can exceed 35% due to inadequate storage facilities and transportation infrastructure (Kitinoja et al., 2019).

Tomato (*Solanum lycopersicum* L.) is a globally significant horticultural crop renowned for its high nutritional content. However, its high moisture content and water-soluble nutrients render it susceptible to various fungal pathogens, leading to significant post-harvest losses (Liang et al., 2021). Among these pathogens, *Alternaria alternata* (Fr.) Keissler is a primary causal agent of tomato fruit rot. This fungus thrives in specific environmental conditions and becomes particularly aggressive when the fruit is injured or weakened during storage. The resulting symptoms typically manifest as dark brown to black, firm, slightly sunken lesions that can expand to several centimeters in diameter (Slathia et al., 2021).

Fungal pathogens significantly contribute to post-harvest losses in tomatoes during long-term storage. Fungicides are commonly employed as a preventive measure to mitigate these losses. However, their application raises environmental concerns, poses risks to human health, and can lead to the development of fungicide-resistant fungal strains (Devi et al., 2021). As an alternative, biocontrol agents like *Trichoderma harzianum* have shown promise in controlling A. alternata. This approach offers a more environmentally friendly and sustainable solution for managing post-harvest diseases in tomatoes (El-Katatny and Emam, 2021).

This investigation aimed to assess the efficacy of *T. harzianum* filtrates in managing *A. alternata*-induced rot in tomato fruits.

Material and Method

Mature, uniformly sized tomato fruits (cv. Firenze) were harvested from a field site in Sidi Bouzid, Tunisia. Following standard sterilization procedures involving NaClO treatment and rinsing, the fruits were wounded with a sterile needle. Each wound was inoculated with either 20 µL of distilled water (negative control, T1), 20 µL of *A. alternata* spore suspension (10^6 spores/mL, positive control, T2), and 20 µL of *T. harzianum* filtrates (T3: Th1, T4: Th2, and T5: Th3). The *Trichoderma* filtrates were applied at a concentration of 100%. After a 2-hour incubation period, tomato fruits were inoculated with the 20 µL of *A. alternata* spore suspension. Treated fruits were placed in plastic containers on sterile, moistened paper towels. Each container held an average of six fruits. These containers were then sealed in plastic bags to maintain a high humidity level (>90%). Subsequently, the containers were incubated in a growth chamber under controlled conditions. The chamber was set to a photoperiod of 8 hours of light and 16 hours of darkness, with a constant temperature of 25°C. The experimental design followed a randomized complete block design. This involved three blocks, each containing 10 containers. The entire experiment was replicated twice (Hajji-Hedfi et al., 2023).

To assess the antifungal efficacy of the treatments on tomato fruits, the extent of Alternaria fruit rot infection was evaluated after a 7-day incubation period. The lesion area covered by *A. alternata* (FAA) was calculated using a ruler (Hajji-Hedfi et al., 2023).

Additionally, the disease severity index (DSI) and resistance level of each treatment were determined. The DSI was calculated using McKinney's formula: DSI (%) = $(\Sigma vn)/(NV) \times 100$, where: v = numeric value of the disease index scale for a specific seedling; n = number of seedlings with a specific disease index value; N = total number of seedlings; V = maximum numeric value of the disease index scale (Hajji-Hedfi et al., 2023).

Statistical analysis was performed using the mean values of the replicates. The data were analyzed by ANOVA using SPSS version 26.0 statistical software (SPSS, SAS Institute, Cary, NC, USA). The homogeneity of the variances and normality was checked by applying Duncan’s multiple range test. The differences between the treatments were determined by Duncan’s multiple range test. All statistical tests were performed with a significance level of 5% ($P \leq 0.05$).

Results and Discussion

The statistical analysis, as indicated by the P-values, confirms the significant differences between the treatments and the control groups ($P < 0.01$). The positive control group, which received no treatment, exhibited the highest DSI (100%) and FAA (7.53 cm) values, indicating severe disease infection. In contrast, the untreated control group, which was not inoculated with the pathogen, showed no signs of disease. Among the three *T. harzianum* filtrates, Th2 demonstrated the most significant reduction in both DSI (7.67%) and FAA (0.25 cm), suggesting its superior efficacy in controlling *A. alternata* infection. Th3 exhibited intermediate efficacy, while Th1 showed the least impact (Table 1).

Treatment with *T. harzianum* Th2 resulted in a significant reduction in disease severity, aligning with previous studies demonstrating the biocontrol potential of *Trichoderma* spp. against *Alternaria* spp. in tomato fruits (Singh et al., 2013; Ruiz-Cisneros et al., 2018). Moreover, *Trichoderma* treatments have been shown to influence the biochemical composition of tomato fruits. Some studies report increased levels of antioxidants and bioactive compounds, such as flavonoids, while others indicate a reduction in these parameters. These contrasting effects may be attributed to the specific *Trichoderma* strain, the plant-pathogen interaction, and the environmental conditions (Borrero et al., 2012; Seo et al., 2014; Silva-Beltrán et al., 2015; Vukelić et al., 2021). The underlying mechanism of *Trichoderma*-induced resistance in tomato fruits involves the activation of defense responses, including the upregulation of defense-related enzymes like polyphenol oxidase, phenylalanine ammonia-lyase, and peroxidase. These enzymes play crucial roles in the synthesis of secondary metabolites that inhibit pathogen growth and development (Konappa et al., 2020; Oszust et al., 2020).

Table 1. Effect of preventive treatments of three species of *T. harzianum* filtrates (Th1, Th2, and Th3) on Disease severity index (DSI) and Area of the tomato fruits covered by *A. alternata* (FAA) in tomato fruits inoculated with *A. alternata* under laboratory conditions.

Treatments	**FAA (cm)**	**DSI (%)**
Positive controls	7.53a[a]	100a
Untreated fruits	0e	0e
Th1	0.7b	20b
Th2	0.25d	7.67d
Th3	0.47c	15.67c
P-value [b]	**<0.01**	**<0.01**

[a] Duncan's multiple range test; the values followed by the various superscripts differ significantly at $P \leq 0.05$.
[b] Probabilities associated with individual F tests.

Conclusion

The statistical analysis unequivocally demonstrates the superior efficacy of *T. harzianum* Th2 in mitigating *A. alternata* infection in tomato fruits. The significant reduction in disease severity and affected fruit area, as indicated by the lowest DSI and FAA values, highlights the potential of this biocontrol agent. Previous studies have underscored the biocontrol capabilities of *Trichoderma* species against *Alternaria* pathogens in tomato fruits. However, the impact of *Trichoderma* treatments on the biochemical composition of fruits remains a subject of debate. While some research suggests an increase in antioxidants and bioactive compounds, others report a decrease. This variability may be attributed to factors such as the specific *Trichoderma* strain, the plant-pathogen interaction, and environmental conditions. The underlying mechanism of *Trichoderma*-induced resistance in tomato fruits involves the activation of plant defense responses. This includes the upregulation of defense-related enzymes like polyphenol oxidase, phenylalanine ammonia-lyase, and peroxidase. These enzymes play a pivotal role in the synthesis of secondary metabolites that inhibit pathogen growth and development. To further advance the application of *Trichoderma* as a biocontrol agent, future research should delve deeper into the specific mechanisms underlying its efficacy against *A. alternata*. Additionally, investigating the impact of *Trichoderma* treatments on the nutritional and sensory quality of tomato fruits is crucial for their commercial adoption. Optimizing application methods and timing can further enhance the effectiveness of *Trichoderma* in controlling plant diseases. Furthermore, exploring the potential of combining *Trichoderma* treatments with other sustainable disease management strategies can provide a more comprehensive and effective approach to disease control.

Acknowledgement

Authors are thankful to the review editor and anonymous reviewers for their invaluable comments and suggestions for improving the clarity of the research paper.

Funding

The authors received no external funding for this article.

Statement of Conflict of Interest

The authors should declare that they are no conflict of interest. The authors report no known financial or personal relationships that could have influenced the work presented in this article.

Authors' Contributions

All authors contributed equally to this work.

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Investigation of Total Phenolic and Flavonoid Content of Sugar Beet (*Beta vulgaris* L.) Collected in Four different Locations in Turkey*

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ABSTRACT: Sugar beet (*Beta vulgaris* L.) is an important industrial plant in the *Amaranthaceae* family. In this study, it was aimed to determine the total of phenolic and flavonoid contents in the plant of sugar beets collected from 4 different locations in Turkey (Diyarbakur, Muş, Bingöl ve Van). Methanol (MeOH) and aqueous (dH_2O) extracts were prepared from the root parts of *B.vulgaris* plant. Diyarbakır water (DW), Diyarbakır methanol (DM), Muş water (MW), Muş methanol (MM), Bingöl water (BW), Bingöl methanol (BM), Van water (VM) and Van methanol (VM) extracts were prepared. The highest yield in methanol extracts was found in DM with 29.32%, while the highest yield in water extracts was found in MW with 53.28%. While total phenolic substance content was not determined in water extracts in total phenolic analyses, it was found that the BM sample had the highest content in methanol extracts as 7.48±1.18 mg GAE/g extract. On the other hand, the highest total flavonoid content was found in the DM sample, while the lowest content was found in the MW sample. According to our study results, it was determined that sugar beet contains low levels of phenolics and flavonoids in its root part. These results show that examining the above-ground parts of the plant may be a more accurate method in studies on the total phenolic and flavonoid content of sugar beet.

Keywords: Extract Yield, Lyophilized Extract, Sugar Beet, Total Phenolic Content, Total Flavonoid Content

INTRODUCTION

Sugar beet or Beet (*Beta vulgaris* L.) is a plant species in the *Amaranthaceae* family with a high energy content, widely grown in Turkey and around the world. *B. vulgaris*, which is resistant to harsh environmental conditions and its production and processing stages are suitable for the use of modern technology, ranked 5th in the world in 2020 with an annual production capacity of 23,000,000 tons in Turkish sugar beet production (Ünsal, 2022). Although sugar beet is mainly used in sugar production, yeast, ethyl alcohol, molasses and wet pulp obtained from sugar beet are used in many areas such as food, cosmetics, animal husbandry and health. Sugar beet is an important plant for food and industry, as well as containing biologically active compounds that are important for health. For example, betaine, found in the structure of sugar beet, is a substance used in health, cosmetics, food industry and diet products. Betaine has a protective effect in alcohol-related liver disease and cancer prevention (Day et al., 2016). Phenolic and flavonoid compounds are important secondary compounds in the structure of sugar beet. Sugar beet contains compounds with strong antioxidant effects such as quercetin, gallic acid, epicatechin and kaempferol (Pyo et al., 2004; Arjeh et al., 2022). Phenolic and flavonoid compounds have different bioactive molecules ranging from simple molecules to polyphenols in different proportions in various parts (Nollet et al., 2018). While flavonoids have medical effects such as diuretic, antispasmodic, antitumoral and anti-inflammatory, phenolic compounds generally have analgesic, antipyretic and anti-inflammatory effects (Chen et al., 2017).

In this study, the extract yield, total phenolic and total flavonoid contents in methanol and water extracts obtained from sugar beet roots collected in four different provinces of Turkey were investigated.

Materials and Method

Sugar beet plants were collected from 4 different locations, Diyarbakır, Muş, Bingöl and Van, by Pharmacist Student Muhammed BOZYEL. The collected sugar beets were sliced with a knife and dried (Figure 1).

Figure 1. Sliced sugar beet samples

The dried sugar beets were ground into powder in a mortar (Figure 2).

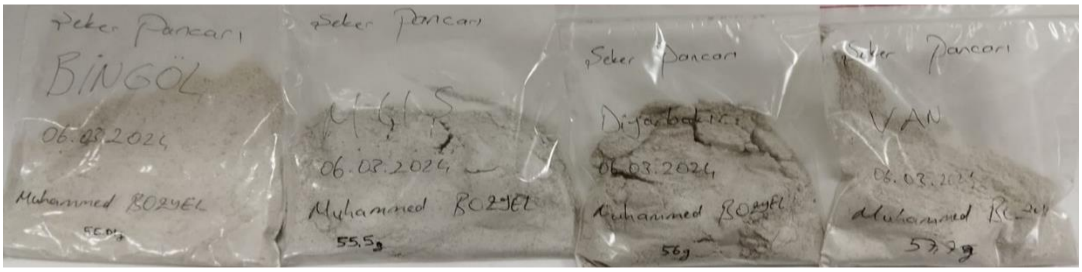

Figure 2. Powdered sugar beet samples

20 g of the powdered samples were weighed and 1 L of water was added (w/v: 1/50) and mixed in a shaker for 1 day. These processes were repeated in the pure methanol fraction. Then, the samples were passed through filter paper and the resulting liquid was evaporated in the evaporator device. The samples that reached a certain consistency were taken into falcon tubes and stored in the freezer for 72 hours. Then, the frozen samples were placed in the lyophilization device and lyophilized extracts were obtained and the yield percentages were calculated.

The total phenolic content of *Beta vulgaris* extracts were determined by mg/g gallic acid equivalent (GAE) according to the gallic acid standard curve (y = 0,5686x, R2 = 0.9996) using Folin-Ciocalteu phenol reagent and sodium carbonate solution (Singleton and Rossi, 1965).

The total flavonoid content of *Beta vulgaris* extracts were determined by mg/g quercetin equivalent (QE) according to the quercetin standard curve (y = 3,2254x, R2 = 0.9968) (Woisky ve Salatino, 1998).

Study was conducted as at least triplicate. For statistical analysis, GraphPad Prism 8 package program One Way Anova Fisher'LSD multiple comparison test was used. Data obtained from this study was presented as average and standard error of mean (SEM). Statistical difference was accepted as $P<0.05$.

Results and Discussion

The yield percentages (%) of DW, DM, MW, MM, BW, BM, VW and VM extracts obtained from sugar beet samples collected from four different locations were found to be 11.42, 29.32, 53.28, 20.36, 24.4, 6.72, 40.08 and 20.96 %, respectively. The highest yield in methanol extract was found in DM with 29.32%, Whereas the highest yield in water extract was found in MW with 53.28%.

Total phenolic contents of *Beta vulgaris* extracts are as shown in Figure 3. According to the findings, while total phenolic content was determined in the methanolic extracts, except the VM sample, total phenolic substance content was not determined in water extracts. In methanol extracts, BM sample was found to have the highest total phenolic content as 7.48±1.18 mg GAE/g extract. In DM and MM samples, it was determined as 6.05±0.71 and 2.64±.50 mg GAE/g extract, respectively.

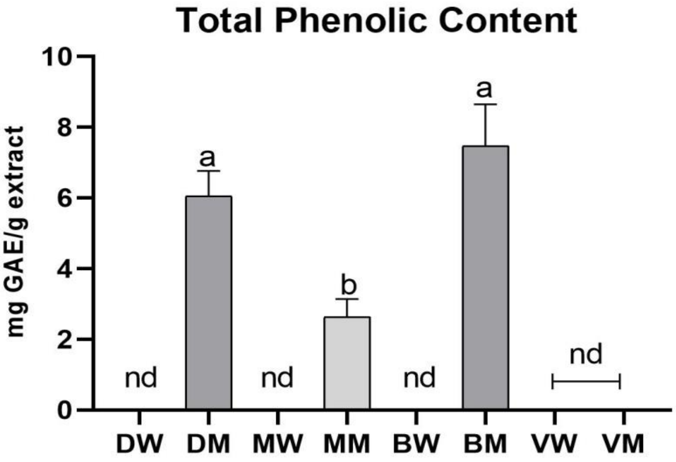

Figure 3. Total phenolic contents of *Beta vulgaris* extracts

The total flavonoid content (TFC) of *Beta vulgaris* plant extracts is shown in Figure 4. The highest TFC was found in the DM sample with 2.43±0.21, while the lowest TFC was found in the MW sample with 0.88±0.23.

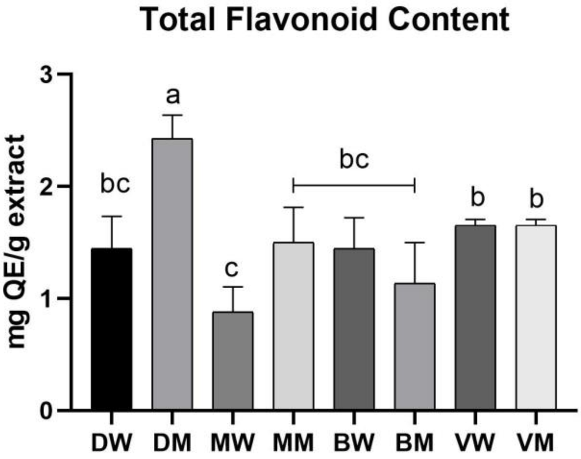

Figure 4. Total flavonoid contents of *Beta vulgaris* extracts

Total phenolic, total flavonoid, and total tannin concentrations were determined in methanolic and ethanolic extracts obtained from the flesh and peel of the *Beta vulgaris* plant (Arjeh et al., 2022). The highest total phenolic content was found in flesh and peel methanol extracts as 8.3±0.0 and 19.7±1.1, respectively (Arjeh et al., 2022). In another study, total phenolic content of 4.2 mg/g dw was observed in the *Beta vulgaris* peel plant (Kähkönen et al. 1999). The total phenol content of the leaf parts of the red and white *Beta vulgaris* plant (red; 128.1 mg/100 g FW, white; 101.5 mg/100 g FW) was determined to be higher compared to the root parts (red; 29.7 mg/100 g FW, white; 23.2/100 g FW) (Pyo et al., 2004). Our findings are consistent with previous research, and methanol may be one of the best solvents for extracting the highest phenolic and flavonoid content.

Conclusion

In this study, the yield %, TPC and TFC of water and methanolic extracts of *Beta vulgaris* collected in 4 different provinces of Turkey were determined. The highest TPC content was detected in the methanol extracts of samples collected in Diyarbakır and Bingöl provinces. Similarly, the highest TFC content was detected in the methanol extract of the sample collected in Diyarbakır province. It was concluded that location and different solvents may be effeztive in content analysis.

Acknowledgement

This study is a part of the Muhammed Bozyel’s graduation project.

Statement of Conflict of Interest

The author(s) should declare that they are no conflict of interest.

Authors' Contributions

MB and AD designed and analyzed the research, MB, AD and AB studies arranged. MB and AD worked on the preparation of pictures and tables. All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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Determination of Agromorphological Characteristics of Some Turkish Oat (*Avena sativa* L.) Genotypes under Sivas Ecological Conditions*

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ABSTRACT: Oats (*Avena sativa* L.), an important cereal crop that belongs to the Poaceae family, are well recognized for their nutritional profile, cultivated in diverse climatic situations, and have higher adaptability to suboptimal soils. Therefore, the characterization of physiological traits to develop new oat cultivars is a crucial goal of the breeders. The current study evaluated a total of 54 oat genotypes for various biological traits under field conditions at Sivas University of Science and Technology in 2023, with the aim of identifying superior genotypes for future breeding programs. The experiment followed a randomized block design with three replicates. Results showed significant genotype effects for all traits. The study revealed significant differences in panicle emergence time among genotypes 50.63 days for Faikbey to 62.49 days for genotype 89; maturation duration ranged between 81.26 days (genotypes 98, 99, 120, and 121) and 93.26 days (genotypes 6, 21, 26, 42, and 64), reflecting diverse adaptability. Plant height varied significantly, with genotypes like Fetih exhibiting minimum (51.73 cm) and Genotype 120 exhibiting the highest plant height (99.03 cm). Panicle length is displayed as ranging from 12.13 cm (Fetih) to 31.64 cm (Genotype 114). Genotype 9 had the highest 2.04 grain weight per panicle, and the genotype 162 had the lowest, 0.63. The study found that Sarı had the highest 1000-grain weight and lowest plot yield (117.89 kg ha^{-1}), while Genotype 59 had the lowest 1000-grain weight. Genotype 124 had the highest 540.92 kg ha^{-1} plot yield, identifying promising candidates for high yield. The study highlights the significance of genetic diversity in oat breeding, suggesting superior traits like yield and panicle length for improved breeding programs.

Keywords: Biological Traits, *Avena sativa* L., Poaceae, Crop Breeding, Sustainable Agriculture Approaches.

INTRODUCTION

Oats (*Avena sativa* L.) are an important cereal crop widely cultivated for their nutritional value and versatility in food products, animal feed, and various industrial uses (Halima et al., 2015). Known for their high fiber content, vitamins, and antioxidants, oats are increasingly recognized for their role in promoting human health and supporting sustainable agricultural practices (Tomar and Sing, 2024). In Turkey, oats are grown primarily in regions with temperate climates, but there is a limited understanding of how different oat genotypes perform in various ecological zones, especially under the specific conditions of Sivas, a city in central Turkey with a continental climate (Tan and Yolcu, 2021).

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*This study is a part of the Ayşe ÖZTÜRK's master thesis accepted by Sivas University of Science and Technology Graduate School of Education

Sivas, characterized by cold winters and hot, dry summers, presents a unique set of challenges for agricultural production, requiring the selection of oat genotypes that are well-adapted to these conditions (Altay et al., 2024). The successful cultivation of oats in this region depends on understanding the interaction between oat genotypes and local environmental factors. Agromorphological characteristics such as plant height, leaf structure, tillering, grain yield, and resistance to biotic and abiotic stresses are key determinants of oat performance (Ma et al., 2021). Evaluating these traits can provide valuable insights into the suitability of various oat genotypes for Sivas' ecological conditions, thus helping to improve oat productivity and resilience. Mathias-Ramwell et al. (2023), conducted a study of 132 oat cultivars revealed high phenotypic diversity (H’ = 0.68 ± 0.18) and moderate genetic diversity (He = 0.58 ± 0.03). Genotype effects were significant ($P \leq 0.05$) for all traits, with most showing moderate to high heritability. Twenty-six superior genotypes were identified for breeding. Genetic subpopulations displayed a low divergence (0.24), suggesting the need for new genetic material to improve long-term yield and quality. Kumar et al. (2023) analyzed the genetic diversity of 38 oat germplasms using 22 ISSR markers, revealing 158 distinct alleles (7.18 alleles/primer). Eight high-yielding genotypes and eight superior for fresh weight were identified. Principal component analysis and UPGMA dendrogram supported these findings, suggesting that cross-compatible germplasms with desirable traits can aid in marker-assisted varietal development. Another study by Erbaş Köse et al. (2022) evaluated the 25 oat genotypes for grain yield, plant height, and quality traits. Genotype, environment, and genotype × environment interactions significantly affected oat characteristics. AMMI analysis identified G1, G3, and G7 as top performers with yields of 4.03, 3.77, and 3.70 t/ha. Genotype-by-trait biplot explained 54.9% of variation, showing positive associations between grain yield and most traits, except plant height.

This study aims to determine the agromorphological characteristics of selected Turkish oat genotypes under the specific ecological conditions of Sivas. By assessing key traits such as plant growth parameters, yield components, and adaptability to local environmental stressors, the research seeks to identify genotypes that perform optimally in this region. The findings of this study can contribute to the development of oat varieties better suited for Sivas, ensuring enhanced productivity and economic sustainability for local farmers. Additionally, the results may have broader implications for oat cultivation in other similar ecological zones, offering a framework for improving oat farming in Turkey and beyond.

Materials and Methods

The research was conducted at the Agricultural R&D Center of Sivas University of Science and Technology during the 2023 oat growing season, over one year. A total of 45 oat genotypes originating from various regions of Turkey, along with 10 cultivated oat varieties (Arslanbey, Kahraman, Kırklar, Yeniçeri, Sarı, Fetih, Checota, Seydişehir, Faikbey, and Albatros), were utilized as experimental materials. The study focused on evaluating a range of important agronomic traits, including days to panicle emergence (DPE), days to maturation (DM), plant height (PH), panicle length (PL), number of grains per panicle (NGP), grain weight per panicle (GWP), thousand-grain weight (TGW), and overall grain yield (GY).

The experimental design employed was an augmented randomized block design, with each oat variety (check) replicated three times. Each genotype was sown in 1-meter-long plots with six rows per plot, spaced 20 cm apart, and a seed density of 450 seeds per square meter. This planting method ensured a uniform stand and allowed for the thorough evaluation of genotype performance across different environmental conditions. Fertilization practices followed a standardized protocol, with 4 kg/da of nitrogen (N) and 10 kg/da of phosphorus (P_2O_5) applied at sowing, followed by an additional 7 kg/da of nitrogen as a top dressing during the growing season to support optimal growth and development.

Statistical Analysis

Data collected during the 2023 growing season were analyzed using the augmented experimental design methodology. Mean comparisons and statistical significance were performed using JMP statistical software (JMP, 2020).

Results and Discussion

The ANOVA results indicated significant genetic variability among the 45 oat genotypes for most of the measured traits, including days to panicle emergence, days to maturity, plant height, panicle length, number of grains per panicle, and plot yield (Table 1). Genotypes exhibited substantial differences in phenological development, plant growth, and yield potential, with significant genotype effects observed for panicle emergence, maturation time, plant height, panicle length, and plot yield ($p<0.01$). However, no significant differences were found for grain weight per panicle or 1000-grain weight, suggesting more stability in these traits across the genotypes. The block effect was minor compared to genotype differences, indicating minimal environmental impact on the results. Overall, the study highlights the potential for selecting high-performing oat genotypes suited to the Sivas region's ecological conditions, with implications for improving oat productivity and adaptability.

Table 1. Analysis of variance for studied traits of oats

	SD	DPE	DM	PH	PL	NGP	GWP	TGW	GY
Genotypes	54	12,62**	15,09**	244,20**	30,25**	217,15**	0,106	34,93**	13498,8**
Block	2	17,33	16,33	49,62	0,19	11,73	0,039	138,66	782,8
Error	18	15,85	16,33	13,27	18,60	69,44	0,061	76,89	1806,6
Total	74	98,04	153,86	235,57	296,63	212,52	0,108	345,46	15462,7

The analysis of agromorphological traits revealed notable differences among the oat genotypes. Days to Panicle Emergence: FAİKBEY (50.63 days) exhibited the earliest panicle emergence, making it suitable for short growing seasons, while CHECOTA (57.00 days) was the slowest (Table 2). Days to Maturity: ARSLANBEY (83.33 days) matured the quickest, beneficial for regions with limited growing periods, whereas CHECOTA (93.00 days) took the longest. Early maturing oat varieties are particularly advantageous, as they can complete their life cycle within 65 to 80 days, making them suitable for environments with limited growing periods (Krotova et al., 2019). Studies indicate that early maturing varieties yield more seeds (e.g., 3702 kg/hm²) than late maturing varieties (2759 kg/hm²) in cold regions(Zhou et al., 2018). Plant Height: Plant height varied from 51.73 cm in FETİH to 85.64 cm in FAİKBEY. Shorter genotypes like FETİH are more resistant to lodging, making them ideal for high-wind areas. Panicle Length: FAİKBEY had the longest panicle (24.07 cm), while FETİH had the shortest (12.13 cm). Longer panicles tend to correlate with higher grain production potential. Studies show a positive correlation between panicle length and grain yield, with longer panicles facilitating more effective tillering and seed development(Mathavaraj et al., 2023) Number of Grains per Panicle: ALBATROS produced the most grains per panicle (55.93 grains), highlighting its potential for higher yield, while ARSLANBEY had the least (25.33 grains). Grain Weight per Panicle: ALBATROS also showed the highest grain weight per panicle (1.54 g), indicating strong yield potential, compared to ARSLANBEY, which recorded one of the lowest (0.91 g). 1000-Grain Weight: ARSLANBEY had the heaviest 1000-grain weight (36.79 g), whereas ALBATROS had one of the lower weights (27.42 g). Larger grain size, as seen in ARSLANBEY, is often linked to better consumer acceptance and milling properties. In a study of 48 oat genotypes, panicle exertion was positively correlated with kernel weight per primary panicle, indicating that longer panicles can enhance grain weight and yield (Premkumar et al., 2017). Plot Yield: The highest plot yield was observed in ALBATROS (320.49 g), while FETİH had the lowest (156.99 g). Given ALBATROS's consistently high performance across several traits, it emerges as a top candidate for high-yield production (Gazal et al., 2014). Güngör et al. (2023) evaluated 15 oat cultivars in Düzce province during the 2021-2022 growing season. Key traits included panicle length (13.23–20.83 cm), grain number per panicle (37.83–86.83), grain weight per panicle (0.96–2.75 g), thousand kernel weight (19.86–42.36 g), test weight (43.45–60.08 kg/hl), groat percentage (74.2–100%), and grain yield (201.4–414.8 kg/da). Biplot analysis showed a positive relationship between grain yield and panicle length, grain number, and weight, while grain yield negatively correlated with test weight and groat percentage. The study conducted by Sönmez et al. (2020) found significant genetic variation in agro-morphological traits among 19 local oat lines, with grain yield ranging from 2.31 to 3.58 t/ha. Lines G13, G16, G19, G21, G22, and G23 showed promising results for regional adaptation.

Table 2. Mean values for studied traits of oats

Genotypes	DPE	DM	PH	PL	NGP	GWP	TGW	GY
Albatros	53,00^{e-h}	88,00^{b}	65,33^{r-t}	16,67^{u-w}	55,93^{a-l}	1,54^{a-g}	27,42$^{c-ı}$	320,49$^{ı-r}$
Arslanbey	51,00^{g-h}	83,33^{c}	69,53^{q-s}	15,47^{v-x}	25,33^{p}	0,91^{h-k}	36,79^{a-b}	283,76^{l-t}
Checota	57,00^{b-c}	93,00^{a}	78,07^{m-p}	19,33^{r-u}	45,27^{d-p}	1,51^{a-h}	33,38^{a-c}	281,59^{m-t}
Faikbey	50,63^{h}	87,48^{b}	85,64^{d-o}	24,07^{c-p}	50,62^{a-o}	1,62^{a-e}	32,68^{a-d}	305,39^{j-t}
Fetih	54,33^{c-f}	88,00^{b}	51,73^{v}	12,13^{y}	31,60^{n-p}	0,90$^{ı-j}$	29,16^{c-g}	156,99^{v-w}
Kahraman	51,67^{f-h}	88,00^{b}	60,00^{t-u}	14,40^{w-y}	33,53^{m-p}	1,06^{f-k}	31,55^{b-e}	215,57^{s-v}
Kırklar	51,00^{g-h}	88,00^{b}	62,73^{t-u}	14,13^{x-y}	31,13^{o-p}	1,05^{f-k}	33,57^{a-c}	243,69^{p-u}
Sarı	57,00^{b-c}	93,00^{a}	64,40^{s-t}	14,00^{x-y}	34,47^{l-p}	1,34^{a-k}	39,40^{a}	117,89^{w}
Seydişehir	53,67^{d-g}	93,00^{a}	76,47^{n-q}	18,60^{t-u}	48,13^{c-o}	1,11^{e-k}	23,18^{f-l}	165,15^{u-w}
Yeniçeri	57,00^{b-c}	93,00^{a}	58,07^{u}	15,73^{v-x}	39,00^{j-p}	0,93^{h-k}	23,98^{e-l}	212,14^{t-w}
6	57,49^{b}	93,26^{a}	93,33^{aj}	27,88^{a-c}	61,05^{a-h}	1,55^{a-g}	25,32^{d-k}	303,57^{j-t}
9	53,49^{d-h}	88,26^{b}	87,73^{a-m}	27,88^{a-c}	71,05^{a-c}	2,04^{a}	28,74^{c-h}	258,68^{o-u}
12	51,49^{f-h}	88,26^{b}	85,53^{d-o}	26,48^{b-g}	34,65^{l-p}	1,03^{f-k}	29,67^{c-g}	264,30^{m-t}
13	57,49^{b}	88,26^{b}	83,93^{g-p}	27,08^{b-e}	43,05^{f-p}	1,10^{e-k}	25,47^{d-k}	323,68^{h-r}
21	53,49^{d-h}	93,26^{a}	88,33^{a-l}	20,68^{n-t}	52,85^{a-m}	1,17^{d-k}	22,06^{f-m}	214,20^{s-w}
26	62,49^{a}	93,26^{a}	84,13^{f-p}	21,68$^{ı-t}$	42,45^{g-p}	0,95^{g-k}	22,24^{f-m}	226,79^{q-v}
28	53,49^{d-h}	88,26^{b}	91,53^{a-l}	21,68$^{ı-t}$	41,45^{h-p}	1,24^{c-k}	29,74^{c-g}	239,20^{p-v}
42	62,49^{a}	93,26^{a}	84,73^{d-p}	18,08^{t-v}	56,05^{a-k}	1,43^{a-j}	25,48^{d-k}	262,40^{n-u}
59	53,49^{d-h}	88,26^{b}	81,13^{k-p}	23,48^{d-q}	53,45^{a-m}	0,97^{g-k}	18,06^{m}	312,33$^{ı-s}$
64	57,49^{b}	93,26^{a}	82,93$^{ı-p}$	21,08^{l-t}	37,65^{k-p}	0,77^{j-k}	20,29^{h-m}	371,84^{e-o}
73	51,49^{f-h}	88,26^{b}	86,13^{c-n}	27,28^{b-d}	75,65^{a}	1,76^{a-c}	23,25^{f-l}	344,93^{f-p}
75	53,49^{d-h}	93,26^{a}	86,33^{c-n}	24,68^{c-n}	57,85^{a-j}	1,27^{b-k}	21,88^{g-m}	310,61$^{ı-s}$
79	53,49^{d-h}	88,26^{b}	87,93^{a-m}	24,88^{c-m}	41,85^{h-p}	0,95^{h-k}	22,53^{f-m}	348,29^{f-p}
89	62,49^{a}	93,26^{a}	97,93^{ab}	25,08^{c-l}	67,05^{a-f}	1,23^{c-k}	18,32^{l-m}	282,70^{l-t}
92	53,49^{d-h}	88,26^{b}	90,13^{a-l}	23,08^{e-r}	50,05^{b-o}	1,36^{a-k}	27,15$^{c-ı}$	380,01^{d-n}
96	50,89^{g-h}	88,26^{b}	93,43^{a-j}	26,64^{b-g}	57,13^{a-k}	1,38^{a-k}	23,46^{f-l}	461,13^{a-e}
97	61,89^{a}	93,26^{a}	98,23^{ab}	25,24^{c-k}	67,53^{a-e}	1,35^{a-k}	19,31$^{ı-m}$	395,19^{b-l}
98	52,89^{e-h}	81,26^{c}	74,03^{p-r}	21,24^{k-t}	33,93^{m-p}	0,95^{g-k}	27,75$^{c-ı}$	376,07^{e-o}
99	50,89^{g-h}	81,26^{c}	76,63^{m-q}	23,04^{e-r}	31,53^{n-p}	0,82^{j-k}	26,03^{d-j}	370,87^{e-o}

104	50,89$^{\text{g-h}}$	88,26$^{\text{b}}$	90,63$^{\text{a-l}}$	26,84$^{\text{b-f}}$	44,13$^{\text{e-p}}$	1,07$^{\text{f-k}}$	23,80$^{\text{f-l}}$	330,99$^{\text{g-r}}$
109	52,89$^{\text{e-h}}$	88,26$^{\text{b}}$	89,23$^{\text{a-l}}$	23,04$^{\text{e-r}}$	44,53$^{\text{e-p}}$	1,05$^{\text{f-k}}$	23,17$^{\text{f-l}}$	360,22$^{\text{e-p}}$
113	52,89$^{\text{e-h}}$	88,26$^{\text{b}}$	83,43$^{\text{h-p}}$	19,84$^{\text{q-u}}$	52,33$^{\text{a-n}}$	1,27$^{\text{b-k}}$	23,78$^{\text{f-l}}$	430,22$^{\text{a-h}}$
114	52,89$^{\text{e-h}}$	88,26$^{\text{b}}$	94,43$^{\text{a-h}}$	31,64$^{\text{a}}$	69,13$^{\text{a-d}}$	1,76$^{\text{a-c}}$	24,72$^{\text{e-l}}$	413,51$^{\text{b-k}}$
120	50,89$^{\text{g-h}}$	81,26$^{\text{c}}$	99,03$^{\text{m-q}}$	25,24$^{\text{c-k}}$	74,33$^{\text{ab}}$	1,68$^{\text{a-d}}$	21,86$^{\text{g-m}}$	497,59$^{\text{a-c}}$
121	50,89$^{\text{g-h}}$	81,26$^{\text{c}}$	97,23$^{\text{a-c}}$	24,64$^{\text{c-o}}$	52,93$^{\text{a-m}}$	1,31$^{\text{a-k}}$	24,10$^{\text{e-l}}$	511,39$^{\text{ab}}$
122	52,89$^{\text{e-h}}$	88,26$^{\text{b}}$	93,43$^{\text{a-j}}$	23,24$^{\text{d-r}}$	39,53$^{\text{j-p}}$	0,90$^{\text{ı-k}}$	22,55$^{\text{f-m}}$	476,21$^{\text{a-d}}$
123	52,89$^{\text{e-h}}$	88,26$^{\text{b}}$	93,23$^{\text{a-j}}$	24,64$^{\text{c-o}}$	44,13$^{\text{e-p}}$	1,28$^{\text{b-k}}$	28,49$^{\text{c-h}}$	509,37$^{\text{ab}}$
124	52,89$^{\text{e-h}}$	88,26$^{\text{b}}$	92,83$^{\text{a-j}}$	30,04$^{\text{ab}}$	62,93$^{\text{a-h}}$	1,80$^{\text{ab}}$	27,79$^{\text{c-ı}}$	540,92$^{\text{a}}$
125	56,89$^{\text{b-d}}$	93,26$^{\text{a}}$	87,83$^{\text{a-m}}$	22,84$^{\text{g-r}}$	54,33$^{\text{a-m}}$	1,19$^{\text{d-k}}$	21,33$^{\text{g-m}}$	406,98$^{\text{b-k}}$
126	52,89$^{\text{e-h}}$	93,26$^{\text{a}}$	95,63$^{\text{a-f}}$	25,64$^{\text{c-ı}}$	57,33$^{\text{a-k}}$	1,41$^{\text{a-j}}$	23,98$^{\text{e-l}}$	359,95$^{\text{e-p}}$
130	52,63$^{\text{f-h}}$	87,48$^{\text{b}}$	96,04$^{\text{a-d}}$	24,87$^{\text{c-m}}$	29,02$^{\text{o-p}}$	0,82$^{\text{j-k}}$	28,45$^{\text{c-h}}$	449,68$^{\text{a-f}}$
133	52,63$^{\text{f-h}}$	87,48$^{\text{b}}$	90,64$^{\text{a-l}}$	24,07$^{\text{c-p}}$	60,82$^{\text{a-ı}}$	1,40$^{\text{a-j}}$	23,75$^{\text{f-l}}$	443,90$^{\text{a-g}}$
139	50,63$^{\text{h}}$	87,48$^{\text{b}}$	82,04$^{\text{j-p}}$	25,27$^{\text{c-j}}$	57,42$^{\text{a-k}}$	1,47$^{\text{a-ı}}$	26,21$^{\text{d-j}}$	373,38$^{\text{e-o}}$
155	56,63$^{\text{b-e}}$	87,48$^{\text{b}}$	92,24$^{\text{a-k}}$	20,27$^{\text{p-t}}$	42,62$^{\text{g-p}}$	1,00$^{\text{g-k}}$	23,85$^{\text{f-l}}$	436,17$^{\text{a-g}}$
156	52,63$^{\text{f-h}}$	87,48$^{\text{b}}$	93,64$^{\text{a-ı}}$	23,47$^{\text{d-q}}$	66,42$^{\text{a-g}}$	1,51$^{\text{a-h}}$	23,50$^{\text{f-l}}$	452,15$^{\text{a-f}}$
158	52,63$^{\text{f-h}}$	87,48$^{\text{b}}$	94,24$^{\text{a-ı}}$	23,67$^{\text{d-q}}$	45,62$^{\text{d-p}}$	1,23$^{\text{c-k}}$	27,42$^{\text{c-ı}}$	429,24$^{\text{a-h}}$
162	61,63$^{\text{a}}$	92,48$^{\text{a}}$	85,04$^{\text{d-p}}$	20,87$^{\text{n-t}}$	33,02$^{\text{m-p}}$	0,63$^{\text{k}}$	19,19$^{\text{j-m}}$	386,63$^{\text{c-m}}$
264	52,63$^{\text{f-h}}$	87,48$^{\text{b}}$	90,44$^{\text{a-l}}$	24,87$^{\text{c-m}}$	47,02$^{\text{c-o}}$	1,32$^{\text{a-k}}$	28,58$^{\text{c-h}}$	414,24$^{\text{b-k}}$
291	56,63$^{\text{b-e}}$	87,48$^{\text{b}}$	95,64$^{\text{a-e}}$	23,47$^{\text{d-q}}$	66,22$^{\text{a-g}}$	1,61$^{\text{a-e}}$	25,07$^{\text{d-k}}$	411,90$^{\text{b-k}}$
296	52,63$^{\text{f-h}}$	87,48$^{\text{b}}$	85,24$^{\text{d-p}}$	20,47$^{\text{o-t}}$	39,02$^{\text{j-p}}$	1,08$^{\text{e-k}}$	28,21$^{\text{c-h}}$	427,42$^{\text{a-h}}$
332	50,63$^{\text{h}}$	92,48$^{\text{a}}$	92,04$^{\text{a-k}}$	22,27$^{\text{h-s}}$	60,62$^{\text{a-ı}}$	1,53$^{\text{a-g}}$	25,97$^{\text{d-k}}$	388,23$^{\text{b-l}}$
333	56,63$^{\text{b-e}}$	92,48$^{\text{a}}$	75,64$^{\text{o-q}}$	20,47$^{\text{o-t}}$	53,82$^{\text{a-m}}$	1,42$^{\text{a-j}}$	27,03$^{\text{c-ı}}$	418,56$^{\text{a-k}}$
345	50,63$^{\text{h}}$	80,48$^{\text{c}}$	80,24$^{\text{l-p}}$	21,47$^{\text{j-t}}$	40,62$^{\text{ı-p}}$	1,20$^{\text{c-k}}$	30,13$^{\text{b-f}}$	453,50$^{\text{a-f}}$
346	56,63$^{\text{b-e}}$	87,48$^{\text{b}}$	94,64$^{\text{a-g}}$	25,67$^{\text{c-h}}$	52,62$^{\text{a-n}}$	1,34$^{\text{a-k}}$	26,02$^{\text{d-j}}$	421,79$^{\text{a-j}}$
347	56,63$^{\text{b-e}}$	87,48$^{\text{b}}$	89,24$^{\text{a-l}}$	19,07$^{\text{r-u}}$	57,82$^{\text{a-j}}$	1,07$^{\text{f-k}}$	18,99$^{\text{k-m}}$	417,16$^{\text{a-k}}$

Conclusion

ALBATROS is the standout genotype, displaying strong agronomic performance and high yield potential. Early maturing genotypes like ARSLANBEY could benefit areas with shorter growing periods. Further research should assess the stability of these genotypes across different agro-climatic zones and explore their resilience to biotic and abiotic stresses.

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The Status of Genotypic Resistance on Wild Grasses against *Fusarium* Root and Crown Rot

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ABSTRACT: *Fusarium* is one of the top destructive soilborne fungi that lived into a range of hosts, including mainly such as agricultural products, animals, human body or soil substrates in across the world. They can also produce secondary metabolites as called mycotoxin that contain a hazardous on human and animals, via contamination of agricultural products using as foods and feeds. *Fusarium* root and crown rot (FCR) is becoming a major disease in many parts of the cereal growing regions worldwide. It can exceed yield losses to 35% by the heavy infection under the dryland fields conditions. The management of this disease recommended different control practices, such as the use of clean and chemically disinfected seed, management of seeding dates, proper fertilization, the use of tillage, crop rotations avoiding other cereals, and the use of cultivars with resistance or tolerance and/or with resistance to water stress. The wild grasses of *Poaceae* are of a great resource to enhance the resistant/tolerant cultivars against FCR. *Aegilops*, *Secale*, *Hordeum*, *Thinopyrum* and *Agropyron* like species in this family are in tertiary gene pool of the cereal breeding and contribute with some of the most important several quantitative trait loci on managing of abiotic and biotic stress factors. Increasing drought stress and climate change phenomena may lead to soil-borne fungal diseases, especially Fusarium crown rot, becoming more aggressive and causing more losses to important cereals such as wheat and barley. Thus, exploiting wild grasses in breeding programs to improving robust wheat lines and cultivars that could be able to overcome crown or root rot disease stress will make a major contribution to the sustainability of cereal production.

Keywords: Wheat, *Fusarium* crown rot, Wild Grasses, QTLs, *Agropyron*

INTRODUCTION

Fusarium is one of the top destructive soilborne fungi that lived into a range of hosts, including mainly such as agricultural products, animals, human body or soil substrates in across the world. This genus has morphologically and phylogenetically distinct seventy-species and identified more than one-hundred fifty its sub-species on various hosts (Leslie et al., 2006). The remarkable property of this genus is that their some species has been caused by major important plant diseases almost in worldwide and thus globally serious economic yield and quality losses in agricultural products. The small grain cereals are among the most common plants of their hosts and they occur disease symptoms on all parts of these plants such as particularly wilts, rots and blights (Gardiner et al., 2012; Kazan and Gardiner, 2018; Miedaner, 1997; Parry et al., 1995). Moreover, *Fusarium* spp. is not only cause to plant diseases but also can produce secondary metabolites as called mycotoxin that contain a hazardous on human and animals, via contamination of agricultural products using as foods and feeds. The naturally occurring *Fusarium* mycotoxins belong to the trichotecenes, zearelenones and fumonisins (Logrieco et al., 2002).

Fusarium crown rot (FCR) is the generic name used to refer to the disease caused by different pathogen species of the genera *Fusarium*. FCR is primarily caused by *F. culmorum* (W. G. Sm.) Sacc., *F. pseudograminearum* (O'Donnell & T. Aoki; group I) (= *Gibberella coronicola*), and *F. graminearum* Schwabe (group II) (= *G. zeae* (Schwein.) Petch) (Burgess et al., 1975; Cook, 2010; Paulitz et al., 2002). Apart from the three mainly *Fusarium* species, *Fusarium avenaceum* (Fr.:Fr.) Sacc., *Microdochium nivale* (Fr.) Samuels & Hallett (= *Fusarium nivale* (Fr.) Sorauer), *F. acuminatum* Ellis & Everh. and *F. equiseti* (Corda) Sacc. has been reported the less virulent pathogens associated with crown rot diseases (Paulitz et al., 2002; Smiley et al., 2005). FCR disease caused by these species is in arid and semi-arid climate and water stresses conditions on worldwide, including Australia, Northwest America, Canada, South America, Africa, Middle East and Chine (Akinsanmi et al., 2004; Castanares et al., 2012 ; Ferreira et al., 2015 ; Mishra et al., 2006 ; Smiley et al., 2005; Tunali et al., 2008; Zhang et al., 2015). Paulitz *et al*. (2002) determined that 76% of the plants in winter wheat fields can be infested with FCR, with estimated losses of 18% in heavily infected fields and a negative impact of US$76 ha-1. In another study, yield losses have been documented as high as 35%, with an accepted average of 9%, while world-wide losses exceeding 30% have been reported (Nicol et al., 2007).

The management of FCR is the principal issue for reducing of damage on field conditions worldwide. Cook (2010) has recommended different control practices, such as the use of clean and chemically disinfected seed, management of seeding dates, proper fertilization, the use of tillage, crop rotations avoiding other cereals, and the use of cultivars with resistance or tolerance and/or with resistance to water stress. No single management strategy has proven effective in eliminating root and crown rots. However, combined practices have proved helpful, even though they do not provide high levels of control.

The aim of this review is to evaluate the current status of genotypic resistance against FCR and the role of the wild grasses on enhancing of breeding strategies for the cereals, particularly wheat and barley.

Status of Genotypic Resistance on Wheat

Resistance to *Fusarium* pathogens has been frequently associated with Fusarium head blight (FHB) resistance or direct resistance to crown rot (FCR) disease (Bai and Shaner, 2004 ; Smiley et al., 2003). Genetic studies have identified several quantitative trait loci (QTL), which are effective in resistance to FHB and QTLs to FHB were founded on all wheat chromosomes except chromosome 7D (Buerstmayr et al., 2009). Some wheat genotypes from Asian origin have been showed strongly genotypic resistance to FHB disease under the severe FHB epidemics (Bai and Shaner, 1994) and remarkable successes like the cultivars “Sumai 3”, “Ning 7840”, “Ning 8331” and other lines developed by the breeders. However, while high resistance to FHB has been described (Bai and Shaner, 2004), work performed by Xie *et al*. (2006) and Li *et al*. (2010) suggested that FHB resistant germplasm did not offer any resistance to FCR. Li et al. (2010) proposed that phenomenon of differential resistance to FCR and FHB in wheat, where one plant genotype displays a resistant phenotype at one development stage but a susceptible reaction to the same pathogen at another stage. Nevertheless, Moya-Elizondo and Jacobsen (2016) conducted that cv. Volt has showed a partial resistance to FHB and FCR in greenhouse experiment with inoculated by *F. culmorum*. In a study that used molecular markers associated with partial seedling resistance to FCR disease of double haploid lines constructed from crosses between ‘2-49’ (partially resistant) and ‘Janz’ (susceptible) parents has been identified QTLs located 1D and 1A chromosomes which at same location that with FHB (Collard et al., 2005). Bovill *et al*. (2006) has been reported that seedling resistance has been linked to QTLs located on chromosomes 2B, 2D and 5D in progenies obtained from a cross between ‘W21MMT70’ (partial resistance) x ‘Mendos’(susceptible). In another study, several significant QTLs for FCR resistance have been documented on chromosomes 1A, 1D, 2B, 3B, and 4B in resistant Australian cultivars by “Sunco” (Woolston, 2000) crossed with two susceptible cultivars (Poole et al., 2012). Liu and Ogbonnaya (2015) reported that FCR QTLs identified, were distributed across 13 of 21 wheat chromosome and lso revealed that the A, B and D subgenomes contain 6, 25 and 11 FCR QTLs, respectively. Pariyar *et al.* (2020) were resulted that mixed linear model analysis revealed seven novel QTLs to *F. culmorum* linked on chromosomes 2AL, 3AS, 4BS, 5BS, 5DS, 5DL and 6DS for growth room and eight QTLs on chromosomes on 3AS, 3BS, 3DL, 4BS (2), 5BS, 6BS and 6BL for greenhouse, and they has been concluded FCR resistance responses in wheat to be complex and controlled by multiple QTLs.

Status of Genotypic Resistance on Wild Grasses

Poaceae communities have large spread areas such as agricultural, aquatic, or arid habitats worldwide. These plants which survive considerably various ecology and soil conditions, can resist abiotic and biotic stress conditions. The wild species of these family also play an important role at based on long term the evolution of their members such as cereals that is economically the most important agricultural products in worldwide. For example, modern bread wheat (*Triticum aestivum* L.) is derived from a combination of three closely related independently genomes (A, B and D) formed by multiple hybridizations among the three different progenitor species, *T. urartu* for A genome, *Aegilops speltoides* for B genome and *A. tauschii* for D genome (Huang et al., 2002; Shewry, 2009).

Wild grasses and cultivated cereals are the constitutive sources of valuable genes for wheat breeding (Ceoloni et al., 2014). According to Friebe *et al.* (1996), tertiary gene pool species have genomes that differ from common wheat subgenomes (homoeologous) and it includes the genera *Aegilops* L. (species with U, C, M, T, X genomes), *Secale* L., *Hordeum* L., *Thinopyrum* Á. Löve, *Agropyron* Gaertn., *Leymus* Hochst., *Haynaldia* L. (= *Dasypyrum*), and *Pseudoroegneria* (Nevski) A. Löve (Friebe et al., 1996; Kroupin et al., 2019; Kumar et al., 2022).

Qcrs.cpi.3B, one of the strongest FCR QTLs, is derived from *Triticum spelta*, a wild relative of hexaploid or bread wheat and it is located on the long arm of chromosome 3B (Ma et al., 2010). Lin *et al.* (2022) reported that genome-wide association (GWAS) mapping using 6,739 single nucleotide polymorphisms (SNPs) revealed that two SNPs on chromosome 2D and four SNPs on chromosome 7D of *A. tauschii* were significantly associated with FCR resistance. Almost all FCR resistance alleles were presented in accessions from the *tauschii* subspecies, and only 4, 11, and 19 resistance alleles were presented in accessions from the *strangulate* subspecies.

A major QTL, located at the distal end of chromosome 4HL, was detected in this wild barley genotype belonging to *Hordeum spontanneum* (L.). The QTL was detected in both of the populations analyzed and it explained up to 45.3% of the phenotypic variance in both glasshouse and field trials (Chen et al., 2013a). In another study of the same researchers that were conducted another study with landraces of *H. vulgare*, two QTL, one located on the long arm of chromosome 1H (designated as *Qcrs.cpi-1H*) and the other on 3HL (designated as *Qcrs.cpi-3H*), were founded to be responsible for the FCR resistance of this genotype (Chen et al., 2013b).

Perennial *Triticeae* species of the *Thinopyrum* genus are among the richest sources of valuable genes/QTL for wheat improvement and has an effective resistance QTL to FHB and FCR, associated with the long arm of *Thinopyrum elongatum* chromosome 7E (7EL) (Ceoloni et al., 2017). In a study of towards understanding the contribution of *Th. elongatum* 7EL to improvement of disease resistance in wheat, a reduction in browning symptoms had been observed as early as 4 d post inoculation in the infected forets of telosomic addition line CS7EL when compared to Chinese Spring, in response to *F. graminearum* inoculation (Konkin et al., 2022).

Conclusion

Fusarium graminearum and *F. culmorum* cause serious yield losses by root and crown rot diseases, especially in wheat plants. The resistance of the host plant during the seedling or adult plant period is critical in the management of these diseases. The use of resistant cultivars in agricultural production is the factor that reducing the cost of plant protection applications and make the greatest contribution to the sustainability of agriculture. For this reason, it is necessary for a common plant such as wheat to enhance resistance against these diseases, caused by a universal disease agent such as *Fusarium* and breeding programs for this purpose should be continued by using developing technological tools. For this purpose, the potential a source of resistance of wild *Poaceae* family members which are in the tertiary gene pool of the cultivated cereals, will be among the most important issues of future studies.

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Modelling of Growth Curves of Twin and Single-Born Male Lambs

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ABSTRACT: In this study, Richards, Brody and Gompertz non-linear growth models were used to predict the growth curves of twin and single born male lambs. The aim of this study was to determine the most appropriate of these three models for our data and to compare the growth performance of twin and single lambs. The Richards model is characterised by its flexibility when the growth rate changes over time, while the Brody model is particularly effective in predicting the long-term growth of animals. The Gompertz model is useful in early growth predictions. The performance of each model was evaluated using statistical criteria such as coefficient of determination (R^2) and mean square error (MSE). The results were found to be 3.576 and 97.9, 4.477 and 97.9 for Brody model; 2.857 and 97.5, 4.144 and 97.1 for Gompertz model; 3.831 and 96.9, 4.85 and 96.9 for Richards model in twin and singleton lambs, respectively. When the results are analysed, it is seen that Brody and Gompertz models have the highest R2 and lowest MSE values. Brody and Gompertz models can be suggested as the most suitable model for comparing the growth curves of twin and singleton lambs due to its less parameters and ease of application. These analyses allowed us to compare the growth curves of twin and singleton lambs and to determine the growth differences between these two groups. The findings obtained will contribute to the development of more efficient strategies in animal breeding.

Keywords: Awassi, Growth Curve, Nonlinear Models

INTRODUCTION

Growth is the expression of age-related changes in body weight and volume. Growth shows a complex structure since it is under the pressure of many environmental factors based on genetic structure (Yakupoğlu 1999). Curves indicating the change of growth over time within a certain period of time are defined as growth curves or age-development curves (Efe 1990). Growth curves provide the opportunity to predict the growth of a creature at a later age, enabling animals with good growth to be used for selection at an early age (Efe 1990; Tekel 1998). The shape of the growth curves may vary according to the species, breed, sex, environmental conditions and the trait analysed. In sheep, the change in the time until reaching adult weight can be described by linear models. However, since the growth rate at later ages is sigmoidal, it does not increase linearly. Therefore, non-linear models have been developed to express the change over time (Efe 1990; Yakupoğlu 1999; Bilgin and Esenbuğa 2003; Lambe et al. 2006; Yıldız et al. 2009).

Describing the growth of sheep using growth curves is very useful in animal husbandry. Growth curves help us to understand how sheep grow and develop over a given age range. These curves are usually constructed using live weight measurements and analysed with different models. Accurate estimation of growth curves in animal husbandry is of great importance for increasing productivity and monitoring the health status of animals. In a study on Malian sheep, the growth curves of sheep from weaning to 48 months of age were analysed. Linear, Quadratic, Cubic, Gompertz and Logistic models were used in the study and it was reported that all models except the linear model were able to describe the growth adequately. Such studies provide important data to breeders to determine the optimal feeding and care conditions for sheep (Aytekin and Zulkadir 2013).

Growth curves can also be used for different sheep breeds and feeding regimes. In another study on Awassi sheep, growth curves were estimated using different non-linear models and Bertalanffy model was suggested as the most appropriate model. Such analyses are very important as they provide important information to optimise the growth performance of sheep (Yağanoğlu 2022).

In this study, nonlinear Richards, Brody and Gompertz growth models were used to predict the growth curves of twin and singleton born male lambs. By comparing the performances of these models, the most appropriate model for our data was determined and the growth performances of twin and singleton lambs were analysed.

Material and Method

The data used in the study consisted of weight data of twin (9 heads) and singleton (16 heads) born male lambs (25 heads in total) measured at regular intervals from birth. These data were analysed using Brody, Gompertz and Richards models. The performance of the models was compared using statistical criteria such as coefficient of determination (R^2) and mean square error (MSE).

Table 1. Nonlinear growth models

Models	Formula
Brody	$\boldsymbol{Y_t = A[1-\beta * \exp(-k * t)]}$
Gompertz	$\boldsymbol{Y_t = A * \exp[-\beta * \exp(-k * t)]}$
Richards	$\boldsymbol{Y_t = A[1-\beta * \exp(-k * t)]^m}$

In the models; Y= body weight, t= age, Yt= observed body weight (kg) at age t months; A= average highest body weight or adult body weight of the individual; β= ratio of body weight gained after birth to adult body weight; Exp= base of natural logarithm; k= maturation rate; m=

the change point that occurs when the change in the estimated growth rate changes from increase to decrease.

Results and Discussion

While the Richards model stands out with its flexibility in cases where the growth rate changes over time, the Brody model is particularly effective in long-run growth forecasts of animals. Gompertz model is useful in early period growth predictions. When Table 1 is analysed, the highest A parameter was determined by Richard model (113.01 and 87.63) and the lowest by Gompertz model (53.14 and 45.30) in twin and single male lambs of Awassi breed. B parameter was estimated similarly in twin and singleton male lambs by Brody and Richards models (0.96 and 0.93). k parameter was estimated similarly by Brody and Richards models (0.01 and 0.04). The parameter m, which is one of the parameters of Richards model, was determined as 0.65 and 1.10 in twin and singleton male lambs. Similar to our study, Kopuzlu et al (2014), Yaldızbaş (2016), Nimase et al. (2018) estimated growth curves using different non-linear models. They reported the results obtained as similar to our study.

When Table 2 is analysed, the highest AUC of twin and singleton male lambs of Awassi breed was determined by Richards model (3.831 and 4.850) and the lowest was determined by Gompertz model (2.857 and 4.144). The highest R^2 values were determined with Brody model (97.9 and 97.9) and the lowest with Richards model (96.9 and 96.9). Gompertz and Brody models, which had the highest R^2 and the lowest AUC values, showed the best fit in the twin and singleton male lambs. The fit of Richards model was lower than these two models.

Table 2. Parameters, AUC, R^2 values and their standard errors estimated by non-linear growth models for twin and singleton born male lambs of Awassi breed

Model		A	B	k	m	MSE	R^2
Brody	Twin	87.99±8.05	0.96±0.01	0.01±0.006		3.576	97.9
	Single	63.92±6.04	0.93±0.01	0.04±0.005		4.477	97.9
Gompertz	Twin	53.14±6.06	0.57±0.06	0.25±0.005		2.857	97.5
	Single	45.30±5.09	0.36±0.11	0.10±0.005		4.144	97.1
Richards	Twin	113.01±23.83	0.96±0.01	0.01±0.006	0.65	3.831	96.9
	Single	87.63±20.02	0.93±0.01	0.04±0.005	1.10	4.850	96.9

Bilgin et al. (2004), Kopuzlu et al. (2014) and Nimase et al. (2018), who used different non-linear models similar to our study, reported Brody model as the best model for predicting lamb growth. They emphasised that it can be recommended because it has fewer parameters and ease of interpretation.

In Fig 1 and Fig 2, the observed live weight data and the growth data predicted by different models are compared with the observed live weight data of the twin and singleton male lambs.

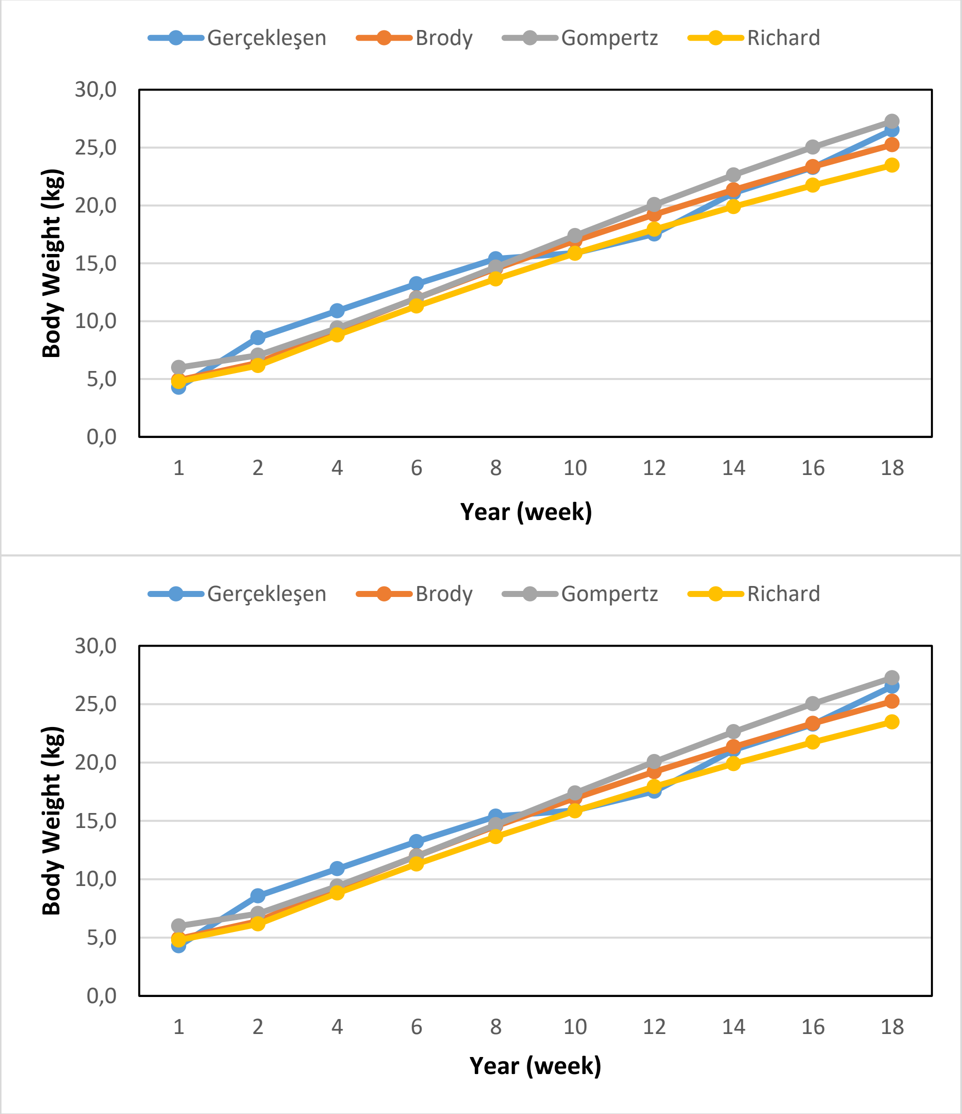

Figure 1. Growth curves observed and predicted by different models for male twin lambs

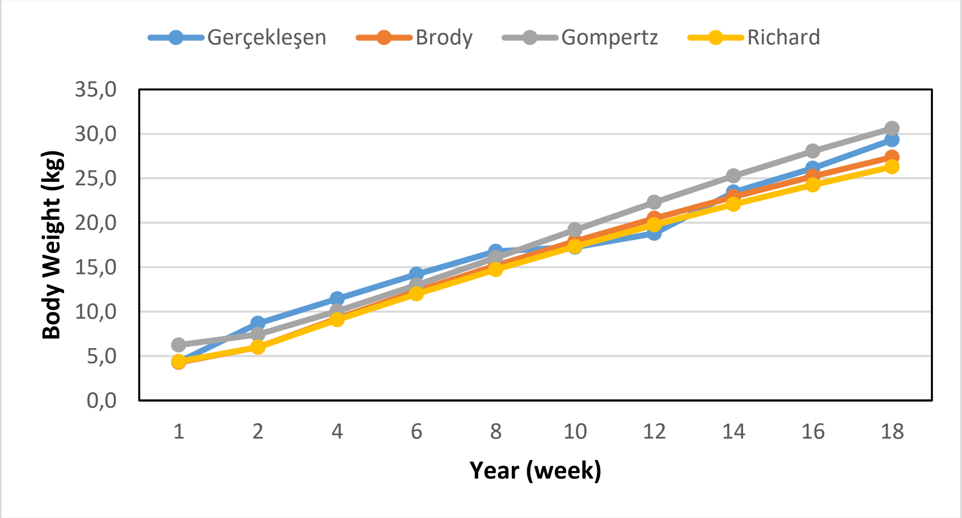

Figure 2. Growth curves observed and predicted by different models for single male lambs

Conclusion

When the results were analysed, it was observed that Brody and Gompertz models had the highest R^2 and lowest AUC values. Brody and Gompertz models are recommended as the most appropriate models for comparing the growth curves of twin and singleton lambs due to their low number of parameters and ease of application. These analyses allowed us to compare the growth curves of twin and singleton lambs and to determine the growth differences between these two groups. The findings obtained will contribute to the development of more efficient strategies in animal breeding.

Statement of Conflict of Interest

The author(s) have no conflict of interest.

Authors' Contributions

Dogan Turkyilmaz, Ulku Dagdelen, and Nurinisa Esenbuga designed and analyzed the research, Dogan Turkyilmaz, Ulku Dagdelen and Nurinisa Esenbuga studies arranged. Dogan Türkyilmaz worked on the preparation of Ulku Dagdelen and Nurinisa Esenbuga pictures and tables. All authors contributed to the writing of the article, and took part in the process of publication of the article and read and approved it.

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Effects of Scandium on Biochemical and Antioxidant Enzyme Activities of Pepper Seedlings

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ABSTRACT: Pepper (*Capsıcum annuum* L.) is a widely cultivated vegetable important for human nutrition but sensitive to environmental stresses such as salinity, drought, and heavy metals. Scandium (Sc), a rare earth element, is not essential for plant growth but interacts with physiological and biochemical processes, influencing stress responses and antioxidant enzyme activity. These enzymes, including superoxide dismutase (SOD), catalase (CAT), peroxidase (POD), glutathione reductase (GR), glutathione S-transferases (GST), glucose-6-phosphate dehydrogenase (G6PD), and ascorbate peroxidase (APX), play critical roles in reducing oxidative stress by preventing reactive oxygen species (ROS) accumulation. This supports plant growth and adaptation to environmental changes. In this study, Sc treatments at 0, 125, 250, 500, and 1000 µM concentrations were applied to pepper seedlings. The results showed that the highest H_2O_2, MDA, proline, CAT, GR, GST, G6PD, and APX activities were observed at 1000 µM Sc. The highest sucrose content was recorded at 250 µM Sc, while POD and SOD activities peaked at 125 µM Sc. These findings suggest that Sc, despite being non-essential, significantly affects antioxidant enzyme activities and stress responses, with concentration-dependent effects on biochemical and physiological parameters.

Keywords: Pepper, Scandium, Antioxidant Enzyme Activity, H_2O_2, MDA, Prolin

INTRODUCTION

Pepper (*Capsicum annuum* L.) is a plant species belonging to the Solanaceae family. Pepper is a rich source of vitamin C and antioxidants. It is also valuable for vitamin A, potassium, fiber and carotenoids. It is an important vegetable in terms of both economic and nutritional value and is widely cultivated around the world. Pepper is highly sensitive to environmental stresses and understanding its physiological and biochemical responses to these stresses is crucial for developing strategies to increase its resilience and ensure sustainable production (Sanati et al. 2018; Mandal et al. 2023).

Scandium (Sc) is an element belonging to the group of rare earth elements (REEs), found in low concentrations in nature and commonly used in metallurgy, aerospace and advanced technologies. However, recent studies have revealed that scandium can affect physiological and biochemical processes in plants. It has shown that scandium can exert both positive and negative effects on growth, stress tolerance and metabolic processes in plants (Horovitz, 2012; Ozturk et al. 2023). Scandium can increase photosynthetic efficiency and promote plant growth when applied at low concentrations. This is mainly attributed to improvements in carbon metabolism and enzyme activities (Hong et al. 2003; Cui et al. 2019).

Oxidative stress occurs as a result of excessive accumulation of reactive oxygen species (ROS) in plants due to environmental factors (such as salinity, drought, heavy metals) and causes damage to biomolecules such as cell membranes, proteins and DNA (Doğru, 2020). Oxidative stress occurs as a result of excessive accumulation of reactive oxygen species (ROS) in plants due to environmental factors (such as salinity, drought, heavy metals) and causes damage to biomolecules such as cell membranes, proteins and DNA (Doğru, 2020). Antioxidant defense systems play a critical role in the protection of plants against oxidative stress. The antioxidant defense system consists of enzymatic and non-enzymatic mechanisms that detoxify these harmful ROS. Enzymatic antioxidants: Enzymes such as superoxide dismutase (SOD), catalase (CAT), peroxidase (POD), ascorbate peroxidase (APX), glutathione reductase (GR) and glutathione S-transferase (GST) regulate ROS levels. Non-enzymatic antioxidants: Compounds such as ascorbic acid, glutathione, carotenoids and tocopherols neutralize free radicals and reduce cellular damage. This system supports plant growth and development by maintaining a balance between ROS production and detoxification (Gill & Tuteja, 2010).

Sc can reduce the effects of oxidative stress by controlling ROS accumulation. This mechanism occurs by increasing the activities of antioxidant enzymes such as SOD, CAT, POD and APX. These enzymes maintain cellular balance by eliminating the harmful effects of ROS and support plant adaptation to stress conditions (Pang et al. 2019; Dridi et al. 2022). Sc treatments can also increase the activities of enzymes that regulate glutathione metabolism, such as glucose-6-phosphate dehydrogenase (G6PD) and glutathione S-transferase (GST). This is critical for detoxifying ROS and optimizing cellular energy metabolism (Elbasan et al. 2020).

In this context, the aim of this study was to investigate the effects of Sc on biochemical parameters and antioxidant enzyme activities of plants by applying various concentrations in pepper seedlings.

Material and Method

Plant Material and Experimental Design

In this study, pepper (*Capsicum annum* L. cv. Yalova Carliston) seeds were used as plant material and the experiments were carried out under controlled conditions at Atatürk University, Erzurum. The temperature and humidity of the greenhouse were controlled by a sensor and kept at an average temperature of 24 (±2) °C during the day and 18 (±2) °C at night. Humidity was kept around 50 (±5) per cent. Pepper seeds were first sown in peat and when three true leaves appeared, the seedlings were transplanted into 1.5 liter pots, one seedling per pot. The pots were composed of garden soil, peat and sand in a ratio of (3:1:1:1, v:v:v:v). Sc was applied at different concentrations (0, 125, 250, 500 and 1000 µM) after about one week. Sc was applied to the seedlings as a foliar spray every 5 days for a total of 3 times.

Determination of H_2O_2 and MDA Content

The levels of hydrogen peroxide and MDA were assessed following the methodology of Sardar et al. 2022. The H_2O_2 concentration was ascertained with a standard calibration curve established with varying concentrations of H_2O_2. MDA was quantified from thiobarbituric acid-reactive molecules, with its concentration determined from the absorbance curve utilising an extinction coefficient of 155 mmol L^{-1} cm^{-1} (Ekinci et al. 2024).

Proline Content

The method of Shams et al. 2016 was employed to quantify proline content, and the proline levels in the tissues were evaluated using a standard curve derived from pure proline.

Antioxidant Enzyme Activities

The activity of antioxidant enzymes (CAT, POD, SOD, APX) were assessed on fresh leaf samples utilising the methodologies of Shams et al. (2020) and Dadasoglu et al. (2021). The GR enzyme and Glutathione-S-transferase (GST) enzyme were quantified following the methodology of Chikezie et al. (2009), with findings expressed as enzyme units per gramme of fresh leaves (Eu/g leaf). The enzyme glucose-6-phosphate dehydrogenase (G6PDH) was quantified following the methodology of Landi et al. (2016). The absorbance of the samples was quantified at 340 nm by assessing NADP+, and the findings were expressed as enzyme units per gramme of fresh leaves (Eu/g leaf).

Statistical Analysis

The statistical analysis was performed using GraphPad Prism 9 software, employing one-way ANOVA within a completely randomized design. To find differences between means at the 0.05 level, Tukey's HSD (honestly significant difference) test was employed. Graphical analysis was conducted with GraphPad Prism 9 software.

Results and Discussion

In this study, the effects of different concentrations of Sc on antioxidant enzyme activities and stress-related biochemical parameters in pepper seedlings were investigated in detail. The results show that Sc treatments have significant effects on oxidative stress, antioxidant defense mechanisms and metabolic processes.

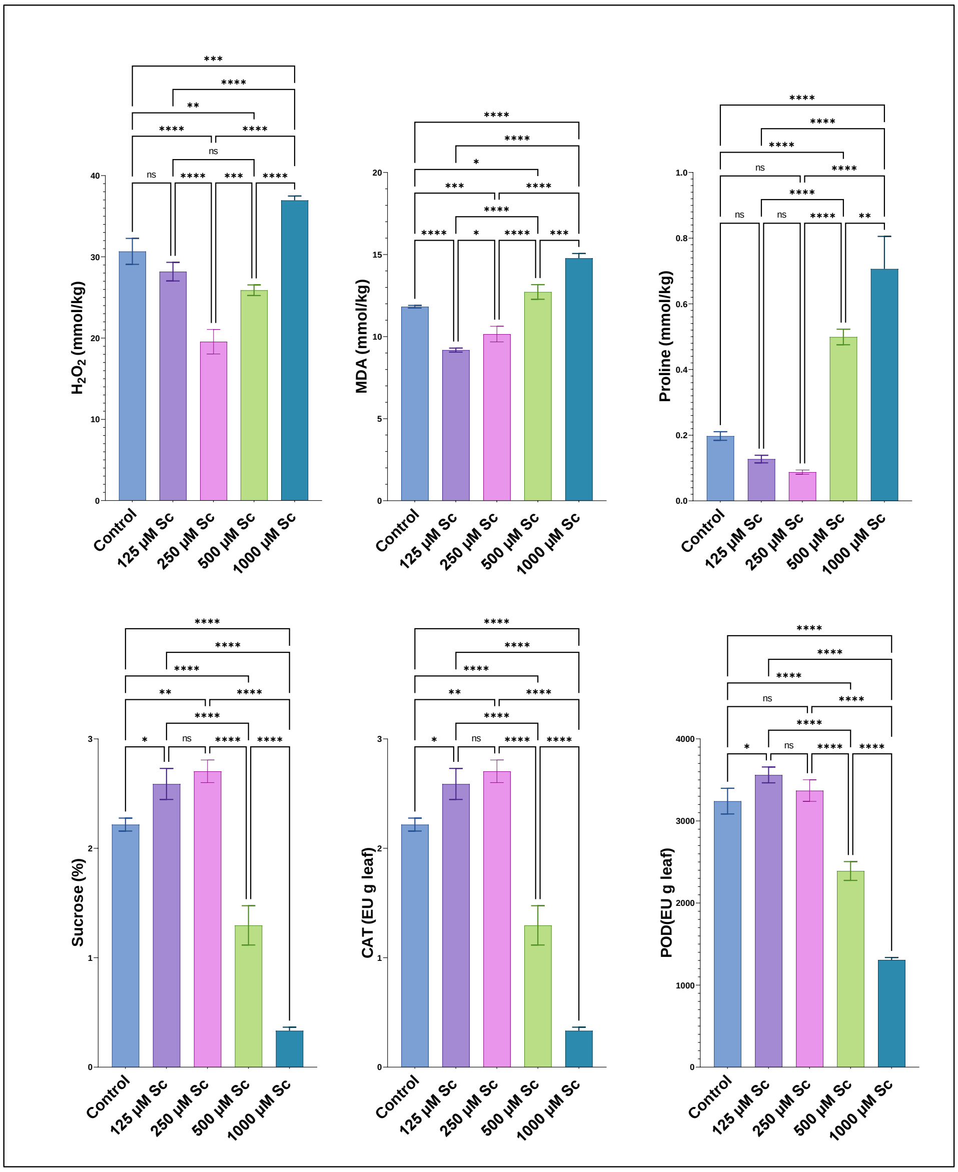

Figure 1. Effect of different concentrations of SC treatments (125, 250, 500, and 1000 µM) on H2O2, MDA, proline, sucrose, catalase (CAT), and peroxidase (POD) levels in plant tissues. Control group (blue) was compared with treatment groups at varying concentrations (purple, pink, green, and dark blue). Significance levels: p<0.05 (), p<0.01 (), p<0.001 (), p<0.0001 (****); ns: no significant difference.

The effect of Sc treatment on H2O2 content in pepper seedlings is shown in Figure 1. In the control group, H2O2 content was measured at ~4 mmol/kg. Treatment with 125 µM Sc showed a significant increase compared to the control group (~5 mmol/kg, ***$p < 0.001$). At 250 µM Sc, H2O2 content remained at a similar level (~5 mmol/kg, ns). However, 500 µM Sc significantly increased H2O2 content (~6 mmol/kg, ****$p < 0.0001$), and the highest level was observed at 1000 µM Sc (~7 mmol/kg, ****$p < 0.0001$).

MDA content; ın the control group, MDA content was measured at the lowest level (~2 mmol/kg). Treatments with 125 µM and 250 µM Sc led to statistically significant increases (~3 mmol/kg, **$p < 0.01$; ~4 mmol/kg, ****$p < 0.0001$, respectively). The highest MDA content was observed at 1000 µM Sc (~6 mmol/kg, ****$p < 0.0001$)(Fig.1).

The proline content; ın the control group, proline content was the lowest (~1 mmol/kg). A slight increase was observed at 125 µM and 250 µM Sc (~2 mmol/kg, ns). However, at 500 µM Sc, proline content showed a significant increase (~4 mmol/kg, ***$p <0.001$), and the highest level was recorded at 1000 µM Sc (~6 mmol/kg, ****$p <0.0001$) (Fig.1).

The control group exhibited a sucrose content of ~5%. A notable increase was observed at 250 µM Sc, where sucrose reached its peak (~7%, ****$p <0.0001$). At higher concentrations (500 and 1000 µM Sc), sucrose content decreased significantly (~4%, ****$p <0.0001$) (Fig.1).

The control group showed CAT activity at ~2 EU/g leaf. Treatments with 125 µM and 250 µM Sc resulted in moderate increases (~3 EU/g leaf, **$p < 0.01$; ~4 EU/g leaf, ***$p < 0.001$, respectively). The highest CAT activity was observed at 1000 µM Sc (~6 EU/g leaf, ****$p < 0.0001$)(Fig.1).

The control group recorded the lowest POD activity (~1.5 EU/g leaf). Treatment with 125 µM Sc showed the highest POD activity (~4 EU/g leaf, ****$p < 0.0001$). However, higher concentrations (250–1000 µM Sc) resulted in a gradual decline in POD activity (~3 EU/g leaf, ****$p < 0.0001$ for all comparisons)(Fig.1).

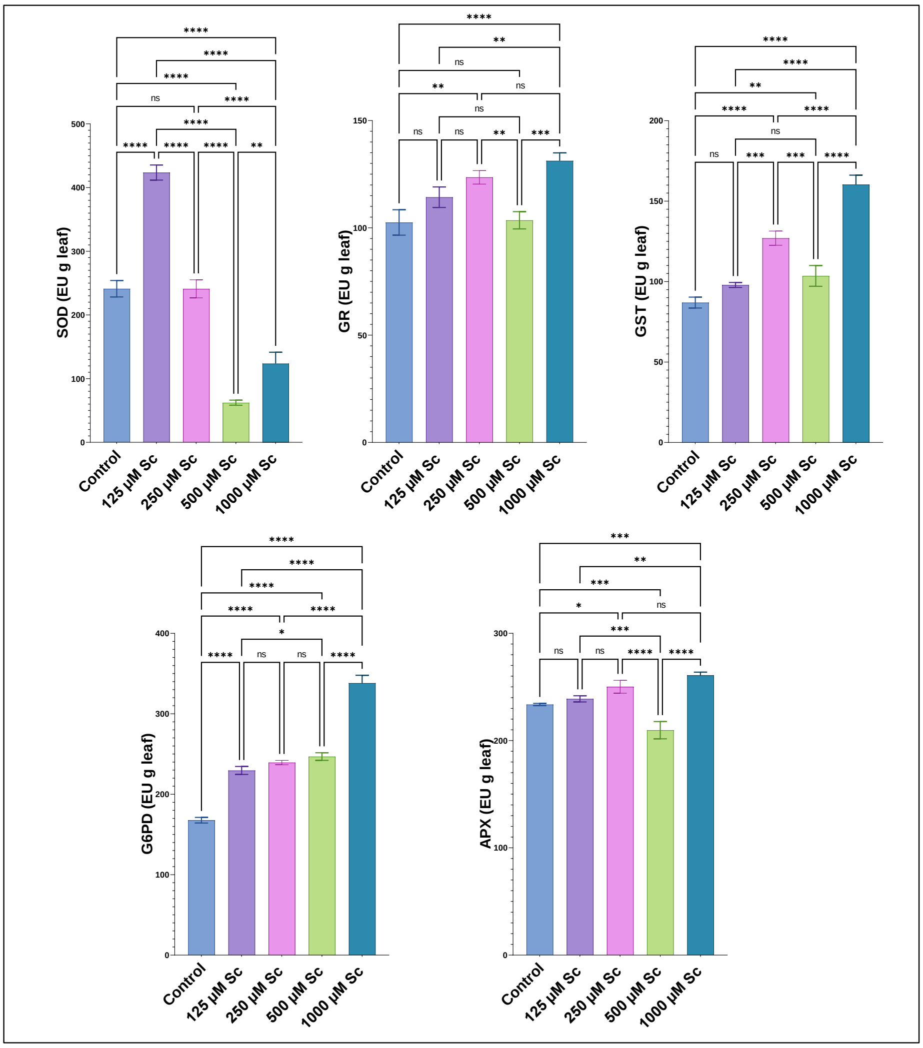

Figure 2. Effect of different concentrations of SC treatments (125, 250, 500, and 1000 µM) on SOD, GR, GST, G6PD, and APX enzyme activities in plant tissues. Control group (blue) was compared with treatment groups at varying concentrations (purple, pink, green, and dark blue). Significance levels: p<0.05 (), *p<0.01 ()*, p<0.001 (), p<0.0001 (****); ns: no significant difference.

In the control group, SOD activity was measured at ~50 EU/g leaf. Treatment with 125 µM Sc significantly increased SOD activity (~150 EU/g leaf, **p <0.01). The highest level was observed at 250 µM Sc (~250 EU/g leaf, ****p <0.0001), while further increases in Sc concentration led to reduced SOD activity (~100 EU/g leaf at 1000 µM Sc, ****p <0.0001) (Fig. 2).

The control group showed GR activity at ~2 EU/g leaf. GR activity steadily increased with Sc treatments, reaching its peak at 1000 µM Sc (~6 EU/g leaf, ****p < 0.0001)(Fig. 2).

The control group exhibited the lowest GST activity (~100 EU/g leaf). GST activity increased significantly at all Sc concentrations, with the highest level recorded at 1000 µM Sc (~300 EU/g leaf, ****p < 0.0001)(Fig. 2).

G6PD activity in the control group was ~100 EU/g leaf. Significant increases were observed at 500 µM Sc (~250 EU/g leaf, ****$p < 0.0001$) and 1000 µM Sc (~300 EU/g leaf, ****$p < 0.0001$)(Fig. 2).

In the control group, APX activity was ~50 EU/g leaf. Treatment with 500 µM Sc significantly increased APX activity (~150 EU/g leaf, ***$p < 0.001$), while the highest level was recorded at 1000 µM Sc (~200 EU/g leaf, ****$p < 0.0001$) (Fig. 2).

The observed increase in antioxidant enzyme activities, such as CAT, GR, GST, G6PD, and APX, at higher Sc concentrations (1000 µM) indicates a robust activation of the antioxidant defense system. This activation is crucial for mitigating oxidative stress caused by the accumulation of ROS under Sc treatment. Similar findings were reported by Kaur et al. (2024), who emphasized the biphasic effects of REEs on plant physiology, with low concentrations promoting antioxidant activity and higher doses triggering stress responses.

The peak activities of POD and SOD at lower concentrations (125 µM) suggest that moderate Sc levels can enhance ROS-scavenging efficiency without inducing significant oxidative damage. This is consistent with the hormetic effects of REEs, as described by He et al. (2022), where low doses stimulate beneficial stress responses while higher doses may lead to toxicity.

The highest levels of proline and MDA at 1000 µM Sc suggest enhanced osmoprotectant accumulation and lipid peroxidation under severe oxidative stress. Proline acts as a stabilizer for membranes and proteins, aiding in stress adaptation, as highlighted in studies on Sc-treated plants (Ramos et al. 2016). However, increased MDA levels indicate that excessive Sc concentrations may also exacerbate lipid membrane damage, reflecting the dual role of Sc in stress regulation.

The maximum sucrose content recorded at 250 µM Sc points to metabolic adjustments that enhance energy storage and stress adaptation at optimal Sc concentrations. This aligns with findings by Liu et al. (2021), who observed improved metabolic efficiency in plants exposed to low-to-moderate levels of REEs.

In a study by Alp et al. 2023, it was reported that Sc increased SOD, APX, GR, GST, monodehydroascorbate reductase (MDHAR) and NADPH oxidase (NOX) activities by reducing Cr-induced oxidative damage in *Lemna minor*. However, in all treatment groups, high H2O2 content and retention of ROS causing lipid peroxidation were effectively eliminate.

In a study investigating the effect of Sc application on Oryza sativa L. under salt and drought stress, it was reported that Sc application to NaCl-treated rice increased SOD, APX, GR, MDHAR and dehydroascorbate reductase (DHAR) and peroxidase (POX). Although Sc increased the activity of MDHAR and DHAR enzymes when combined with PEG, it did not increase APX activity and therefore did not fully maintain the redox balance of AsA (ascorbate). However, the GSH pool could be replenished by induction of DHAR and GR enzymes in this group. In rice plants subjected to NaCl and PEG stress, Sc treatment increased APX and MDHAR activities, especially at a concentration of 25 µM. Thanks to Sc's enhancement of antioxidant enzyme activities, the H2O2 and TBARS (an indicator of lipid peroxidation) content under stress conditions was significantly reduced (Elbasan et al. 2020).

These results underscore the potential of scandium as a modulator of antioxidant defense and stress tolerance in plants. However, the concentration-dependent effects highlight the importance of precise dosage management to avoid oxidative damage. Future research should focus on elucidating the molecular mechanisms underlying Sc-induced stress responses and its long-term effects on plant growth and productivity

Conclusion

This study demonstrates the dose-dependent effects of scandium (Sc) on biochemical and physiological parameters in Capsicum annuum L. seedlings. Low to moderate concentrations of Sc (125-250 µM) increased stress tolerance by stimulating antioxidant enzyme activities and improving metabolic balance. High Sc concentrations (1000 µM) induced oxidative stress, as indicated by high H2O2 and MDA levels, but also triggered antioxidant defense mechanisms to counteract this stress. Furthermore, sucrose content peaked at 250 µM Sc, indicating a positive effect on energy metabolism, while proline accumulation at 1000 µM suggests its role in osmotic adjustment under stress conditions. These results emphasize the dual effects of scandium on plants, providing potential benefits at optimal doses, while carrying a risk of toxicity at higher concentrations. This study provides valuable insights into the physiological roles of scandium and highlights the importance of dose optimization for agricultural applications. Future research should focus on understanding the long-term effects and exploring scandium utilization in various plant species under different environmental stress conditions.

Funding

This research was not financially supported by any institution.

Statement of Conflict of Interest

The authors declare no competing interests

Authors' Contributions

Esra YAPRAK prepared the manuscript. Sümeyra UÇAR, Merve YÜCE, and Metin TURAN conducted laboratory experiments and collected data. This manuscript was proofread by Ertan YILDIRIM and Murat AYDIN. All authors approved the final form of the manuscript.

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International Conference on
Food, Agriculture and Animal Sciences
19-22 December 2024, Erzurum, TÜRKİYE

Reproductive Characteristics of Rainbow Trout (*Oncorhynchus mykiss*) and the Effects of Two Different Commercial Feeds on the Growth of Their Fry

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ABSTRACT: In this study, the incubation period for these eggs was found to be 36 days, with a hatching rate of 93.37%. Rainbow trout that had consumed their yolk sacs were fed with commercial feeds of brands A and B for 90 days. The condition factor was determined as 0.96 and 0.99 for feeds A and B, respectively, while the organ index was 8.68 and 9.24, respectively. Among the growth parameters, the specific growth rate was determined to be 2.76 for feed A and 2.59 for feed B, and the feed conversion ratio was 0.99 for feed A and 1.15 for feed B. During the experiment, the weight gain in the group fed with feed A increased from 0.83 g to 9.87 g at the end of 90 days, while in the group fed with feed B, it increased from 0.83 g to 8.93 g. The hepatosomatic index values were calculated as 1.03 for feed A and 0.78 for feed B. At the end of the study, the weight-specific growth values were determined to be 215.46 and 196.79 for the groups fed with feeds A and B, respectively ($p<0.05$).

Keywords: Rainbow Trout, Growth Parameters, Hatching Rate

INTRODUCTION

The rapid increase in the world population has necessitated a corresponding rise in food production. With terrestrial food resources reaching their upper production limits, humanity's focus has shifted to aquatic resources. From past to present, aquatic products have played a significant role in meeting human nutritional needs. The production of aquatic products can be categorized into two main areas: fishing and aquaculture (Şahin, 2004). Over the past 30 years, the production of aquatic products has shown significant advancements under the term aquaculture. Aquaculture has been reported by FAO as the fastest-growing food sector worldwide (Vannuccini, 2004). The recent decline in fish stocks has accelerated efforts to increase product diversity in aquaculture. There are various trout species being farmed globally and in our country, including rainbow trout (*Oncorhynchus mykiss*), and others under domestication studies such as the Black Sea trout (*Salmo trutta labrax*), brook trout (*Salvelinus fontinalis*), and brown trout (*Salmo trutta fario*) (Çelikkale, 1994; Çakmak et al., 2007; Kocaman et al., 2009). The success of introducing new species into aquaculture depends on the incubation stage, and success during this period is closely linked to egg quality. High-quality eggs positively influence the hatching rate, incubation performance, and efficiency of the incubation process (Güner and Tekinay, 2002). Feed quality is one of the most critical factors influencing success in aquaculture. The primary goal in fish nutrition is to prepare feed mixtures that meet the needs of the fish and ensure significant live weight gain (Lovell, 1989).

In this study, the hatching efficiency of rainbow trout (*Oncorhynchus mykiss*) eggs, the most significant species in inland waters of our country, and the growth performance of fry during the juvenile stage fed with two different commercially available feeds were evaluated.

Material and Method

In the study, the fish material consisted of 11 female and 11 male rainbow trout (*Oncorhynchus mykiss*) (Figure 1) reared at the Atatürk University Faculty of Fisheries Inland Fish Application and Research Center.

Figure 1. Female and male rainbow trout (*Oncorhynchus mykiss*) used in the fertilization process (Original image).

A total of 52,241 eggs were obtained, and the fertilized eggs were incubated in the hatching cabin (Figure 2).

Figure 2. Fertilization of trout eggs (Original image).

Table 1. Chemical composition of the A brand feed.

Chemical Composition A Feed	**%**
Crude Protein	55
Crude Lipid	18
Ash	10.5
Cellulose	0.5
Phosphorus	1.7
Calcium	2.5
Sodium	0.5

In the experiment, six trays measuring 0.50 x 0.30 x 0.25 cm were placed inside two raceway-type pools, each with dimensions of 2.0 x 0.50 x 0.40 m.

Table 2. Chemical composition of the B brand feed.

Chemical Composition B Feed	**%**
Crude Protein	55
Crude Lipid	15
Ash	10.5
Cellulose	0.9
Phosphorus	1.8
Calcium	2.5
Sodium	0.7

Total of 48,776 fry were obtained. After completing the weaning period and reaching an average weight of 0.83 g, they were divided into 2 groups with 3 replicates each for feeding trials and fed with A and B feeds (Table 1 and Table 2). Fry were randomly selected and placed in each tray, with 35 fish per tray. The daily feed amounts (as a percentage of body weight) required for trout of different weights at varying water temperatures were provided six times a day for a period of ninety days. Growth parameters;

The condition factor was determined using the formula below (Lagler, 1956; Ricker, 1975; Bagenal and Tesch, 1978).

$$K=(W/FL^3)\times 100$$

The following formula was used to obtain the hepatosomatic index value (Cheng et al., 2005):

$$\text{Hepatosomatic Index (HSI)} = (\text{Liver Weight}) / (\text{Total Body Weight}) \times 100$$

The following formula was used to obtain the viscerosomatic index value (Cheng et al., 2005)

$$\text{Viscerosomatic Index (VSI)} = (\text{Total Weight of All Internal Organs}) / (\text{Total Body Weight}) \times 100$$

Live weight gain was calculated using the formula below (Boylu, 2014).

$$\text{Weight Gain (LWG)} = Wt - (Wt\text{-}1)$$

Weight-specific growth was calculated using the formula below (Korkut et al., 2007).

$$\text{Weight-Specific Growth (WSG)} = [(\text{Ln } Wt - \text{Ln } Wt\text{-}1) / t] \times 100$$

Feed conversion ratio was calculated using the formula below.

$$\text{Feed Conversion Ratio (FCR)} = \text{Feed Consumed (g)} / [\text{Final Live Weight (g)} - \text{Initial Live Weight (g)}]$$

$$\text{Specific Growth Rate (SGR), \%} = \{[\text{Ln (Final Weight)} - \text{Ln (Initial Weight)}] / \text{Duration of Experiment}\} \times 100.$$

$$\text{Weight Relative Growth (WRG): } [(Wt - Wt\text{-}1) / Wt\text{-}1] \times 100.$$

$$\text{Survival Rate (SR)} = (Nt / Nt\text{-}1) \times 100.$$

The data obtained in the study were analyzed using the Student's t-test in the SPSS 18 software package. The means of significantly different variation sources were compared using the DUNCAN multiple comparison test.

Results and Discussion

At the end of the 90-day feeding trial, the condition factor of rainbow trout (*Oncorhynchus mykiss*) was calculated as 0.96 and 0.99 for feed types A and B, respectively, and the difference between the groups was not found to be statistically significant (Table 3). Brannon (1991) reported that the condition factor for newly feeding trout fry is 0.95, indicating that as fish gain weight, feed utilization efficiency increases, and this value rises to 1.2 or 1.3 as weight increases. A condition factor close to 1 under good feeding conditions is considered ideal (Martinez et al., 2001). Similarly, Tunçelli and Memiş (2024) found it to range between 1.16 and 1.38.

Table 3. Condition Factor (K)

Groups	The Condition Factor ^{NS}
	Mean / Standard Error
A Feed	0.96±0.03
B Feed	0.99±0.02

NS: Not significant

The hepatosomatic index (HSI) values were calculated as 1.03 and 0.78 for feeds A and B, respectively. This difference was not found to be statistically significant (Table 4). The variation in HSI values between the groups can be associated with the high lipid content in the liver (Cheng et al., 2005). Marjanović et al. (2024) reported HSI values ranging from 2.28 to 2.68 and stated that, unlike our results, the feed composition had a significant impact on these values.

Table 4. Hepatosomatic Index (HSI)

Groups	Hepatosomatic Index (HSI) ^{NS}
	Mean / Standard Error
A Feed	1.03±0.05
B Feed	0.8±0.04

NS: Not significant

The viscerosomatic index (VSI) results were calculated as 8.68 and 9.24 for rainbow trout fed with feeds A and B, respectively. This difference was not found to be statistically significant (Table 5). Morteza Yousefi et al. (2024) reported VSI values ranging from 6.40 to 7.88 and stated, unlike our results, that these values were significantly affected by feed composition and additives.

Table 5. Viscerosomatic Index (VSI)

Groups	Viscerosomatic Index (VSI) ^{NS}
	Mean / Standard Error
A Feed	8.68±0.21
B Feed	9.24±0.33

NS: Not significant

During the trial period, the live weight increased from 0.83 g to 9.87 g in the group fed with feed A and to 8.93 g in the group fed with feed B. The group, as a main source of variation, was determined to be statistically insignificant for live weight gain (Table 6). Anderson et al. (2024) reported that trout fry fed with commercial feed achieved weight gains ranging from 7.0 to 7.4 and, unlike our results, found this to be significantly affected.

Table 6. Weight Gain (WG)

Groups	Weight Gain (WG) ^{NS}
	Mean / Standard Error
A Feed	9.87±0.28
B Feed	8.93±0.28

NS: Not significant

Weight-Specific Growth Rate (WSGR) was determined to be statistically insignificant as a main source of variation (Table 7). To assess growth, it is necessary to relate live weight to the elapsed time (Korkut et al., 2007). Salem and Ibrahim (2024), in their study on juvenile sea bass, reported that WSGR varied based on the days and the type of feed.

Table 7. Weight-Specific Growth

Groups	Weight-Specific Growth (WSG) ^{NS}
	Mean / Standard Error
A Feed	143.72±1.49
B Feed	141.02±1.49

NS: Not significant

At the end of the study, the feed conversion ratio (FCR) was calculated as 0.99 for rainbow trout fed with feed A and 1.15 for those fed with feed B (Table 8). The difference between the groups was found to be statistically insignificant. Mahato and Paudel (2024), in their research on rainbow trout fry, similarly reported that FCR was not statistically affected.

Table 8. Feed Conversion Ratio (FCR)

Groups	Feed Conversion Ratio (FCR)^{NS}
	Mean / Standard Error
A Feed	0.99±0.05
B Feed	1.15±0.08

NS: Not significant

To determine growth, it is necessary to relate weight to the time elapsed during weight gain, and this relationship is referred to as the "Growth Rate" (Korkut et al., 2007). In the study findings, the specific growth rate (SGR) was calculated as 2.76 for rainbow trout fed with feed A and 2.59 for those fed with feed B (Table 9). The difference between the groups was not found to be statistically significant. The growth course of fish showed a decline in percent specific growth rate (SGR) with each successive stage, recording the highest value for the hatchling-fry stage (12.38%/day) and the lowest for the juvenile-adult transition (0.44%/day) (Nabi et al., 2024).

Table 9. Specific Growth Rate (SGR)

Groups	Specific Growth Rate (SGR)^{NS}
	Mean / Standard Error
A Feed	2.76±0.04
B Feed	2.59±0.09

NS: Not significant

At the end of the study, the survival rate was found to be 93.33% for rainbow trout fed with feed A and 88.57% for those fed with feed B (Table 10). No statistical difference was found between the groups. Cardona et al. (2024), in their study on trout fry, stated that survival rates could be influenced by various factors such as diet and additives.

Table 10. Survival Rate (%)

Groups	Survival Rate (%) ^{NS}
	Mean / Standard Error
A Feed	93.33±2.52
B Feed	88.57±4.95

NS: Not significant

Conclusion

At the end of the study, the average live weight gain in the groups fed with feed A increased from 0.83 g to 9.87 g over 90 days, while in the groups fed with feed B, it increased from 0.83 g to 8.93 g over the same period. The survival rate was found to be 93.33% for rainbow trout fed with feed A and 88.57% for those fed with feed B. These differences are thought to be due to the protein, lipid, and cellulose percentages in feeds A and B, as well as the composition of the compounds contributing to these percentages. Because the effects of feeds on the hatching efficiency, survival rate, and growth of trout are critical for evaluating feed performance.

In summary, feed quality plays a pivotal role in the hatching success, survival and growth of trout.

Acknowledgement

Thanks to İbrahim BİNGÖL and Muhammed Adem PİROL.

Funding

Atatürk University Scientific Research Projects Unit: Project ID: 392-PRJ2015/185*

Statement of Conflict of Interest

There is no conflict of interest.

Authors' Contributions

Corresponding author is Esat Mahmut KOCAMAN. Esat Mahmut KOCAMAN and İsmail KARADAĞ designed, analyzed the research and studies arranged by authors. Fatih KORKMAZ worked on the preparation of pictures and tables. All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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Seaweed

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ABSTRACT: Hunger and malnutrition, which have been the most fundamental problems of humanity since ancient times, continue to be important today. The rapid increase in the world population, the increase in the need for food in proportion to the great concern of famine, and the fact that humanity is faced with the threat of famine, have led to the use of new and unusual food sources and the development of existing resources. Although many alternative sources have been suggested, one of these alternative food sources is algae. In addition to being the food source of many aquatic creatures, algae are very important in terms of producing two-thirds of the photosynthetic carbon requirement of the entire world and preserving the integrity of the entire ecosystem. Seaweed is a macroalgae commonly found in the ocean and an important marine biological resource. They are sold commercially and are primarily used in the food industry, pharmaceuticals, cosmeceuticals and other related industries. Various biological activities associated with bioactive compounds obtained from seaweed have the potential to expand the value of health benefits in the food and pharmaceutical industries.

Keywords: Seaweed, Nutrition, Food, Algae

INTRODUCTION

Nutrition plays an important role in both sustaining life and regulating growth, development and physiological functions. In today's world where epidemics are on the rise, consumers' demands for healthier and more natural products are also increasing day by day. In addition, the increase in the world population, the decrease in agricultural resources and the variability of economic conditions have led to studies on the production of easy-to-grow, high-quality and natural alternative additives. Algae are one of these natural alternative additives and have a reliable consumption from the past to the present (Seyitoğlu, 2017).

Algae, which make up approximately 90-95% of marine flora and can grow in a wide variety of water sources, are organisms that can also produce food through photosynthesis (Nale, 2021). Algae are one of the most important producers in the food chain (Muştu et al., 2019).

Algae are rich in highly digestible proteins, lipids, carbohydrates, essential fatty acids, water-soluble fiber, as well as minerals such as iron, magnesium, potassium, and zinc, which are important in human nutrition. They also contain significant amounts of vitamins such as

Vitamin K, Vitamin E, riboflavin, thiamine, and niacin (Ünver Alçay et al., 2017; Diaz et al., 2023; Matin et al., 2024).

Algae are mostly eukaryotic organisms with a cellulose wall, simple structure, thallus structure that does not show real root, stem and leaf structure and can be observed in different morphologies from single-celled and filamentous microscopic forms to plants a few meters tall in terms of their external appearance. Algae, which can live in a very wide range of aquatic and semi-aquatic environments such as oceans, rivers, freshwater lakes, streams, creeks, polar lakes, puddles, etc., are autotrophic and photosynthetic organisms (Sasa et al., 2020).

Algae, one of the most important living resources of the seas, are used in food, agriculture, cosmetics, medicine, pharmacy and industry. Algae contain numerous bioactive molecules have a variety of health benefits such as antioxidant, antibacterial, antiviral, anticarcinogenic, anti-inflammatory and antiobesity effects (Aktar and Cebe, 2010; Chénais, 2021).

Algae are a heterogeneous group of organisms commonly classified according to their size as microalgae (phytoplankton) and macroalgae (seaweed-filamentous algae) (Mendes et al., 2022).

Microalgae

Microalgae are organisms with dimensions expressed in microns that do not have movement organelles, but even if they do, they can move with water movements (Ak, 2016). Products obtained from microalgae are used in many areas such as food, pharmacy, agriculture, textile, cosmetics, farming, environment (Oktor, 2018). Microalgae are an important source because they contain high-value products such as polyunsaturated fatty acids (PUFA), vitamins, pigments, high quality proteins, essential amino acids, carbohydrates, lipids, minerals, polysaccharides, phycobiliproteins, phytotoxins and carotenoids (Uzuner and Haznedar, 2020).

There are more than fifty thousand species of microalgae, only a small part of which has been well studied and classified. Bioactive peptides produced from microalgae proteins have been shown to have anticancer, antihypertensive, anticoagulant, antioxidative, antineoplastic, hypolipidemic, hepatoprotective and immunomodulatory activities (Öksüz and Alkan, 2024).

Microalgae play an important role as a food source, especially for marine aquaculture (Şirinyıldız and Yorulmaz, 2022). In aquaculture, microalgae are used as pigment sources in the cultivation of trout, shrimp, ornamental fish and salmon, and in addition to their coloring properties, they are important for increasing the survival rate and rapid development of fish. (Duru and Kargın Yılmaz, 2013).

Macroalgae

Macroalgae, known as seaweeds, are aquatic plants that are commonly distributed along the coast or in the benthic zone. Macroalgae differ from other marine plants, such as seagrasses and marine mangroves, in that they lack leaves, roots, stems, branches, flowers, and vascular bundles. Seaweeds have been recognized since World War II for their potential bioactive compounds that benefit humanity. A wide variety of forms and species of seaweeds are present in coastal areas around the world, especially in Japan, the Philippines, Malaysia, Singapore, Thailand, the United States, Australia, India, and European countries with long coastlines (Torun and Konuklugil, 2020).

Macroalgae have more than 1200 species and are widely found in marine environments and freshwater (Guo et al., 2022). Seaweeds are one of the main components of primary biomass production in coastal marine ecosystems and play essential ecological roles as habitat and substrate for invertebrates, fish, mammals and birds (Rebours et al., 2014). Macroalgae are organisms that provide nutrition, shelter and reproduction for living things, ranging in length from 1-2 cm to 40-50 m. They are classified as brown (Phaeophyceae), red (Rhodophyceae) and green (Chlorophyceae) algae according to the pigments they contain (İrkin, 2020; Choudhary et al., 2021).

Macroalgae are used in food, agriculture, cosmetics, medicine, pharmaceutical and energy industries (Figure 1) (Rahikainen et al., 2021). Macroalgae are rich in protein, lipids, unsaturated fatty acids, vitamins and various bioactive substances, and are one of the foods with the richest mineral content known (Polat and Polat, 2022).

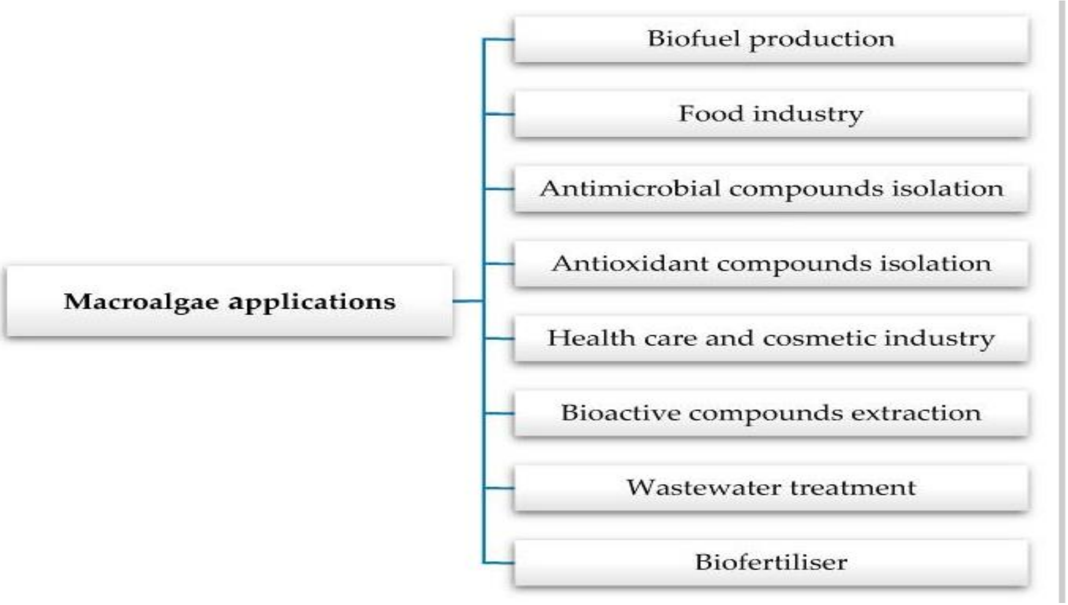

Figure 1. The main applications of macroalgae (Biris-Dorhoi et al., 2020).

Additionally, seaweed has been used as a food in many countries for decades due to its health and nutritional benefits. Seaweed contains bioactive compounds that are beneficial against various pathological conditions, including cancer, type 2 diabetes, and neurological disorders (Hyderi et al., 2024).

Funding

No financial support was received in conducting this study.

Statement of Conflict of Interest

The authors declare that there is no conflict of interest for this article.

Authors' Contributions

POY designed the study. POY, GA; Literature review; POY, GA; Article writing. Both authors read and approved the final version of the article

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International Conference on
Food, Agriculture and Animal Sciences
19-22 December 2024, Erzurum, TÜRKİYE

Optimal Smart Agriculture Technologies and Solutions in the Future of Farming

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ABSTRACT: Precision agriculture technologies have been developed and are still being developed to increase the efficiency of agricultural processes, optimize resource utilization, and support environmental sustainability. One of the most important ways to solve food shortages is the use of modern technology and the integration of artificial intelligence in agriculture to increase productivity. Smart farming uses technologies such as optical, mechanical, and electrochemical sensors; air flow and location tracking; drones; satellite imagery; artificial intelligence; and the Internet of Things to monitor, analyze and manage farm practices. Smart agricultural technologies are utilized in a wide range of areas, including pest management, weed control, plant monitoring, storage management, irrigation management, disease management and control, weather forecasting and monitoring, yield estimation, soil composition analysis, and agricultural machinery management. By utilizing real-time data and intelligent decision-making systems, smart agriculture aims to increase productivity, reduce resource waste, improve sustainability, and address the challenges posed by a growing global population. Another goal of precision agriculture technology is to automate data collection and analysis processes, enabling farmers to make more informed decisions while reducing the cost of agricultural inputs and increasing productivity. The use of digital technologies in agriculture and livestock is rapidly increasing. Smart monitoring systems enhance agricultural efficiency, whereas digital technologies improve productivity, sustainability, and effectiveness. Smart greenhouses, irrigation, and fertilization systems support agricultural sustainability by monitoring environmental and plant parameters. In this study, the opportunities, benefits, future trends, and effects of the use of precision agriculture technologies on sustainable agriculture and food production are discussed.

Keywords: Smart Agriculture, Intelligent Technologies, Machine Learning, Data Mining, Agricultural Efficiency

INTRODUCTION

Considering the limited agricultural land, lack of water, climate change and ever-changing environmental conditions, new and innovative smart agriculture solutions must be developed to meet the demand for food and agricultural products. Smart agriculture refers to the integration of technology, such as the Internet of Things (IoT), sensors, robotics, artificial intelligence, machine learning, deep learning, smart supply chains, big data analytics, cloud computing, and blockchain, into the agriculture industry (Jararweh et al., 2023). The main purpose of smart agriculture, which can generally be described as an agricultural system integrated with data analytics and machine learning, is to develop a decision-making support system for farming management. The development of precision smart farming systems significantly depends on the latest technologies, such as the Internet of Things (IoT), unmanned aerial vehicles (UAVs), augmented reality (AR) systems and machine learning (ML) algorithms (Ponnusamy and Natarajan, 2021). The smart agriculture system aims to use efficient water and resources, increase the quantity and quality of production, reduce waste, reduce human effort, increase accurate farm evaluation, improve performance, increase profitability, enhance sustainability, provide a good and acceptable product, and improve animal health. This system also optimizes the inputs of applications such as environmental conditions, growth status, soil conditions, irrigation water, pests and fertilizers, weed management, and greenhouse production, reducing costs and increasing agricultural productivity (Çakmakçı, 2022).

In smart agriculture (SA), key applications of intelligent technologies include pest management, soil and field monitoring, weed control, monitoring agricultural products, storage management, disease management and control, equipment and remote monitoring, autonomous robotics and mobile devices, satellite monitoring, weather forecasting and monitoring, smart water and irrigation management, yield prediction, soil composition and management, machinery management, and smart greenhouses. Managing the agricultural production supply chain, measuring soil variability, improving agricultural production and management, reducing resource usage, monitoring water consumption, enhancing agricultural processes, identifying agricultural risks and hazards, and optimizing decision-making are crucial application areas of agricultural technologies. The use of digital technologies in agriculture and livestock is rapidly increasing. Optical, mechanical, and electrochemical sensors, air flow, and location tracking technologies provide early warnings for diseases and pests, optimizing harvest processes. Smart monitoring systems enhance agricultural efficiency, whereas digital technologies improve productivity, sustainability, and effectiveness. Smart greenhouses, irrigation, and fertilization systems support agricultural sustainability by monitoring environmental and plant parameters.

In livestock management, environmental and body sensors improve animal health and living conditions. Machine learning algorithms are effective in detecting mating behaviors and diseases in livestock. Precision livestock systems monitor health and welfare parameters, increasing productivity and protecting animal health. Artificial intelligence (AI) and machine learning (ML) applications are effective in analyzing soil data, plant phenotyping, and carbon stock estimation. Smart irrigation systems contribute to water conservation and increased efficiency. Additionally, smart harvesting systems help achieve sustainable production with lower costs and increased productivity. These technologies enhance the sustainability of agriculture and livestock by strengthening the capacity to manage productivity and environmental impacts. This article discusses the topics mentioned above.

Smart Technologies in Precision Agriculture

Smart farming technologies have been described as modern and advanced solutions that improve the productivity of the agricultural sector, reduce costs, save time, improve the health and safety of producers, increase product quality, and reduce losses on and off the field (Collado et al., 2018). Smart farming, on the other hand, is a promising solution in urban agriculture, and farmers can monitor their crops and ensure early detection of diseases and pests so that pesticides are applied to specific target areas, thus minimizing the cost and negative impact on beneficial insects and the environment (Balyan et al., 2024). Smart agricultural technologies help sustainable agriculture by ensuring smart post-harvest management, such as cold chain monitoring, quality control, and efficient transportation, maintaining the freshness and quality of harvested products, ensuring a longer shelf life, and reducing waste.

Farmers using AI-powered smart agriculture technologies can identify areas that need irrigation, fertilization, or pesticide treatment, thereby using fewer chemicals, improving harvest quality, increasing profits, and achieving significant cost savings (Javaid et al., 2023). In agricultural terms, machine learning and artificial intelligence can be used primarily in crop management areas, such as yield prediction, weed, disease, nitrogen, and water stress detection, detection and classification of crop quality characteristics, and identification and classification of plant species (Çakmakçı, 2022). Smart farming technologies improve the overall health of the farming system, reduce the challenges faced by farmers and significantly reduce their dependence on fertilizers and chemicals (Chicaiza et al., 2024). Precision agriculture technologies improve the productivity, resilience, and environmental performance of farms (Gebresenbet et al., 2023), provide greater economic stability and better livelihoods for smallholder producers (Chandra and Collis, 2021), and support climate change mitigation and biodiversity enhancement through environmentally sustainable practices (Javaid et al., 2023; Gebresenbet et al., 2023).

Precision agriculture (PA) technologies are utilized in a wide range of areas, including pest management, plant monitoring, storage management, irrigation management, yield estimation, soil composition analysis, and agricultural machinery management. These technologies have been developed to increase the efficiency of agricultural processes, optimize resource utilization, and support environmental sustainability.

Another key objective of precision agriculture technologies is to reduce the cost of agricultural inputs and ensure the sustainability of agricultural production by increasing productivity. In this context, smart systems used in agriculture automate data collection and analysis processes, enabling farmers to make more informed decisions. In the future, by expanding IoT and sensor networks in agriculture, farmers can make data-driven decisions with real-time insights into crops, leading to increased efficiency and productivity, resource savings and improved overall sustainability (Balyan et al., 2024).

Plant Monitoring

To meet the demand for food and raw materials and to increase productivity in a sustainable manner, the optimization of crop management from planting to product distribution is essential. In this respect, automatic monitoring systems are an important step in the smart digital agriculture concept that enables farmers to make and implement fast and accurate decisions at the right time (Çakmakçı and Çakmakçı, 2023). The use of various types of sensors, such as optical, mechanical, and electrochemical sensors, enables the monitoring of plant growth. Sensors can provide images for farmers to make accurate and more informed decisions at the appropriate time and for early warning of disease and pests, whereas smart monitoring provides the ability to optimize harvest, monitor crop quality traits and increase revenue (Goedde et al., 2020). IoT sensors placed in fields wirelessly collect and transmit data such as pH levels, soil and crop nutrient levels, moisture content, and temperature to a central system. Using these data, decisions can be made about soil parameters, soil fertility, plant health, crop rotation, and disease prevention, and quality food can be produced with the right time and amount of fertilizer application, such as sulfur, liming, nitrogen, and phosphorus (Cadavid et al., 2018; Kumar et al., 2024). This approach can optimize resource use and enable informed decisions about crop management on the basis of data, reduce input use, improve growth and food quality, reduce costs, and promote environmentally friendly practices (Monteiro et al., 2021; Kumar et al., 2024). Unmanned aerial vehicles and IoT-based smart farming help reduce crop waste by adapting better field monitoring, accurate data acquisition, and data processing (Islam et al., 2021).

Weather forecasting, irrigation, the agricultural supply chain, soil management, pest protection, weed protection, intelligent spraying, decision-making, harvesting, and warehousing are important among the parameters monitored by artificial intelligence in agriculture (Javaid et al., 2023). The use of remote sensing for agriculture has recently started, and it can provide comprehensive information about biomass and yield and monitor stress factors and rotations. With the use of remote sensing and monitoring technologies, water quality can be evaluated (Gholizadeh et al. 2016), soil maps can be captured at medium resolution (Gómez et al., 2016), biological diversity can be monitored, and species-specific data can be captured (Hodgson et al., 2018).

Image recognition and sensor technologies allow farmers to make timely and informed decisions for the early detection of diseases and pests. Additionally, artificial intelligence (AI) and machine learning (ML) algorithms are used in plant yield predictions. These technologies facilitate better management of agricultural processes and optimize plant health, resulting in increased efficiency and cost savings.

Unmanned aerial vehicles (UAVs) are also widely used to monitor plant growth and optimize agricultural practices such as irrigation and fertilization. UAVs provide high-resolution imaging for precision agriculture, allowing real-time monitoring of plant growth and enabling rapid intervention when needed. Furthermore, UAVs integrated with sensors play a significant role in determining plant stress conditions, water, and nutrient needs.

Animal Monitoring

Smart animal monitoring generally covers applications such as health monitoring, welfare monitoring, remote monitoring, behavioral monitoring, safety monitoring, activity monitoring and real-time monitoring. Smart farming systems use monitoring, GPS-based animal care, robotic milking, feeding, and watering, smart health collars, and predictive disease control innovations to improve livestock productivity, sustainability, and animal welfare (Dayoub et al., 2024). Smart animal monitoring and control involves a variety of devices, including tracking collars for location, wearables, environmental controls, remote sensors, automated feeding systems, animal trackers, behavior sensors, robotic management, and cloud-based management. These systems increase farm efficiency, productivity, and sustainability (Alabdali et al., 2023; Dayoub et al., 2024). In large-scale livestock management, body and environmental sensors are used to monitor the health and living conditions of animals. Animal welfare and living conditions can be optimized when data such as body temperature, movement patterns, feeding behavior, environmental conditions, location, activity level, and heart rate captured by sensor technologies covering wearable devices and environmental monitoring systems are combined with AI algorithms (Neethirajan, 2020, 2024; Mishra and Sharma, 2023). Body sensors and environmental sensors can monitor temperature and water consumption, prevent disease and epidemics, detect hazards, and adjust weather and heat in barns to improve living conditions (Çakmakçı and Çakmakçı, 2023). The integration and adoption of sensor technologies and artificial intelligence in livestock farming are critical in the evolution of animal husbandry and the improvement of animal welfare. IoT-enabled monitoring tools contribute to more efficient resource sharing and management (Alshehri, 2023) and enable farms to make appropriate decisions regarding food plans, grazing land management and pesticide applications (Kumar et al., 2024). Smart animal monitoring technologies benefit conservation efforts, shape the animal care environment and revolutionize animal welfare.

Machine learning algorithms analyze animal behavior and health status, providing insights for farmers that increase animal welfare. This, in turn, increases animal productivity and allows for early intervention in health issues (Neethirajan, 2024). The integration of smart devices and artificial intelligence contributes significantly to monitoring and improving animal health, as evident in early disease detection (Alipio and Villena,2023). Smart animal monitoring and sensing technologies are rapidly developing, enabling animal feeding programs to be improved (Ruuska et al., 2016), animal health to be monitored, and animal welfare to be assessed and improved by regulating medication administration (Singh et al., 2022; Jiang et al., 2023). Smart technologies are used to monitor the drinking and feeding behavior, health status, and environmental impact of cattle and to control the productivity, health, and welfare parameters of the animals (Çakmakçı, 2022). Smart farming technologies help to identify the locations where animals graze in open areas within large stables, as well as help to measure the status of ventilation and air quality on farms and detect harmful gases from excrement (Islam et al., 2021). Digital technologies can reduce diseases and crises in livestock farming, analyze animal welfare and provide information on animal behavior, changes in housing conditions, the impact of climate change on animals, animal health, welfare, reproduction and performance data and animal management (Gebresenbet et al., 2023).

Additionally, animal monitoring technologies contribute to increased automation in farm management and maximization of efficiency. Continuous monitoring of temperature, heart rate, mobility, and other biometric data improves both productivity and animal health. Smart animal monitoring systems are crucial, particularly for the management of large herds, and enable the development of early warning systems to prevent disease outbreaks. The continuous monitoring of animals' temperature, heart rate, mobility, and other biometric data enhances both productivity and animal health. Smart animal monitoring systems are particularly vital for managing large herds and enable the development of early warning systems to prevent the spread of diseases.

Plant Phenotyping and Natural Resource Monitoring

Artificial intelligence (AI) and machine learning (ML) techniques are used in important processes such as soil analysis, plant phenotyping, and carbon stock estimation via satellite images and spectroscopic data. AI and advanced computer-based technologies in agriculture are changing the agricultural industry; improving crop quality, yield detection, and weed identification; enhancing agricultural productivity; and real-time monitoring, harvesting, and processing (Balyan et al., 2024). In recent years, advances in the field of plant phenomics have made precision farming more possible, and AI features have been integrated into imaging methods, increasing the efficiency of data collection and analysis. Pphenomic data management is based on the development of models for the relationships between genotype and phenotype and the interactions in the environment, the management of databases for the exchange of information and resources, and the development of programs to transform sensory data into phenotypic information.

Sustainable crop production depends on field phenotyping, and AI-assisted crop phenotyping and yield predictions can improve crop phenotyping (Bang et al., 2020; Yang et al., 2020; Nabwire et al., 2021; Song et al., 2021; Kumar et al., 2022). Phenotyping platforms have been proven to be successful in identifying plant growth stages in wheat and maize (Yang et al., 2020), segmenting plant images (Bang et al., 2020), segmenting plants and weeds (Kumar et al., 2022), phenotyping crop disease resistance (Song et al., 2021), and increasing crop productivity (Selvaraj et al., 2020). Researchers have emphasized that with the use of remote sensing and monitoring technologies, biological diversity can be monitored, and species-specific data can be captured (Hodgson et al., 2018). Aerial remote sensing and monitoring technologies increase the effectiveness of high-resolution mapping, wildlife counting and biodiversity monitoring (Çakmakçı, 2022).

These technologies contribute to making agricultural production processes more efficient and environmentally friendly, supporting the sustainable use of natural resources. By analyzing the physiological and morphological characteristics of plants, plant phenotyping enables genetic improvements in agricultural production.

Real-time monitoring of large agricultural areas using satellite images and spectral analysis methods allows for the assessment of plant health and yield potential. These analyses support the efficient use of natural resources and enhance environmental sustainability. Applications such as soil health indicator estimation and carbon stock management are highly important for minimizing the environmental impact of agricultural production.

Control and Optimization

Control in IoT-based smart agriculture is the result of active monitoring in an automated system, where the monitored variables are automatically adjusted to predefined thresholds (Islam et al., 2021). AI-based autonomous systems and monitoring based sensors such as temperature, pH, humidity, wind speed trackers, cameras, lights, NPK, light-dependent resistors, floods and soil moisture enable the automation of applications such as irrigation, fertilization, and pest control in agricultural greenhouses (Kumar et al., 2024). The opportunities offered by IoT can reduce farming risk, optimize processes and build a more stable food chain, increasing efficiency, productivity and sustainability. In smart irrigation systems, moisture and soil temperature can be used to control irrigation (Goap et al., 2018), whereas sensors installed on tractors and UAVs can be used to control variable rates of nutrition, fertilization and site-specific weed control technologies (Villa-Henriksen et al., 2020). Forecasting plays an important role in farm management and control, thus increasing stability, productivity, and measurement accuracy, and by predicting drought and nutritional conditions, irrigation and plant nutrition can be activated, thus reducing yield losses and enabling resource use.

These systems are an essential part of sustainable agricultural practices, aiming to optimize pesticide and herbicide use to minimize environmental impact. Additionally, advanced sensing and data analytics capabilities allow for more efficient management of agricultural inputs. Smart irrigation systems accurately determine the amount of water required by plants, ensuring the efficient and sustainable use of water resources.

As a result, water conservation is achieved, and optimal conditions for plant growth are created. Furthermore, real-time monitoring and control of environmental conditions in agricultural greenhouses make it possible to maintain optimal growth conditions for plants. These automated control systems save labor while enhancing agricultural productivity and product quality.

Harvest Systems

Intelligent modern harvesting systems using technologies such as smart sensors, robotic systems, UAVs, faster region-convolutional neural networks (R-CNNs), IoT devices, artificial intelligence and machine learning-based computer vision techniques help achieve sustainable production with more cost-efficient production, less labor and lower harvest costs, yield optimization and increased productivity (Horng et al., 2020; Zhang J. et al., 2020; Zhang, X, 2020; Sharma et al., 2021). These systems increase the efficiency of agricultural production and reduce labor costs. Automatic harvesting robots can determine when a crop is ready to be harvested, increasing output while reducing labor expenses and the time spent on the task (Balyan et al., 2024).

These systems provide a cost-effective and sustainable production process, enhancing the efficiency and profitability of agricultural operations. Robotic harvest systems determine the ripeness level of fruits and vegetables using sensors, ensuring that they are harvested at the optimal time. This helps maintain product quality and reduce waste rates. Additionally, the use of robotic systems offers significant advantages in addressing labor shortages and enables faster and more efficient execution of agricultural activities. UAVs, on the other hand, play a crucial role in identifying areas that need to be harvested by using high-resolution images and advanced algorithms.

How to Teach and Integrate These Systems for Farmers

To maximize smart farming and IoT technology efficiency, adapting solutions to local conditions, farms and specific crop characteristics is important. This requires designing flexible technological solutions for irrigation and monitoring systems according to the product and environmental conditions. Despite its potential, the widespread adoption of IoT in smart farming faces challenges, including a lack of education, technology, and financial resources; resistance to the adoption of new technologies; and a lack of knowledge among farmers (Chicaiza et al., 2024). For the spread and success of digital technologies, the adoption of new technologies, the gathering of temporal and spatial data, an interdisciplinary approach, state and private sector support, training programs and high-quality data assurance are deemed necessary (Çakmakçı and Çakmakçı, 2023). The adoption of smart farming technologies requires dealing with challenges such as managing resistance from older farmers, preventing a gap between farmers and technology providers, and addressing the high costs associated with new technologies.

Conduct hands-on training workshops to demonstrate the use of precision agriculture tools in real farming scenarios.

-Provide easy-to-use mobile applications that guide farmers step-by-step in the use of these technologies.

-Partners with local agricultural cooperatives should introduce technology gradually and provide ongoing support.

-Offer incentives or subsidies for farmers adopting precision agriculture technologies to reduce initial costs.

-Produce low-cost, suitable machinery for small and local farmers, and develop sensor-driven driverless tractors for large-scale farmers.

-Create success stories from early adopters to showcase the benefits and motivate other farmers to integrate these systems.

-Establish community-led tech hubs where farmers can access resources, share experiences, and seek expert advice on new technologies.

Conclusion

Precision agriculture technologies leverage advanced sensors, artificial intelligence, machine learning, and autonomous systems to increase efficiency, reduce costs, and ensure sustainability at every stage of agricultural processes. Plant and animal monitoring, sustainable use of natural resources, control and optimization processes, and modern harvest systems make agricultural production both efficient and environmentally friendly. These integrated approaches are crucial steps toward more sustainable and profitable agricultural production in the future. Smart agriculture will gradually develop toward improving production and efficiency, labor and cost and will provide methods and solutions that will guarantee food safety. Smart farming technologies optimize resource use, reduce labor requirements, improve agricultural management, and contribute to increased agricultural productivity, profitability and sustainability. Artificial intelligence technologies offer innovative and precise solutions to the important agricultural problems and agricultural food production bottlenecks faced by farmers, and it is clear that they will offer new opportunities for yield optimization in the future.

Statement of Conflict of Interest

The authors declare that they have no conflicts of interest.

Authors' Contributions

M.F. Çakmakçı designed this review. M.F. Çakmakçı and F.B. Günay conducted the literature investigation. M.F. Çakmakçı prepared the review. F.B. Günay and M.F. Çakmakçı worked on the writing - review & editing. All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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Investigation of Color, Total Phenolic Content, Total Flavonoid Content and Antioxidant Properties of Nori Samples Offered for Sale in Turkey

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ABSTRACT: Nori is widely cultivated as an important seafood, commonly used in sushi, soups, and salads. It is reported that nori has various pharmacological activities such as immunomodulation, anticancer, antihyperlipidemic, and antioxidative activities. For these reasons, in this study, color, total phenolic content (TPC), total flavonoid content (TFC), and antioxidant properties (DPPH, ABTS, FRAP, and CUPRAC) of nori samples from 8 different companies sold in the Turkish market were determined. For this purpose, extracts were obtained by applying two different solvents (80% methanol and purified water) and ultrasonic extraction process. The L*, a*, b*, C*, and H° values of the nori extracts analyzed in the study varied between 40.83-48.77, (-3.65)-(+0.04), 14.95-21.86, 17.85-24.30 and 59.82-94.75 respectively. Color values showed significant changes according to brand and solvent type ($p<0.01$). The amounts of TPC and TFC were found to vary between 7.12-15.08 mg GAE/g and 2.90-8.11 mg QE/g, respectively. The antioxidant activities determined by DPPH, ABTS, FRAP, and CUPRAC methods ranged between 3.18-11.38 mM TE/100 g, 1.17-12.66 mM TE/100 g, 1.57-7.61 mM TE/100 g, and 2.61-9.43 mM TE/100 g, respectively. TPC, TFC, and antioxidant properties (DPPH, ABTS, FRAP, and CUPRAC) showed significant changes according to brand and solvent type ($p<0.01$). According to the results determined in the study, it is thought that the inclusion of these nori in diet, supplements or functional foods will increase the functional properties of new products.

Keywords: Nori, Color, Phenolic Content, Flavonoid Content, Antioxidant Activity

INTRODUCTION

Seaweeds (Macroalgae) are plant-like organisms of marine origin, widely distributed in oceans and aquaculture farms worldwide. So far, more than 50,000 species of seaweed have been identified in 132 countries. The seaweed sector is one of the fastest-growing industries, with around 49 countries actively engaged in seaweed farming. Seaweeds generally are quite diverse, but they are mainly classified as Rhodophyta (red), Chlorophyta (green), and Ochrophyta (brown) according to their dominant pigmentation. Their varied chemical composition makes them useful in many industries (Rioux et al., 2017; Darko et al., 2024).

Seaweeds contain numerous nutritionally and gastronomically important components. These sea vegetables have a nutrient composition rich in fiber, minerals, proteins, vitamins, and low in lipids. They may also provide nutrients such as iron, iodine, and vitamin B12, which are typically foun in lower amounts in plant-based diets (Lafeuille et al., 2024). They also contain numerous proteins/peptides, polyphenols, and polyunsaturated fatty acids (omega-3). The polyphenol content of seaweeds can range from 4 to59 mg GAE (Gallic acid equivalent) per gram dry weight (DW). Phenolic compounds found in seaweeds have potent antioxidant activity, as well as hypotensive, cardioprotective, and neuroprotective anti-inflammatory, along with beneficial effects on gut function and microbiota. In addition, polyphenols can interact with various proteins to limit their activity. Seaweed phenolic extracts can inhibit α-amylase and/or α-glucosidase, two enzymes that regulate the glycemic index through starch digestion (Rioux et al., 2017). Seaweeds are also known to be an excellent carriers of umami taste (the fifth taste), which is considered a flavor enhancer and contains numerous volatile organic compounds that contribute tothe overall flavor through olfactory stimulation (Lafeuille et al., 2024).

In particular, their distinctive umami flavor makes them highly desirable among Asian consumers. Umami components, including various free amino acids, 5'-ribonucleotides, and umami enhancers (such as sugars, oligopeptides, organic acids, and their derivatives), are abundant in seaweeds. The harmonious interaction of these substances results in the umami flavor. Glutamic acid (Glu) and aspartic acid (Asp) are the primary contributors to the umami flavor, while glycine (Gly), alanine (Ala), and serine (Ser) provide foods with a sweet undertone. Inosine 5'-monophosphate (IMP) stands out as a prominent umami component among the 5'-ribonucleotides found in seafood. Additionally, other nucleotides, such as guanosine monophosphate (GMP), adenosine monophosphate (AMP), sugars and organic acids enhance the umami flavor (Yuan et al., 2024).

Seaweeds are processed in the food sector, either as whole or as ingredients in food products (Darko et al., 2024). In the Pacific regions (Indonesia, Philippines, New Zealand Maoris, and Hawaii) and Asian cultures (China, Japan, and Korea), seaweeds have long been consumed raw in a variety of dishes, including salads, soups, cookies, stews, and condiments (Rioux et al., 2017). Although seaweed consumption has a long-tradition in many Asian countries, it has not yet played a significant role in the Western diet. However, recent studies show a growing interest in seaweed consumption in Western countries, especially due to consumers' desire to eat healthier foods. Factors such as high nutritional and health benefits, a low carbon footprint and sustainability also play a role in this shift (Maksan et al., 2025). In addition, de Boer et al. (2013) suggested that algae-based products may play a role as 'trendsetters', with highly engaged consumers valuing authentic sources of protein, particularly algae products. Building on this, the findings of Birch et al. (2019) suggest that health-conscious consumers are more inclined to include seaweed in their diets. In addition, the migration of Asian populations worldwide has encouraged the discovery of new ingredients from seaweeds and increased the number of chefs in restaurants creating new dishes (seaweed chips, seaweed-enriched milk-based powder preparations, seaweed biscuits, seaweed instant mashed potatoes, seaweed tagliatelle, Wakame salad, and more) (Rioux et al., 2017).

Among the macroalgae traditionally consumed by Asian populations, Ulva, Laminaria, and *Porphyra* are well-known. Species such as Wakame or Kombu require cooking to overcome their chewy texture, whereas others, like Nori and sea lettuce, can be eaten raw . The utilization of seaweed as a sea vegetable usually involves drying or salting. Drying seaweed is one of the primary steps to allow transportation (Rioux et al., 2017). Two species, *Neopyropia yezoensis* and *Pyropia haitanensis*, with a rich cultivation history spanning centuries in East Asian countries, particularly China, Japan, and Korea, have emerged as commercially viable options. These species have been used as traditional food sources, especially in coastal areas where they are integral components of popular Asian dishes like nori and sushi (Yuan et al., 2024).

Porphyra sp. (nori, seaweed) is widely cultivated as an important seafood (Bito et al., 2017). Nori is generally used in sushi, soups, and salads (Akşar, 2012). It is known that the main bioactive compounds are phenolic compounds, sulfated polysaccharides and peptides. Noriis also a source of dietary fiber, essential fatty acids, vitamins, and minerals. In nori, fluorotanins have been reported to show antioxidant activity and protection against UV light (Coelho et al., 2023).

Dried nori contains numerous nutrients, including vitamin B12, the only vitamin not found in plant-based food sources. Nori also contains large amounts of iron compared to other plant-based foods and eicosapentaenoic acid, an important fatty acid found in fish oils. Nori also contains many bioactive compounds that show various pharmacological activities such as immunomodulation, anticancer, antihyperlipidemic, and antioxidative activities. This is an indication that nori consumption is beneficial for human health. However, *Porphyra* sp. contains toxic metals, such as arsenic and cadmium, and/or amphipod allergens whose levels vary significantly among nori products (Akşar, 2012; Bito et al., 2017).

The compound content of each seaweed depends on the species. However, geographical and environmental factors also play an effective role in the composition (Coelho et al., 2023). Some studies have been conducted to determine the antioxidant activity of nori (Onofrejová et al., 2010; Coelho et al., 2023). However, the studies are not sufficient. For this study, it was aimed to determine the physicochemical and antioxidant properties of eight packaged nori samples from eight companies sold in the Turkish market by four different antioxidant activity assay methods (DPPH, ABTS, FRAP, and CUPRAC) using two different solvents (80% methanol and purified water). Furthermore, according to the results reported here, it may be recommended to develop new and natural products by including these seaweeds in diet, supplements or functional foods.

Material and Method

Nori samples were purchased from 8 different companies in the Turkish market, 7 from South Korea and 1 from China. Nori samples were stored in sealed metallic bags and used for direct analysis.

Color Determination

The color values of nori samples were measured with a colorimeter (Konica Minolta CR-400, Korea). This samples color intensities were determined with a colorimeter making three-dimensional measurements in the CIE (L*, a*, b*, C*, H°) system (Şengül et al., 2023).

Extraction

Nori samples were first passed through a waring blender and turned into powder. Then, 3 g of the samples were weighed and 45 mL of pure water and 80% methanol (methanol:pure water) were added separately. Then, it was left for extraction in an ultrasonic water bath for 30 minutes. At the end of the period, the samples were taken into falcon tubes and centrifuged at 6000 rpm at 4° C for 15 minutes. Extracts were obtained by filtering the mixture through Whatman No:1 filter paper. The obtained extracts were used in TPC, TFC, DPPH, ABTS, FRAP, and CUPRAC analyses.

Total Phenolic Content (TPC)

To calculate the total phenolic content of nori samples (Şengül et al., 2023), 0.1 ml of the extracts were taken and transferred to glass tubes. Then 0.2 N 2.5 ml of FCR (Folin-Ciocalteau reagent) was added and vortex process was applied. After 3 min of waiting time, 2 ml of 7.5% sodium carbonate (Na_2CO_3) solution was added to the samples and vortexed again. The mixture was incubated for 2 hours. The absorbance values of the samples were then determined by reading at 760 nm wavelength with a spectrophotometer (PG Instruments T60V, UK). Total phenolic acid content of the samples was given as gallic acid equivalent.

Total flavonoid content (TFC)

To determine the total flavonoid content of the samples (Şengül et al., 2023), 250 µL of the extracts were taken and 1250 µL of distilled water was added and vortexed. Then 75 µL 5% $NaNO_2$ was added to the mixture and vortexed. Then the mixture was incubated for 6 min. At the end of the time, 150 µL $AlCl_3$-$6H_2O$ was added to the mixture and vortexed again and kept for 5 min. Finally, 500 µL 4% NaOH was added and vortexed. The mixture was incubated for 15 min and then read at 510 nm wavelength in a spectrophotometer (PG Instruments T60V, UK). Total flavonoid content was given as mg quercetin equivalent (QE)/100 g.

Antioxidant Assays

DPPH scavenging activity

To analyze the DPPH radical scavenging activity (Brand-Williams et al., 1995), 25 µL sample extracts were taken. 0.1 mM 2475 µL DPPH solution prepared previously was added to the samples. The samples were then vortexed and mixed homogeneously. The samples were then incubated in the dark and at room temperature for 30 min. After the end of the time, the absorbance values of the samples were read with a spectrophotometer (PG Instruments T60V, UK) at 517 nm wavelength. A calibration curve was drawn with Trolox solution prepared in the range of 5-25 micromoles. The results were calculated as mM Trolox equivalent (TE)/100 g using the equation obtained from the calibration curve.

$ABTS^+$ Scavenging Activity

ABTS (2.2́-Azino-bis (3-ethylbenzthiazoline-6-sulfonic acid) solution was prepared the night before in order to investigate the ABTS radical scavenging activity of nori extract samples. For this purpose, potassium persulfate solution was added to the ABTS solution in the dark, mixed and kept for 16 hours. The absorbance of the solution was measured with a spectrophotometer at a wavelength of 734 nm and adjusted to 0.700±0.025. 10 µl of the extracts were transferred to tubes. Then 990 µl ABTS radical was added and vortexed. The samples were then incubated in the dark for 6 minutes. At the end of the time, the absorbance values of the samples were read at a wavelength of 734 nm in a spectrophotometer (Özkan et al., 2007). A calibration curve was drawn with Trolox solution prepared in the range of 5-25 micromoles.

The results were calculated as mM Trolox equivalent (TE)/100 g using the equation obtained from the calibration curve.

Fe^{3+} Reduction Capacity (FRAP)

FRAP method was used to determine the antioxidant activity of nori extract samples. The principle of this method is based on the reduction of Fe^{3+} in the $Fe(TPTZ)^{3+}$ mixture, which is the radical used in the analysis, to the blue colored $Fe(TPTZ)_{2+}$ complex in acidic medium (Koçak et al., 2018). Determination of antioxidant activity by FRAP method was used by modifying the method proposed by Koçak et al. The solutions used in the study were prepared using the following formulations;

1- Each day, 3.1 g of sodium acetate + 16 mL of acetic acid solution was dissolved in 1 L of solution and prepared as acetate buffer (pH 3.6) in three solutions,

2- 0,156 g TPTZ (2,4,6-tripyridyl-s-triazine) dissolved in 50 mL ethanol,

3- 0.5404 g $FeCl_3{\cdot}6H_2O$+2 mL HCl (37% m/m) dissolved in 100 mL solution.

After the preparation of the solutions, 80 mL of solution 1 was taken and 8 mL of solution 2 and 8 mL of solution 3 were mixed to prepare the FRAP reagent. 0.1 mL of sample extracts were taken and 0.9 mL of FRAP reagent was added. The mixture was vortexed and kept for 4 minutes. The absorbance values of the samples were then measured at 593 nm wavelength. A calibration curve was drawn with Trolox solution prepared in the range of 5-25 micromoles. The results were calculated as mM Trolox equivalent (TE)/g using the equation obtained from the calibration curve.

Cu^{2+} Reduction Capacity (CUPRAC)

For the CUPRAC method (Apak et al., 2004), 100 µL of the extracted samples were placed in test tubes and 1000 µL distilled water was added and the tubes were vortexed. Then 1000 µL 10 mM $CuCl_2.2H_2O$ solution, 1000 µL 1 M NH_4AC solution and 1000 µL 7.5 mM $C_{14}H_{12}N_2$ solution were added to the tubes respectively. The tubes were vortexed after the addition of each solution to ensure homogeneity. The samples were incubated for 30 min in the dark and at room temperature and read against the blind at 450 nm with a spectrophotometer (PG Instruments T60V, UK). A calibration curve was drawn with Trolox solution prepared in the range of 5-25 micromoles. The results were calculated as mM Trolox equivalent (TE)/100 g using the equation obtained from the calibration curve.

Statistical Analysis

The data obtained in triplicate were analyzed with the SPSS 20.0 program. The results were expressed as mean values with standard deviation (±SD). One-way analysis of variance (ANOVA) was carried out to determine the significant group differences between the means ($p \leq 0.05$, $p \leq 0.01$). Duncan's multiple range test was used to compare mean values.

Results and Discussion

Nori samples L* (bright: 100, dark: 0), a* (red: +60, green: -60), b* (yellow: +60, blue: -60), C* (Chroma, color saturation), and H° (Hue angle) values were determined as a result of the readings, and all readings were performed on a white background at 20±2°C (Şengül et al., 2023). The color intensity analysis results of nori samples are given in Table 1. The L*, a*, b*, C*, and H° values of the nori extracts analyzed in the study varied between 40.83-48.77, (-3.65)-(+0.04), 14.95-21.86, 17.85-24.30 and 59.82-94.75 respectively. Color values showed significant changes according to brand and solvent type ($p<0.01$).

Table 1. Color values of nori samples

Brand (B)	L*	a*	b*	C*	H°
1	40.83±10.83^{d}	-0.44±10.36^{a}	21.86±13.01^{a}	24.30±11.89^{a}	77.15±32.00^{b}
2	43.38±7.73^{c}	0.04±13.63^{a}	17.73±17.19^{bcd}	24.15±12.60^{a}	59.82±55.37^{d}
3	46.33±0.73^{b}	-0.46±8.63^{a}	14.95±12.14^{d}	17.85±10.39^{c}	67.68±43.91^{c}
4	46.75±2.90^{b}	-3.65±7.24^{d}	20.63±8.53^{ab}	21.71±9.28^{ab}	94.75±17.99^{a}
5	45.59±2.04^{b}	-1.72±8.92^{b}	18.47±13.08^{bc}	20.86±11.90^{b}	75.21±39.50^{bc}
6	48.77±1.51^{a}	-2.57±5.42^{c}	17.51±4.39^{cd}	18.25±4.97^{c}	94.64±16.02^{a}
7	48.62±0.75^{a}	-3.15±7.61^{cd}	20.20±8.61^{abc}	21.37±9.26^{b}	91.34±20.21^{a}
8	41.19±10.87^{d}	-0.54±10.66^{a}	21.43±13.39^{a}	24.10±12.14^{a}	76.02±33.91^{b}
	**	**	**	**	**
Solvent type (ST)					
Water	41.21±6.92^{b}	6.69±3.42^{a}	9.00±4.53^{b}	12.34±2.16^{b}	50.44±25.33^{b}
Methanol	49.15±2.08^{a}	-9.81±1.46^{b}	29.19±4.72^{a}	30.81±4.85^{a}	108.71±1.81^{a}
	**	**	**	**	**
BXST	**	**	**	**	**

When the color intensity results of nori samples were examined according to solvent type, it was observed that the averages of L*, b*, C*, and H° values were higher in methanol extracts. a* values were higher in extracts prepared with water (Figure 1). As additional information, nori seaweed is known to represent a major source of R-phycocyanin (R-PC) as a natural food colorant because it can be grown in large quantities. However, it should be noted at this point that R-PC generally has a moderate pH stability and temperature increase above 40 °C causes a significant decrease in protein stability and color intensity (Veličković et al., 2023). The color differences between the extraction solutions in the study are thought to be caused by differences in the pH of the solutions.

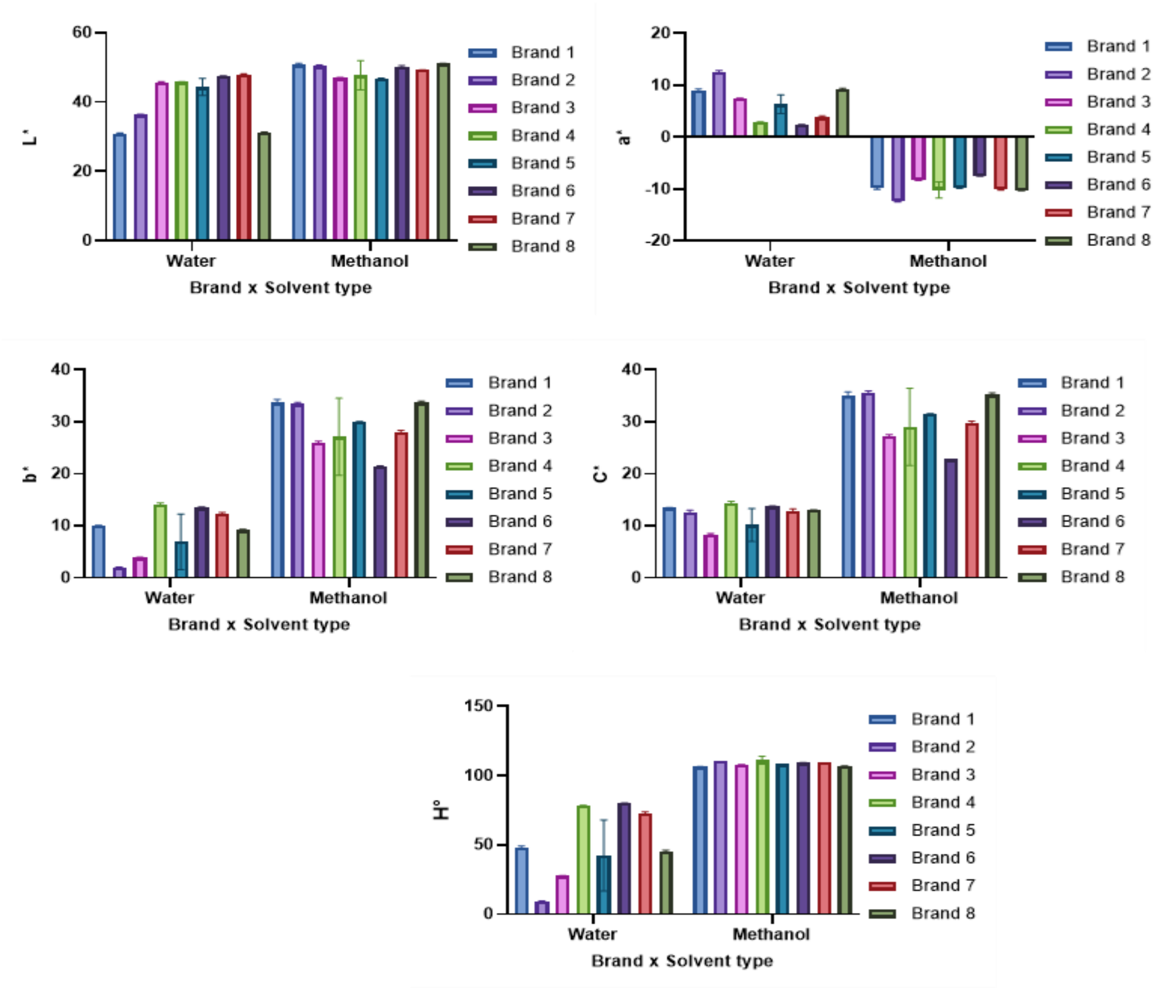

Figure 1. Change in color values of nori samples according to brand x solvent type

The results of TPC, TFC, and antioxidant activity analysis of nori samples were given in Table 2. The amounts of TPC and TFC were found to vary between 7.12-15.08 mg GAE/g and 2.90-8.11 mg QE/g, respectively. The antioxidant activities determined by DPPH, ABTS, FRAP, and CUPRAC methods ranged between 3.18-11.38 mM TE/100 g, 1.17-12.66 mM TE/100 g, 1.57-7.61 mM TE/100 g, and 2.61-9.43 mM TE/100 g, respectively. TPC, TFC, and antioxidant properties (DPPH, ABTS, FRAP, and CUPRAC) showed significant changes according to brand and solvent type ($p<0.01$). Rioux et al. (2017) reported that the polyphenol content of seaweeds can vary between 4 to 59 mg GAE /g dry weight (DW). The results obtained in the study were found to be between these values.

Table 2. TPC, TFC, and antioxidant activities (DPPH, ABTS, FRAP, and CUPRAC) of nori samples

Brand (B)	TPC	TFC	DPPH	ABTS	FRAP	CUPRAC

	(mg GAE/g)	(mg QE/g)	(mM TE/100 g)	(mM TE/100 g)	(mM TE/100g)	(mM TE/100g)
1	11.39±4.34^{e}	8.11±0.84^{a}	3.18±0.84^{h}	1.65±1.20^{e}	2.18±0.88^{de}	4.06±1.86^{e}
2	8.97±2.52^{g}	5.02±1.91^{c}	4.96±0.79^{e}	2.19±1.13^{d}	2.41±0.83^{d}	3.49±0.78^{f}
3	15.08±3.60^{a}	4.61±1.61^{d}	11.38±0.67^{a}	9.83±3.92^{b}	4.96±1.81^{c}	9.43±1.78^{a}
4	7.12±1.64^{h}	3.97±2.46^{e}	4.14±0.24^{f}	1.17±0.73^{f}	1.57±0.30^{f}	2.61±0.27^{g}
5	13.26±4.11^{c}	6.48±3.68^{b}	9.66±2.92^{d}	5.46±2.13^{c}	6.07±2.33^{b}	6.78±1.84^{c}
6	14.41±5.49^{b}	2.90±0.49^{g}	10.45±1.66^{b}	12.66±9.10^{a}	7.61±3.68^{a}	8.28±2.99^{b}
7	12.32±3.59^{d}	3.29±1.23^{f}	9.98±2.36^{c}	5.56±1.61^{c}	5.81±2.12^{b}	6.36±1.57^{d}
8	10.58±4.81^{f}	6.50±0.13^{b}	3.54±0.43^{g}	1.72±1.25^{e}	2.10±0.80^{e}	3.77±1.85^{ef}
	**	**	**	**	**	**
Solvent type (ST)						
Water	15.07±3.44^{a}	3.91±2.37^{a}	8.00±4.27^{a}	7.42±6.38^{a}	5.12±3.20^{a}	7.06±2.90^{a}
Methanol	8.21±2.00^{b}	6.31±1.86^{b}	6.33±2.60^{b}	2.64±2.12^{b}	3.06±1.85^{b}	4.14±1.97^{b}
	**	**	**	**	**	**
BXST	**	**	**	**	**	**

When the results of TPC, TFC, and antioxidant properties (DPPH, ABTS, FRAP, and CUPRAC) of nori samples were evaluated according to the solvent type, it was observed that the averages of these analysis results of nori extracts prepared with water were higher than methanol extracts (Figure 2). Here, it is thought that the changes in the compound composition due to the pH difference between the extract solutions reveal these results.

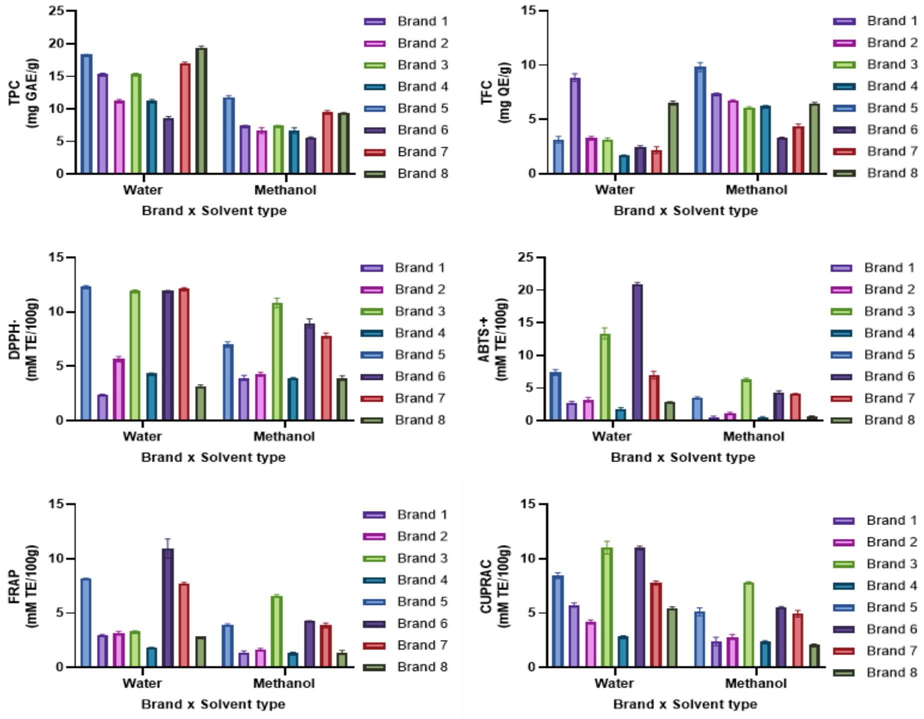

Figure 2. TPC, TFC, and antioxidant activities (DPPH, ABTS, FRAP, and CUPRAC) of nori samples by brand x solvent type

Conclusion

In general, seaweed contains a wide range of nutritional components with various functional properties that can lead to many culinary innovations. Collaboration with creative chefs in gastronomy can increase the visibility and acceptance of this resource by offering recipes or dishes created with seaweeds. Future studies linking culinary and food science could support the use of seaweed for different purposes at home, but also in food products. The results of this study show that nori seaweed extracts, due to their antioxidant properties, have a promising potential for use in the improvement of human health and management of diseases, including those associated with oxidative stress and neurodegeneration.

Acknowledgement

The authors thank the TÜBİTAK BİDEB 2211/A National PhD Scholarship Program for supporting Isa Arslan Karakutuk.

Statement of Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Authors' Contributions

Memnune ŞENGÜL and Sefa AKSOY designed and analyzed the research, İsa Arslan KARAKÜTÜK studies arranged. Melek ZOR worked on the preparation of Nursaç AKYOL KUYUCUOĞLU pictures and tables. All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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Phytochemistry and Antioxidant Activity of *Plantago ovata* Forsk. Seeds Extract

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ABSTRACT: Herbs are alternative medicines for treatment of various diseases due to their assumed acceptability, effectiveness, affordability, safety and low cost. This study aims to enhance the medicinal plants of Algeria and explore its exploitation potential. We chose the seeds of *Plantago ovata* Forsk. (Plantaginaceae), used in traditional medicine. Phytochemical analyses of the methanol extract obtained by maceration were carried out. The evaluation of the antioxidant activity was made; Phytochemical analysis of the methanol extract revealed the presence of polyphenols, flavonoids, condensed tannins and quinones. According to our study, the methanolic extract of *Plantago ovata* Forsk. seeds showed a low amount of polyphenols with a value of 4,7± 1,20 (ug EAG/mg ES), the respective contents of total flavonoids were 1,71± 0,14 ug EQ/mg ES, and that of flavones and flavonols of 15.7 ± 0.5 µg EQ/mg ES, condensed tannins were 1,25 ± 0 ugEC/mg ES . The evaluation of the antioxidant activity of the methanol extract by the DPPH and FRAP methods revealed that the seed extract has a low antioxidant activity, whereas with the phosphomolybdate test (CAT) the antioxidant activity was acceptable. These preliminary results could be used to justify the traditional use of this plant.

Keywords: Medicinal Plant, *Plantago ovata* Forsk.Seeds, Methanolic Extract, Phytochemical Analysis, Antioxidant Activity.

INTRODUCTION

Medicinal plants are considered a very important natural source for the treatment of many diseases due to their richness in secondary metabolites, in varying proportions depending on the plants and environmental conditions. According to the World Health Organization, 80% of the global population relies on traditional medicine to meet primary healthcare needs. It is estimated that at least 25% of all modern medicines are derived, directly or indirectly, from medicinal plants, mainly due to the application of modern technologies to traditional knowledge.

In this present work, we have chosen to study the seeds of *Plantago ovata* Forsk. is a plant species belonging to the family Plantaginaceae. An ethnobotanical survey conducted with 100 people revealed that the seeds of this plant are mainly used as an infusion to treat various ailments, particularly colon problems and constipation. In the Sétif region, the plant is known as "bezr elkatouna."

Material and Method

The methanolic extract of the leaves was obtained by maceration, and the phytochemical screening of *Plantago ovata* Forsk. seeds (psyllium seeds) was carried out to detect polyphenols, flavonoids, tannins, and quinones. The colorimetric determination of total polyphenols was performed using the Folin-Ciocalteu method (Singleton et al., 1999), while the determination of flavonoids, flavones, and flavonols was carried out using the aluminum trichloride method (Kosalec et al., 2004). Tannins were identified using the vanillin method (Sebai et al., 2013).

The free radical scavenging activity (DPPH test) (Sanchez-Moreno, 2002), reducing power (Oyaizu, 1986), and total antioxidant capacity (ammonium phosphomolybdate test) were evaluated using spectrophotometric methods (Umamaheswari and Chatterjee, 2007).

Results and Discussion

Phytochemical Screening

The results obtained (Table1) show that psyllium seeds contain polyphenols , flavonoids, tannins and quinones.

Phytochemical tests by Manish et al., (2016) on seeds of the same species of *Plantago ovata* showed the presence of alkaloids, tannins, terpenoids, flavonoids, saponins and glycosides.

Table 1. The different chemical groups present in the methanolic extract of *Plantago ovata* seeds.

	Secondary metabolites	Tube reaction results	Intensity of the reaction
1	Polyphenols	green color	+
2	Flavonoïds	couleur bleu /bleu violacé	+
3	Tannins	green color	+
4	Saponosides	Absence	-
5	Quinones	Red ring at the bottom	+
6	Anthraquinones	Absence	-
7	Terpenoïds	Absence	-

(+): Presence, (-): Absence

Quantitative analysis

According to our study, the metanolic extract of Plantago ovata Forsk seeds. showed a low amount of polyphenols with a value of 4.7 1.20 µg EAG/mg ES, this content is much lower than that obtained by maceration of the seeds of psyllium from India whose value is 286.8 6.05 (mg GAE/gDW) for the' ethanolic extract (Khedher et al., 2022). Similarly, our result is significantly lower than the results found by Shivanjali et al., (2018) for 14.5 0.095 and 43.8 0.092 (mg GAE/g dry wt.) for metanolic extract from envelopes and leaves of *P.ovata*. the respective total flavonoid levels were 1.71 0.14 µg EQ/mg ES, and the flavones and flavonols levels were 15.7 0.5 µg EQ/mg ES.

This result showed that the extract of *Plantago ovata* seeds contains total flavonoids. From the bibliographical data, it is clear that the total flavonoid content differs according to geographical distribution. In addition, Shivanjali et al. (2018) also estimated the content at 83.4 0.052 (mg Rutin/g dry wt.) dry weight of psyllium husks and 320.9 0.052 (mg Rutin/g dry wt.) dry weight of leaves.

In our study the content of condensed tannins in the extract is 1.25 0 µg EC/mg ES., our result is significantly lower than the results found by with Khedher et al., (2022) determined this content of tannins condensed on extracts of seeds of the same species obtained with ethanol and the same method, this content was 39.33 1.52 (mgCE/gDW).

Antioxidant activities

The crude methanolic extract was evaluated for its antioxidant activity in vitro by three different methods: free radical trapping (DPPH), ammonium phosphomolybdate (CAT) and iron reducing power (FRAP).

DPPH Radical Control Test

BHA is expressed in IC50 (µg/ml). This parameter is defined as the sample concentration required to reduce the DPPH* radical by 50% in the reaction medium. It is determined from the equation of the calibration lines representing the percentage inhibition as a function of the concentration of the dry extract (Fig. 1). The radical control activity is inversely proportional to the IC50 value.

The results show that the extracts of seeds of *P. ovata* species. Weakly trap DPPH* free radicals with an IC50 of 204.53 µg/ml.

This activity is much lower than that of the standard BHA, which is 4.29µg/ml (Fig. 2).

In another study, the IC50 of methanolic extract from envelopes and leaves of P.ovata was 133.74 µg/ml and 13. 65 µg/ml respectively (Shivanjali et al.,2018).

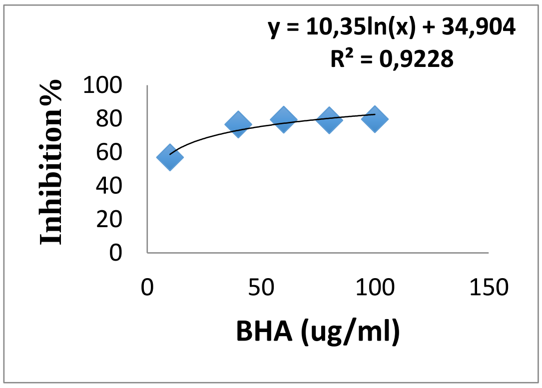

Figure 1. Variation of DPPH inhibition as a function of concentration of P. ovata seeds extract

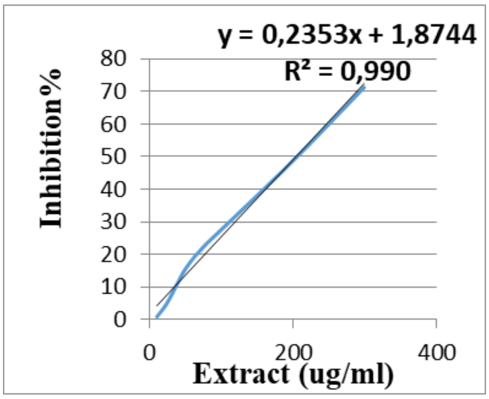

Figure 2. Variation of DPPH inhibition as a function of BHA

Total antioxidant capacity (TAC)

The extract showed a total antioxidant capacity of 22.75% in terms of ascorbic acid for the volume of 0.3 ml (Fig. 3) and a percentage of 52.29% in terms of quercetin (Fig 4).

In work published by Shivanjali et al. (2018) on *P.ovata* seeds that were macerated in methanol (80%), the total antioxidant capacity was 99.55 0.1 (µg AAE/mg) for envelopes and 164.00 0.2 (µg AAE/mg) for leaves.

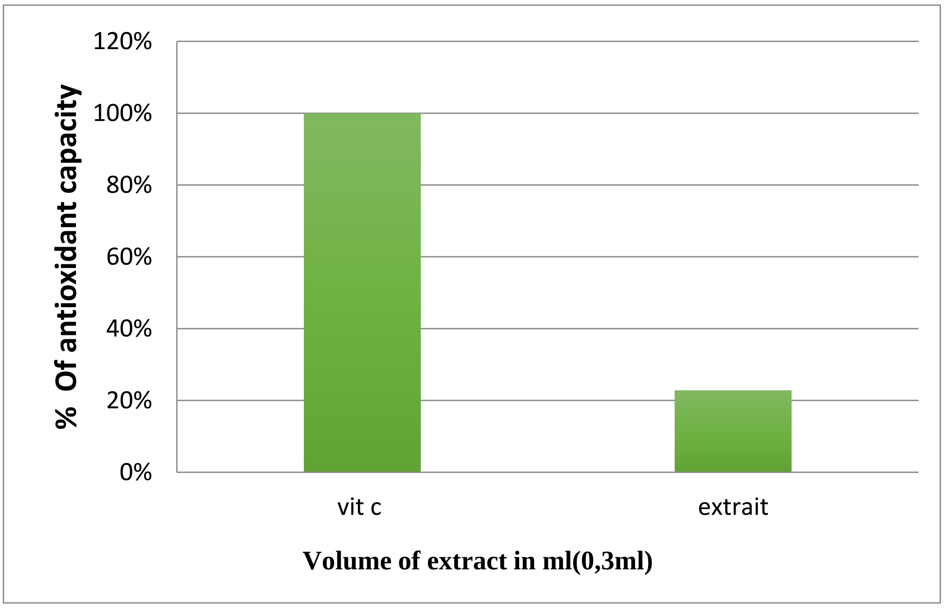

Figure 3. Histogram of the total antioxidant capacity of *P. ovata* seeds extracts in relation to ascorbic acid.

Figure 4. Histogram of the total antioxidant capacity of *P.ovata* seeds extracts in relation to quercetin.

Test du Pouvoir Réducteur du Fer (FRAP)

This test revealed that our methanolic extract has a reducing activity, with an EC50 equal to 19530 µg/ml (19.530mg/ml) The result is determined from the calibration curve (Fig. 5) which showed that the reduction power of Fe3+ in Fe2+ is proportional to the sample concentration. The psyllium seeds extract gives a very low reducing activity compared to the standards used (BHA and quercetin). Furthermore, the reducing power of BHA and quercetin (Fig. 6; Fig. 7) is 84.91 and 56.97 µg/ml respectively. Our results are not consistent with those of Khedher et al. (2022), who determined a EC50 value of 59.97 1.03 mg/mL for macerated ethanolic extract.

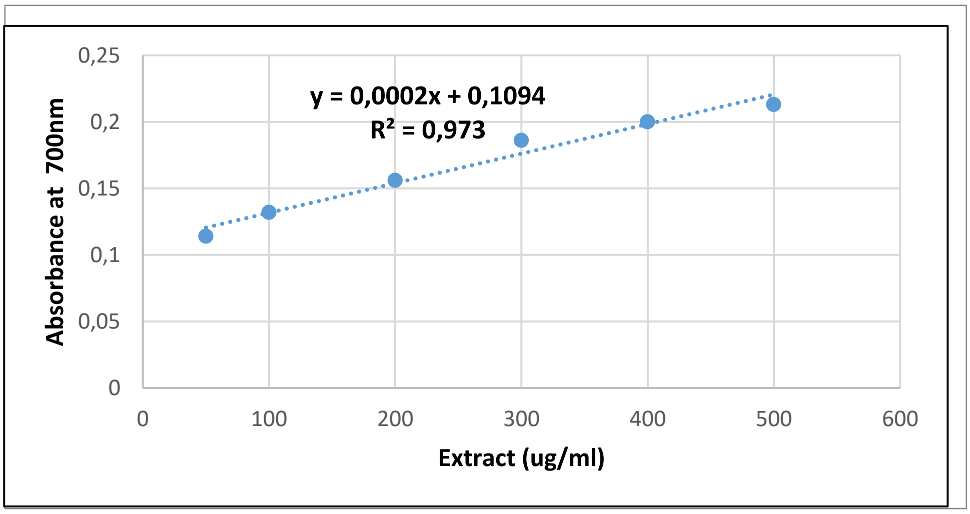

Figure 5. Calibration curve for the reducing power of the methanolic extract from *P.ovata* seeds

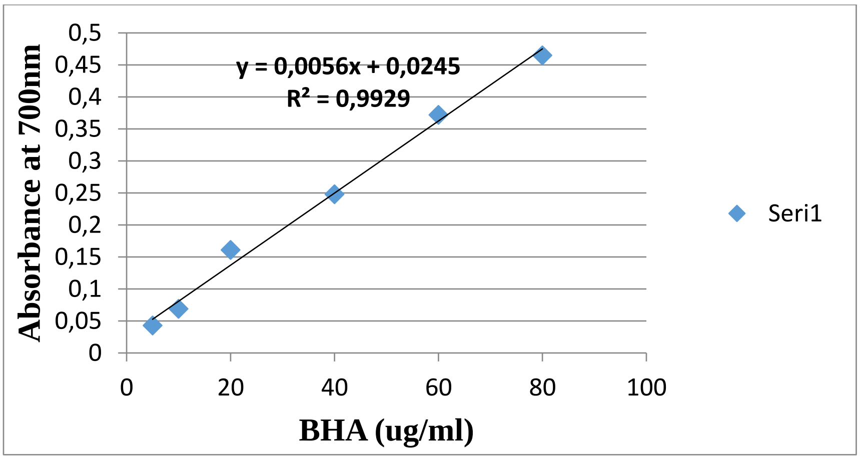

Figure 6. Calibration curve of the reducing power of BHA

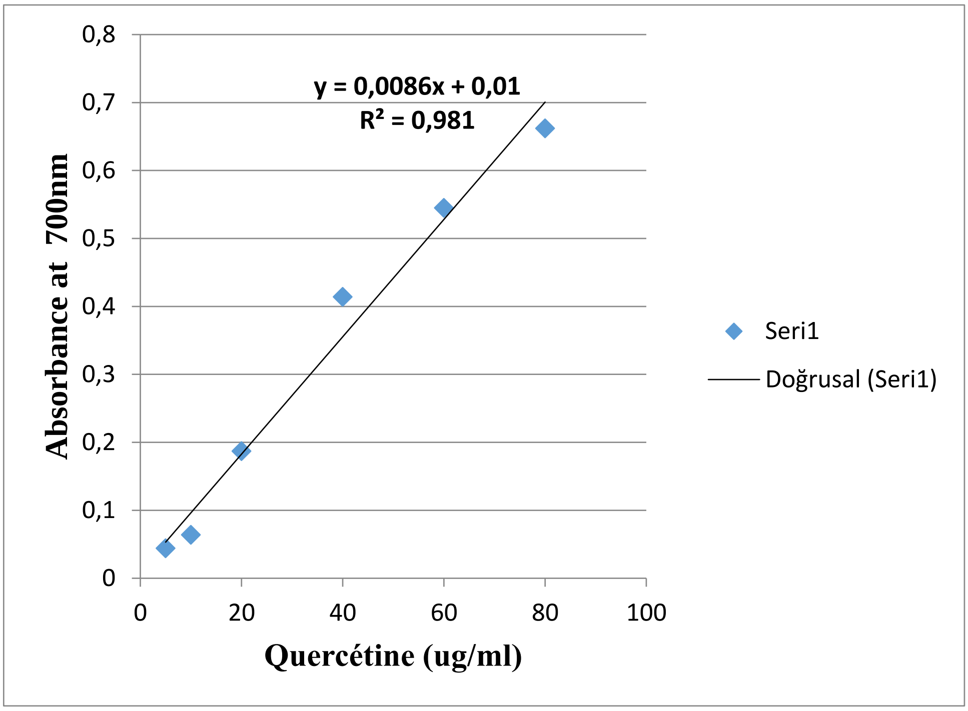

Figure 7. Calibration curve for the reducing power of quercetin.

Conclusion

This study focused on an ethnobotanical study in the Sétif region and its surroundings, phytochemical analyses and antioxidant activities of *Plantago ovata* seeds. These studies have yielded interesting results.

In fact, the qualitative analyses carried out have revealed the presence of phenolic compounds, flavonoids, condensed tannins and quinones in the methanolic extract of the seeds. The chemical evaluation revealed dominant concentrations of total polyphenols and flavones and flavonols, whereas tannins and flavonoids are detected in small quantities.

The evaluation of the antioxidant activity of methanolic extract by DPPH and FRAP methods revealed that the seed extract has low antioxidant activity, whereas with the phosphomolybdate (CAT) test the antioxidant activity is acceptable.

These promising results encourage us to develop further research in the future such as:

- Continue phytochemical study of the plant Plantago ovata to isolate other active ingredients.

- Perform in vivo tests to look for other interesting activities.

- Manufacture herbal products with this plant in various galenic forms (ex: syrup, capsules, tablets...).

Acknowledgement

We would like to thank Algerian Ministry of High Education and Research for the financial support as well as the Applied Microbiology Laboratory, University F.A.Setif1 for technical assistance.

Statement of Conflict of Interest

We declare that we have no conflict of interest.

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Role of Heart Rate Variability on Emotional and Behavioral Regulation in Animals

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ABSTRACT: A well-functioning cardiac state is important for a better life. Changes in cardiac functioning is associated with normal physiological conditions and behavioral changes. Welfare, stress and cardiovascular health can be characterised by healthy heart beats. In order to accurately analyse the beats, determining of long or short measurements periods are necessary. Accordingly, heart rate variability (HRV) is accepted as the most remarkable measure for identifying the autonomic nervous system function in both animals and humans. Additionally, various portable equipment and specific algorithms for recording and analysing cardiac activity are available to determine the heart rate variability. The domain measures of HRV are SDNN (Standard deviation of N-N intervals), SDANN (Standard deviation of the mean of N-N intervals), RMSSD (The square root of the mean of the sum of the squares of differences between successive beats), NN50 (Number of pairs of successive inter beat intervals differing by more than 50 ms) , pNN50 (NN50 count divided by the total number of all beats), and also the geometric measures as HRV index and Lorenz plot. HRV in animal researchers has been an increasing attend nowadays, especially in animal training, therapeutic applications, clarifying behavioral problems. In this study, it'll be tried to identify the heart rate variability in several animals, the methodologies and researches.

Keywords: Animal Behavior, Heart Rate Variability, Stress, Welfare

INTRODUCTION

There is a strong link between heart and life quality. It was reported that heart diseases have a wide range of mobidity and mortality over the years. To measure welfare and stress status of animals, monitoring and measuring cardiac health is necessary. To analysis the cardiac health, besides biochemical blood variables or stress hormones, some physiological parameters have been used especially heart rate and heart rate variability (Rasmussen et al., 2012; Pirintr et al., 2012; Bogucki and Noszczyk-Nowak, 2015).

Heart rate is a simple parameter to measure the cardiac activity. Nevertheless, heart rate variability (HRV) is measured with the changing temporal distance between success R-R intervals. HRV is a non-invasive technique to determine the functions of autonomic nervous system. In addition, the balance of the sympathetic and vagal activity can be clarified by HRV (Bennet et al., 2009). There are important studies about HR and HRV parameters in animals reviewed by some researchers (von Borell et al., 2007; Kahankova et al., 2022). Some studies determined that no significant in HRV parameters among animals while some of them reported either lower and higher values of HRV for animals' welfare.

The sensing technology for humans has several possibilities to monitor vital signs. However, for animals, the measurements are more complicated due to animals' physical structure and psychological health. This study is aimed to summarize the examples of the practical measuring of animal cardiac activity via HRV, and evaluate the monitoring technologies.

Material and Method

HRV can determined by several intervals, especially time and frequency intervals. The time domain parameters include NN (the time interval between two consecutive normal beats), SDNN (standard deviation of NN intervals), and rMSSD (root mean square of successive NN interval differences), as comprehensively reviewed by Billman (2011). In additionally, some geometric measures are used as well as time domain intervals to assess the HRV. These measures are based on the histogram of inter-beat intervals where inter-beat intervals are converted into a scale (Table 1). The most important geometrical measurements are HRV index, TINN index and Lorenz plot.

Frequency domain analysis is a complex technique that identify how much of signals lies with one more frequency bands. It was reported that frequency domain analysis observed that a unique and a non-invasive tool for determine the autonomic function (Table 2). Studies in investigating positive emotional states are limited, and only a small room of research investigating both time and frequency domain HRV indexes.

Table 1. Time domain measurements of HRV (modified from the European Society of Cardiology and von Borell et al., 2007)

Variable	**Description**	**Units**
Statistical measures		
SDNN	Standard deviation of all inter-beat intervals	ms
SDANN	Standard deviation of the mean of inter-beat intervals in all 5-min segments	ms
SDNN index	Mean of the standard deviations of all inter-beat intervals for all 5 min segments of the entire data set (24 h).	ms
RMSSD	The square root of the mean of the sum of the squares of differences between successive inter-beat intervals.	ms
NN50	Number of pairs of successive inter-beat intervals differing by more than 50 ms.	
pNN50	Number of pairs of successive inter-beat intervals differing by more than 50 ms.	%
Geometric measure		

HRV index	Total number of all inter-beat intervals divided by the height of the histogram of all inter-beat intervals measured on a discrete scale with bins of 7.8125 ms (1/128 s).	
TINN index	Baseline width of the minimum square difference triangular interpolation of the highest peak of the histogram of all inter-beat intervals.	ms
Lorenz plot	XY-diagram of each inter-beat interval of the data set plotted as a function of the previous inter-beat interval.	

Table 2. Frequency domain measurements of HRV (Modified from Bogucki and Noszczyk-Nowak, 2015)

Variable	**Description**	**Frequency range**	**Units**
TP	Area under entire power spectral curve (≤0.4), variance of all normal N-N intervals	≤0.4	ms2
ULF	Ultra low frequency power	≤ 0.003 Hz	ms2
VLF	Very low frequency power	(0.003-0.04) Hz	ms2
LF	Low frequency power	(0.04-0.15) Hz	ms2
HF	High frequency power	(0.15-0.40) Hz	ms2
LFnu	Normalized low frequency power	LF/LF+HF	Nu
HFnu	Normalized high frequency power	HF/LF+HF	nu
LF/HF	Ratio of the low-to high frequency power	ND	

For measuring HRV parameters, Holter or smart telemetric systems are available today. HRV applied in animal researches, methodology is important. It was reviewed that especially in pigs, there are two main themes for this topic. One of them is for biomedical models of human diseases, and the second is using as a stress indicator applied to welfare of animals (von Borell et al., 2007). The activity of the autonomic nervous system has been investigated in recent years in several animal species, especially in dogs, horses and pigs. Also, in ruminants and poultry, there has been notable studies.

Results and Discussion

The findings showed that HRV and electrocardiographic monitoring in animals, especially in cattle, sheep, horses, dogs and pigs have been studied over the years. Research topics were covered in relation of HRV caused by stress due to lameness in cattle and horses; by special diseases such as grass sickness, gastrointestinal diseases and laminitis; by assessing presence of pain and illness.

There are severity studies addressing the HRV in ruminants, including pathological diseases and stressors (Pomfrett et al., 2004; Hall et al., 2004). In ruminants heat and crowded stress are important. According to studies, ruminants showed anticipatory changes in cardiac activity via in short term variability (RNSSD) and long-term viability (SDNN) of HRV in stressful situations. It was reported that while HRV existing, RMSSD and SDNN parameters decreased. However, some researchers reported that no significant differences were found in both time and frequency domain parameters of HRV of lactating cows (Mohr et al., 2002). Studies in goats and sheeps are limited. Some researchers studied to analysis the resting behavior or stress with HRV, and found increasing activity. It was recommended that HRV in all ruminants are crucial to identify their stressful even in healthy conditions or pathological diseases (Von Borell et al., 2007; Kahankova et al., 2022).

There is an acceptable amount of literature reveals in HRV and horses with several techniques. It was rewieved that HRV in horse reports can be found in behavioral, clinical and physiological conditions. There are several Holter systems using for horses, especially for their welfare. Both time and frequency domains can be used for horses. It was reported that HF spectral power at night is an important value for these animals (Kuwahara et al., 1999; Eager et al., 2004). According to studies in horses, clinical conditions, training and wellbeing have been investigated and, also severity results were reported by researchers (Von Borell et al., 2007; Kahankova et al., 2022). Horses are emotional animals. HRV analysis have been based on this purpose, and measurement of physical and emotional stress have been more important. HRV in horses can be recommended especially for their welfare and training.

There have been some studies about biomedical researches in pigs (Mesangeau et al., 2000; Vos et al., 2004; Kuwahara et al., 2004). Researchers reported that the effects of pair housing on HRV parameters in pigs. Also some researchers were indicated the analysis methods of HRV parameters on gestation, social stress, restraint stress, grooming (Marchant-Forde et al., 2004Geverink et al., 2002; Hansen 2000).

Studies in poultry has been focused on the ultradian rhythms of cardiac activity. However, there is limited study to analysis the HRV, especially for emotional states and metabolic diseases (Mohr et al., 2002; Von Borell et al., 2007; Kahankova et al., 2022). To understand the relationship between feather pecking and coping style, sudden death syndrome by stressors and transports have been studied by researchers. It was reported that HRV analysis has been an increasing attend in birds to appears stress and welfare of these animals.

HRV can be assessed via several methods in dogs even in long- or short-term electrocardiogram recordings. Some studies have determined that the short-term monitoring has more advantages than 24-hour monitoring, some of them reported long term advantages in training (Handlin et al., 2011; Bogucki and Noszczyk-Nowak 2015; Kahankova et al., 2022). There have been some studies among several dog breeds reported the HRV differences (Manzo et al., 2009). Also, it was reported that negative emotional stress can decrease the HRV in dogs (Zupan et al., 2016). Some studies reported that HRV had several results such as increases and decreases in strange situations and stress (Gacsi et al., 2013; Rehn et al., 2013; Seyidoglu et al., 2023).

HRV measurement has become more significant and popular noninvasive tool as it is easy to perform, and also has become more clarity to our knowledge about animals and their welfare status.

Conclusion

HRV has been used more by the researchers and cardiologists in the veterinary field, due to its easy application and sensitivity. It can be used as a model in clinical studies as well as treatment process of animals. To assess stress and wellbeing under stressors, to study basic cardiovascular regulation, to evaluate the pathological conditions, behavioural disorders and management problems, HRV have been used in animals during last decade. Todays, HRV has been known as a crucial index to measure the physical activity and evaluate the emotional status, and thereby to improve the animal welfare. It can be suggested that HRV can be an essential measure for clarifying scientific and clinical understanding in animals' field

Statement of Conflict of Interest

The author(s) should declare that they are no conflict of interest.

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Intercropping of Sorgum x Sudangrass Hybrid with Forage Pea for Forage Quality

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ABSTRACT: Second crop forage production is widespread and beneficial under irrigated semi-arid conditions of Anatolia. Growers prefer forage pea for its high-quality forage and suitability for second-crop production in terms of vegetation period. However, yield is an issue, and therefore, the high-yielded species, mostly C4, are also preferred in the region for second-crop production. Intercropping annual grass-legume systems are also suggested for second-crop forage production in the area but it is a concern how forage quality changes as the species ratio changes in the mixture. In this research, forage pea (FP) and Sorghum x Sudangrass hybrid (SSH) intercropping were examined in terms of forage crude protein, NDF, and ADF contents. For this purpose, FP (100 % suggested amount) was intercropped with SSH at different ratios (25 and 50 % decreased from the suggested amount) and sown using different intercropping methods (same rows, alternate rows, cross-seeding) for 2 years (2019 and 2020). Results showed that intercropping methods are only effective on NDF content, which was the highest at the cross-seeding method. Sole-sown FP had the highest CP content as expected and 25 or 50 % reduced SSH addition to FP similarly decreased the CP content of forage. However, FP + 50 % reduced SSH intercropping gave better results regarding fiber contents, which is highly related to digestibility. In addition, yearly climatic variations are very effective on forage quality. FP is a high-quality forage source as the second crop in the region but it could be intercropped with a 50 % reduced amount of SSH for good-quality forage production under second crop conditions of Anatolia.

Keywords: Forage pea, Intercropping, Second crop, Sorghum x sudangrass

INTRODUCTION

Good-quality forage production is a critical issue in livestock nutrition. However, growers prefer industrial crops under irrigated conditions mostly due to high income, especially in Anatolia where semi-arid climatic conditions prevail. Second crop forage production is suggested for irrigated lands to overcome high-quality forage shortage in Turkey (Parlak and Sevimay, 2007; Kördikanlıoğlu and Gülümser, 2021). Growers mostly use maize and Sorghum x Sudangrass hybrids (SSH) due to high yielding potential of the species but second crop maize production has been affected from severe drought event in recent years. Therefore, SSH production came into prominence because this species is less-affected from drought in second crop season (Ramatoulaye et al., 2016; Erecek et al., 2023).

Sorghum x Sudangrass hybrids are widely used for fodder production especially in arid and semi-arid regions of the world (Gonulal, 2020; Kushkhov et al., 2021; Sarkar and Northup, 2023). This species second crop performance was also good (Mut et al., 2017; İleri et al., 2021) but forage quality, especially crude protein content, is not meeting the demands in animal nutrition (Eskandari et al., 2009; Stefaniak et al., 2012). Some mixture practices such as intercropping with legumes could increase the forage quality (Eskandari et al., 2009; La Vallie et al., 2020) and forage pea is one of the most appropriate legume species to intercrop with SSH regarding their positive competition (İleri et al., 2021).

Forage pea (FP) is an annual forage legume containing desirable amount of crude protein (nearly 20 %) and appropriate for intercropping with SSH (Iqbal et al., 2018; Kara and Sürmen, 2023). However, this species faces severe lodging problem as monoculture and a companion crop is required in most cases to produce this high-quality forage resource (Uzun et al., 2005; Gungaabayar et al., 2023). Therefore, FP – SSH intercropping could be considered as a good mixture for high quality forage production. However, the quality of the mixture is a question and might be affected from various cultural applications and seeding ratios.

This study was conducted to determine the forage quality of FP – SSH intercropping. Different intercropping methods and two different reduced amount of SSH seed were applied in the second crop season of 2019 and 2020 years in semi-arid irrigated conditions and the forage quality was examined.

Material and Method

The study was carried out at the Experimental Field of Eskisehir Osmangazi University, Faculty of Agriculture, Eskisehir District during 2019 and 2020 years. The area is located in the Central Anatolia, where semi-arid climate conditions prevail. Therefore, summer seasons are hot and dry (Table 1), winter seasons are cold and mostly snowy in the region.

Table 1. Average temperature, precipitation, and humidity data for the study area during the experiment months of 2019 and 2020.

Months	**Temperature (°C)**			**Precipitation (mm)**			**Humidity (%)**		
	2019	**2020**	**LTA**	**2019**	**2020**	**LTA**	**2019**	**2020**	**LTA**
July	**21.3**	**23.2**	**23.3**	**33.5**	**1.2**	**14.0**	**62.3**	**58.0**	**75.8**
August	**22.3**	**23.4**	**22.9**	**2.4**	**1.0**	**7.8**	**61.0**	**52.1**	**74.1**
September	**18.1**	**21.5**	**20.0**	**5.0**	**6.0**	**14.4**	**62.1**	**59.9**	**68.1**
October	**14.2**	**16.1**	**12.9**	**18.3**	**37.0**	**27.0**	**70.1**	**73.8**	**79.6**
Tot./Mean	*18.9*	*21.0*	*19.8*	*59.2*	*45.2*	*63.2*	*63.8*	*60.9*	*74.4*

LTA: Long-term average

According to the soil analyses, the 0-30 cm depth of the experimental soil was slightly alkaline and clay-loam. The lime content was 14.6 %, organic matter content was 1.62 %. Soil P2O5 and K2O contents were 61.6 kg ha-1 and 1688.0 kg ha-1 respectively and has no salinity problem (Soil Survey Laboratory Staff, 1992).

Forage pea (Pisum sativum ssp. arvense cv. Tore) and Sorghum x Sudangrass hybrid (Sorghum bicolor x Sorghum sudanense Stapf cv. Gozde-80) were used as intercropping species in the study. Intercropping was applied using three different sowing methods, which were sowing into the same rows, alternative rows, and cross-seeding. Forage pea (FP) sown solely and by mixing with two different ratio of Sorghum x Sudangrass hybrid (SSH) in intercropping. Sowing ratio for FP was 150 kg ha-1 seeds and SSH ratios were 2.5 and 5 kg ha-1 which were applied by decreasing 75 % and 50 % of the suggested amount (10 kg ha-1) by Acikgoz (2021).

Seedbed was prepared by ploughing wheat stubble and then by using a rotator on 4th and 21st of June in 2019 and 2020 years respectively. Sowing was carried out quickly after preparing the seedbed into the plots, each were 5 x 1.5 m (7.5 m2). The row spacing was 30 cm and 15 cm for same rows and alternate rows methods respectively. In the alternate rows, different species were sown for each rows. Cross-seeding method was applied by sowing the species in alternate rows but in different directions using 30 cm row spacing. After sowing, 30 kg ha-1 nitrogen and 70 kg ha-1 P2O5 (as Di-ammonium phosphate) were applied as fertilizer. Irrigation by sprinkler and weeding by hand hoeing were repeated considering the plant and field conditions.

Harvest date was determined considering the pod fill stage of forage pea because Fraser et al (2001) suggested the pod fill stage as harvest maturity of forage pea when cultivated for fodder. All plots were harvested simultaneously by sickle and dried at 60°C for 48 hours. Dry samples were grounded in laboratory mill and prepared for forage quality analyses. The crude protein ratio (%) of the samples were measured according to the method of AOAC (2003); NDF and ADF contents (%) were measured according to Van Soest et al. (1991).

The data were subjected the analysis of variance, and the means were compared using Tukey Multiple Comparison Test ($p \leq 0.01$) in SAS statistical software (SAS Institute, 2011).

Results and Discussion

Crude Protein Content

The average crude protein (CP) content was 16.3 % and it ranged between 11.1 % and 24.7 % depending on the applications (Table 2). Climatic variations among the experimental years caused a significant variation of CP content (Table 3). However different row configurations did not affect CP content of the mixtures. The CP content of sole-sown forage pea was higher about 5 % considering the mixtures with Sudan grass but rate of Sudan grass in the mixture did not change CP content statistically (Table 3). Two-way interactions of year × mixture and row configuration × mixture were significantly occurred ($p \leq 0.01$) (Figure 2).

Table 2. Descriptive statistics for the investigated characteristics

	Mean	Min.	Max.	Skewness	Kurtosis
Crude protein content (%)	16.3	11.1	24.7	1.260	0.651
NDF content (%)	38.6	30.9	52.3	0.645	-0.850
ADF content (%)	27.0	20.3	36.6	0.360	-0.692

Intercropping systems involving sorghum and legumes, such as forage peas, have been widely studied for their potential to enhance forage quality and yield, particularly in terms of crude protein (CP) content. The integration of legumes into cereal cropping systems is known to improve the nutritional profile of the forage produced, primarily due to the nitrogen-fixing capabilities of legumes, which contribute to increased protein levels in the resulting forage mixtures.

Table 3. Means for the investigated characteristics and ANOVA results

Years (Y)	**CP (%)**	**NDF (%)**	**ADF (%)**
2019	14.6^{B}	35.4^{b}	24.4^{b}
2020	17.9^{A}	41.7^{a}	29.5^{a}
Row Configuration (R)			
Same	16.3	37.8^{B}	27.2
Alternate	16.2	38.1^{B}	27.0
Cross-seed	16.4	39.7^{A}	26.7
Mixture (M)			
Forage Pea (FP)	19.5^{A}	34.3^{C}	25.4^{b}
FP + 25% Sudangrass	14.5^{B}	39.8^{B}	27.7^{ab}
FP + 50% Sudangrass	14.9^{B}	41.6^{A}	27.9^{a}
Mean	16.3	38.6	27.0

The nutritional quality of the dry matter produced through intercropping is a critical consideration. Research by Salem et al. indicated that intercropping legumes with sorghum not only increased dry matter yield but also enhanced the crude protein content of the forage produced (Salem et al., 2019). This is particularly important for livestock feeding, where the nutritional quality of forage can significantly impact animal performance. The findings from Oliveira et al. further support this, showing that intercropping systems can produce silage with improved nutritional parameters compared to monoculture systems, thereby enhancing the overall value of the forage produced (Oliveira et al., 2020). Research indicates that intercropping sorghum with legumes can significantly enhance crude protein yields compared to monoculture systems. For instance, studies have shown that the inclusion of legumes in sorghum intercropping can lead to an increase in CP content, with some reports indicating improvements in protein yield when compared to sole cropping systems (Salem et al., 2019; Iqbal et al., 2019). The intercropping of sorghum with legumes like cowpea and field pea has been particularly effective, as these legumes not only provide additional protein but also enhance overall forage quality by improving digestibility and reducing fiber content (Han et al., 2013; Iqbal et al., 2018).

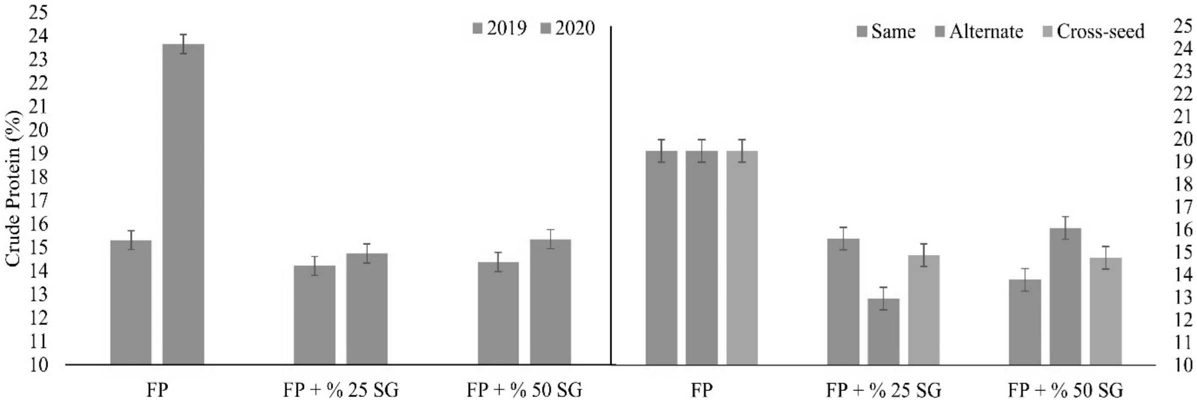

Figure 1. Year × mixture (left) and year × row (right) interactions for CP content

NDF-ADF Contents

The NDF and ADF contents were varied between 30.9 – 52.3 % and 20.3 – 36.6 % respectively. Both NDF and ADF contents significantly increased in the second year from 35.4 % to 41.7 % for NDF, and from 24.4 % to 29.5 % for ADF content (Table 3). Row configuration had a significant effect only on NDF content. The cross-seeding application appeared to increase the NDF content to 39.7 %, while it did not vary significantly between same rows (37.8 %) and alternate rows (38.1 %) configurations. The effect of mixtures was significant for NDF ($p \leq 0.01$) and ADF ($p \leq 0.05$) contents. Integrating Sorghum x Sudangrass hybrid in the mixture also increased the NDF and ADF contents. The highest NDF content was 41.6 % (forage pea + 50 % Sorghum x Sudangrass hybrid) among the mixtures and it was 7.3 % higher than sole-sown forage pea (Table 3). Although the forage pea + 50 % Sorghum x Sudangrass hybrid mixture had 2.5 % higher ADF content than sole-sown forage pea, the changing Sorghum x Sudangrass hybrid ratio in the mixture did not affect ADF content significantly (Table 3). Year

× row configuration and year × mixture interactions were significant for both NDF ($p \leq 0.01$) and ADF ($p \leq 0.05$) contents.

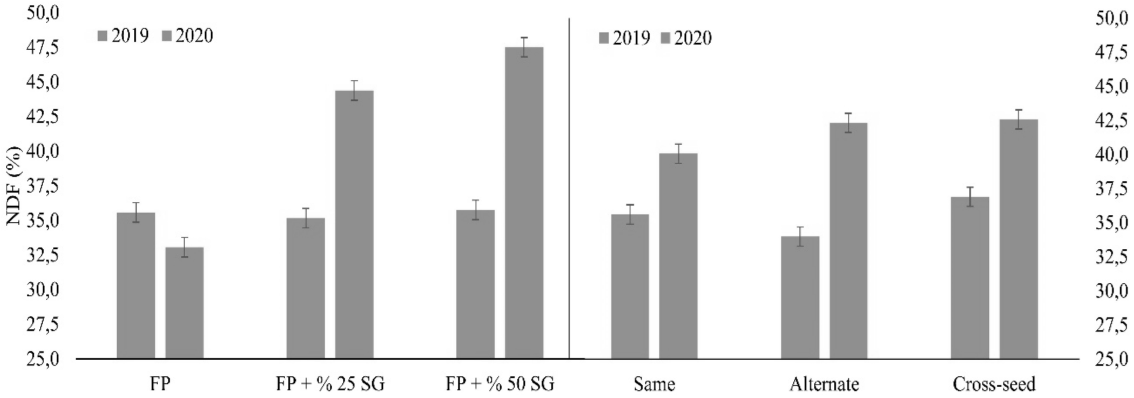

Figure 2. Year × mixture (left) and year × row (right) interactions for NDF content

The importance of Acid Detergent Fiber (ADF) and Neutral Detergent Fiber (NDF) content in forage crops is critical for assessing their nutritional quality and digestibility, which directly impacts livestock productivity. ADF primarily consists of cellulose and lignin, while NDF includes cellulose, hemicellulose, and lignin. Both ADF and NDF are negatively correlated with digestibility; higher concentrations of these fibers typically indicate lower digestibility of forage, which can adversely affect animal performance (Li et al., 2015; Wei et al., 2020; Xie et al., 2011). This relationship underscores the necessity of monitoring ADF and NDF levels in forage crops to ensure optimal livestock nutrition. Research indicates that different row configurations can significantly affect NDF levels. For instance, Erkovan's study found that cross-seeding configurations led to a notable decrease in NDF content compared to sole, same, and alternate row configurations, suggesting that the spatial arrangement of crops can mitigate competition and heat stress, thereby enhancing forage quality (Erkovan, 2022). This is consistent with findings from Fotohi Chiyaneh, who noted that intercropping patterns generally resulted in lower ADF and NDF levels, attributed to improved nutrient availability and environmental efficiency (Fotohi Chiyaneh, 2023). Such reductions in fiber content are essential as higher ADF and NDF levels are associated with decreased digestibility and energy levels in forage (Fotohi Chiyaneh, 2023). This indicates that the success of intercropping systems in reducing NDF and ADF levels may depend not only on the chosen configurations but also on the prevailing environmental conditions during the growing season (Figure 2, 3).

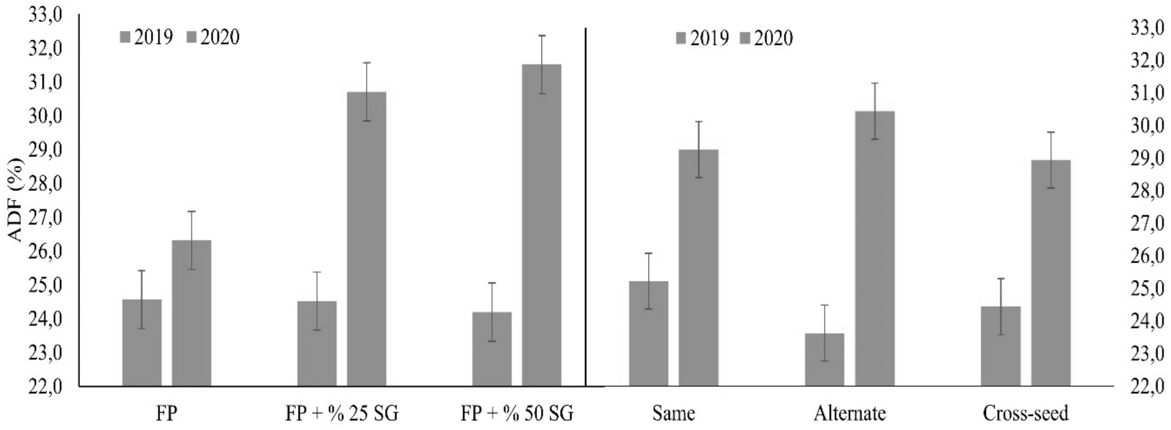

Figure 3. Year × mixture (left) and year × row (right) interactions for ADF content

Conclusion

It was clear that year by year climatic variations have a huge impact of the forage quality of intercrops. Intercropping methods and mixtures were also effective and should be considered as manageable parameters. Study results indicated that FP – SSH intercrops are beneficial in terms of forage quality. Forage produced in cross seeding method had higher quality in 150 kg ha-1 FP + 2.5 kg ha-1 SSH but if SSH ratio is increased up to 5 kg ha-1 in the mixture, species should be sown into alternate rows. Under second crop conditions intercropping of 150 kg ha-1 FP + 5.0 kg ha-1 SSH and sowing into alternate rows gave the best results regarding forage quality but further studies are needed to reveal the effects of other agronomic methods on grass-legume mixtures.

Funding

No funding acquired.

Statement of Conflict of Interest

The author(s) should declare that they are no conflict of interest.

Authors' Contributions

The authors equally contributed to the research

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The Effect of Single and Triple Bacteria Based Bio-Formulations, Mineral and Organic Fertilizers on the Growth, Yield and Oil Content of Rosemary*

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ABSTRACT: There is an increasing need to use microorganisms for safe crop production for consumers, as well as to prevent environmental pollution and ensure the sustainability of agriculture and agricultural resources. Microorganisms are important in agriculture in order to promote the circulation of plant nutrients and reduce the need for chemical fertilizers as much as possible. The objective of this study was to evaluate possible effects of mineral NPK fertilizer (100 kg ha^{-1} N, 100 kg ha^{-1} P and 50 kg ha^{-1} K), farmyard manure (FM: cattle manures 2 t ha^{-1}), and N2-fixing and P-solubilizing bacteria based bio-fertilizers formulations in single (*Pseudomonas fluorescens* RC512; *Pseudomonas fluorescens* RC536, *Bacillus megaterium* RC16, *Bacillus subtilis* RC210, *Bacillus licheniformis* RC502) and three strains combinations (RC512 + RC210 + RC16 and RC536 + RC210 + RC502) on the growth, yield, and oil content and yield and essential oil components in rosemary (*Rosmarinus officinalis* L.) under field conditions of Çanakkale. The experiment was arranged as a completely randomized block design with ten treatments and three replicates. Manure and Fertiliser applied at the time of land preparation by broadcasting prior to planting, and biofertilizers inoculation involved dipping the root system of the seedling into a suspension of bacteria formulations for 60 min, prior to planting. According to field trial results, inoculation of Rosemary with RC512, RC536, RC16, RC210, RC502, RC512 + RC210 + RC16 and RC536 + RC210 + RC502 increased plant height by 27.8, 1.5, 8.4, 12.4, 31.2, and 21.6% as compared to the control; branch number per plant by %10,2, 6,8, 15,3, 14,2, 18,9, 27,1, and 33,8%; fresh herb yield by 11.2, 2.6, 2.7, 14.1, 10. 7, 30.0, and 23,9%; dry herb yield by 6.6, 3.5, 4.7, 16.7, 8.5, 26.3, and 23.7%; fresh leaf yield by 9.6, 4.7, 5.8, 17.8, 9.5, 29.8, and 24.4%; dry leaf yield by 11.3, 8.1, 6.8, 19.2, 11.0, 28.6, and 26.1%; essential oil ratio by 1.1, 4.2, 1.0, 6.3, 5.3, 10.5, and 7.4%; and essential oil yield by 12.5, 12.9, 8.0, 26.9, 17.1, 42.3, and 35.6%, respectively. NPK and FM applications, however, increased the height of plants up to 32.9 and 14.5%, branch number per plant by 30.3 and 6.7 %, fresh herb yield by 32.7 and 16.4%, dried herb yield by 25.7 and 18.0 %, yield of fresh leaves by 29.6 and 16.2%, yield of dry leaves by 28.1 and 20.1 %, and essential oil ratio by 1.1 and 13.7% and yield of essential oil 29.7 and 36.2%, respectively.

Keywords: Rosemary, Bio-fertilizers Formulation, Farmyard Manure, Herb and Leaf Yield, Essential Oil Content

INTRODUCTION

Rosemary (*Rosmarinus officinalis* L.), a member of the Lamiaceae family and one of the characteristic plants of the Mediterranean region, is one of the important perennials, economically important aromatic plants that is widely used as widely used in the world as a medicinal, perfumery, aromatic and ornamental plant, and its fresh or dried leaves are also used

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*This study is a part of the study financially supported by the University Students Research Projects Support Programme (2209/A) provided by the Scientific and Technological Research Council of Turkey (TUBITAK) as a spice. It is used for culinary, medical, cosmetic, and decorative purposes in fresh, dried, and/or essential oil extracted. In addition to its use as a food additive and medicine due to its many pharmacological and biological activities, rosemary extract is frequently used in cooking and aromatherapy due to its unique characteristic aroma and flavor. In Turkey, it is naturally distributed in the coastal strips where the Mediterranean climate prevails and in the Eastern Mediterranean region, especially in Mersin and Adana, as well as in Çanakkale, Tarsus and Hatay regions. Rosemary is a perennial plant that is 50-100 cm high, has a bush form, does not shed its leaves in winter, and has pale blue flowers, and is widely used in the world as a medicinal, aromatic and ornamental plant.

The inoculation of beneficial microbiomes as biofertilizers to soil, seeds or seedlings to improve the availability and uptake of nutrients from the soil has emerged as an innovative and environmentally friendly technology for improving soil fertility and plant growth (Kumar et al., 2022). Bacterial inoculation can affect the growth, yield, essential oil content, yield and chemical content of medicinal and aromatic herbs, seeds, roots, tubers, bulbs and rhizomes (Çakmakçı et al., 2020). According to some research findings in recent years, some preliminary ideas have been given that plant growth promoting bacterial inoculations can be an effective biotechnological tool that stimulates the secondary metabolite production mechanism in plants, and some research has been carried out on this subject in recent years (Cappellari et al., 2015; Mosber et al., 2019; Kutlu et al., 2019; Çakmakçı et al., 2020). Research that will improve the yield, composition and content of essential oils using different plant growth regulators and create opportunities to change the composition of some molecules of economic importance is gaining importance. On the other hand, many medicinal and aromatic species are consumed without any further processing after harvest, which requires that these plants do not contain any synthetic compounds at harvest. As a result, plant growth-promoting bacterial applications are increasingly gaining importance in terms of both plant production and improvement of quality parameters in medicinal and aromatic plants.

Plant growth promoting bacterial applications can stimulate secondary metabolite response (Banchio et al., 2010; Kutlu et al., 2019), and increase oil yield, essential oil components, mono terpene production and accumulation (Nourafcan et al., 2014; Banchio et al., 2009, 2010; Cappellari et al., 2015; Ghorbanpour et al., 2016; Kutlu et al., 2019) in medicinal and aromatic plants. In previous studies, it was reported that the menthone, menthol content in *Mentha piperita* (Santoro et al., 2011), and the citronellol and geraniol content in *Pelargonium graveolens* (Dharni et al., 2014), carvacrol ratio in *Origanum syriacum* subsp sinaicum (Alraey et al., 2019), the total ginsenosides content in *Panax ginseng* (Ji et al., 2019), geranyl acetate in *Dracocephalum moldavica* (Amini et al., 2020), and the content methyl chavicol, eucalyptol, linalool, and β-pinene in *Ocimum basilicum* var. thyrsiflorum (Dehsheikh et al., 2020) plant could be significantly increased by bacterial inoculations.

In previous studies, the inoculations of PGPB, also had a positive effect on the essential oil yield in *Satureja hortensis* (Farahani, 2015), *Mentha arvensis* (Bharti et al., 2016; Singh et al., 2019), *Salvia officinalis* (Ghorbanpour et al., 2016), *Origanum onites* (Kutlu et al., 2019), *Ocimum basilicum* var. thyrsiflorum (Dehsheikh et al., 2020), *Dracocephalum moldavica* (Amini et al., 2020; Nejatzadeh, 2020), *Foeniculum vulgare* (El-Serafy and El-Sheshtawy, 2020; Jeet and Baldi, 2021), and *Origanum onites* (Çakmakçı et al., 2023).

According to some research findings in recent years, some preliminary ideas have been given that plant growth promoting bacterial inoculations can be an effective biotechnological tool that stimulates the secondary metabolite production mechanism in plants, and some research has been carried out on this subject in recent years. Therefore, use as biofertilizers for sustainable agriculture is important. Biological fertilizers are an important component of nutrient management as an environmentally and human-friendly, cost-effective, and renewable resource management strategy. However, promoting plant growth by developing and using effective bacterial strains and biological fertilizer formulations in directly consumed medicinal aromatic plants is an important research area of great importance in terms of the natural environment and consumer health. Although these studies are important in terms of plant nutrition, environment, soil, and human health, biological fertilizer research is still in its infancy and its inoculations are very insufficient. Therefore, this study was carried out to investigate the effects of single and combined bacterial formulations developed from local bacteria isolated from natural conditions of Turkey and inorganic NPK fertilizer and farmyard manure applications on the development, yield, oil content and yield of rosemary.

Material and Method

The objective of this study was to evaluate possible effects of mineral NPK fertilizer (100 kg ha^{-1} N, 100 kg ha^{-1} P and 50 kg ha^{-1} K), farmyard manure (FM: cattle manures 2 t ha^{-1}), and N_2-fixing and P-solubilizing bacteria based bio-fertilizers formulations in single (*Pseudomonas fluorescens* RC512; *Pseudomonas fluorescens* RC536, *Bacillus megaterium* RC16, *Bacillus subtilis* RC210, *Bacillus licheniformis* RC502) and three strains combinations (*Pseudomonas fluorescens* RC512 + *Bacillus subtilis* RC210 + *Bacillus megaterium* RC16; *Pseudomonas fluorescens* RC536 + *Bacillus subtilis* RC210 + *Bacillus licheniformis* RC502) on the growth, yield, and oil content and yield and essential oil components in rosemary (*Rosmarinus officinalis* L.) under field conditions of Çanakkale. The experiment was arranged as a completely randomized block design with ten treatments and four replicates. Manure and fertiliser applied at the time of land preparation by broadcasting prior to planting, and biofertilizers inoculation involved dipping the root system of the seedling into a suspension of bacteria formulations for 60 min, prior to planting.

First, frozen bacterial culture was cultivated on a nutrient agar-containing medium and incubated for 24 hours at 27°C for the single and triple bacteria formulation. For the preparation of the microorganism-based biofertilizer candidate bioformulation, the bacterial culture was grown in flasks containing Nutrient Agar (NA) on a rotary shaker at 27°C for 24 hours. For liquid-based bio-formulation equal volumes (10^8 CFU ml-1 of each inoculant) of each culture were mixed and then used. Subsequently, 24-h cultures were developed in a horizontal shaker incubator, inoculated into NB containing liquid culture medium previously prepared by the fermenter, and sterilized by autoclaving for 20 min at 120°C (Çakmakçı et al., 2013). Bacteria were grown by providing optimum pH, oxygen, and temperature for 24 hours and then inoculated at a ratio of 1:10 to the liquid carrier mixture, which was completely sterilized by steam. The bacteria-inoculated organic liquid carrier was incubated in the bioreactor under optimum growth conditions. When the number of viable bacteria per milliliter exceeds 1 x 10^8 cells (CFU) at the end of 48 hours, the product was packaged under sterile conditions and stored in a cold room at 5 °C until use (Çakmakçı et al., 2013). The inoculated seedlings were planted without waiting and uniform water was applied to all inoculated and uninoculated seedlings after planting. The remainder of the suspension was uniformly delivered to the root zone by drip irrigation, while control plants were given 5 ml of diluted liquid carrier free of bacteria.

Rosemary cuttings were planted in the greenhouses of Çanakkale University Faculty of Agriculture Dardanos Campus on January 5, 2021. The rooted cuttings were then transplanted to the trial areas of Çanakkale Onsekiz Mart University Dardanos Campus ÇOMÜ Faculty of Agriculture Farm Plant Production Research and Application Unit on May 2, 2022. In the experiment, which was carried out according to randomized factorial design. This research was carried out under field conditions on a rosemary plantation created from 2-year-old seedlings with 50 cm x 50. Field experiments were set up according to a randomized plot design with four replications, with 10 saplings in each replication, thus there were 40 rosemary plants in each treatment. The second bacterial application under field conditions was injected into the plant root zone in the spring, with 5 ml of bacterial suspension per seedling. All the phosphorus and potassium fertilizer and half of the nitrogen fertilizer were applied during planting, and the remaining half of the nitrogen fertilizer was applied before the first hoeing. Hoeing was done by hand and repeated as required. While weeds were controlled by hand hoeing, there was no disease or insect attack on the crop during the growth period. Sprinkler irrigation was applied after planting, maintenance, hoeing and irrigation were done on time and appropriately.

Harvests were carried out on 22.06.2023 in the first year by harvesting the herb part from 8-10 cm above the ground at the beginning of flowering stage after measuring the height of 10 plants in the plots in the second year. The second harvest was carried out on 18 September, but the second harvest data was excluded from the evaluation due to water restrictions in the August period in the experimental area. Data on various parameters of rosemary, namely, plant height and branch number of the plant, fresh and dry herb yield per plant and per hectare, fresh and dry leave yield per plant and per hectare, essential oil ratio, essential oil yield, and composition were recorded at harvest time. Plants at the at the beginning of flowering were collected by cutting the aboveground part of the stem from a height of 8-10 cm and dried at 35°C, the essential oil content was extracted from air-dry material by distillation. The data for basil genotypes were subjected to analysis of variance using STATISTICA 12 and the means were separated according to Duncan’s multiple range test.

Results and Discussion

As all selected treatments had promising positive effects on the growth and yield parameters of rosemary under field conditions. Except for single inoculation *Pseudomonas fluorescens* RC536 and *Bacillus megaterium* RC16, all treatments tested significantly increased plant height and fresh herb yield per hectare of rosemary compared to control. Triple inoculation with RC536+RC210+RC502 and RC512+RC16+RC210, single RC210, RC16 and NPK fertilizer increased branch number per plant, while the other treatment groups was similar to the control (Table 1). Except for single RC512, RC536, RC16, and RC502, other bacterial inoculation, farmyard manure and NPK fertilizer application significantly increased dry herbage yield, fresh leaf yield, dry leaf yield and essential oil content in rosemary compared with control. Also, except for RC512 and RC16 formulations, other bacterial inoculation significantly increased essential oil yield, whereas only the triple inoculation with RC536+RC210+RC502 and RC512+RC16+RC210, and farmyard manure increased the essential oil content of rosemary.

Except for single inoculation *Pseudomonas fluorescens* RC512 and *Bacillus megaterium* RC16, other bacterial inoculation and NPK fertilizer and farmyard manure application significantly increased essential oil yield in rosemary. The best effects were obtained in essential oil yield with mixed combination of the three (*Pseudomonas fluorescens* RC512+ *Bacillus subtilis* RC210+ *Bacillus licheniformis* RC601) and triple inoculation with *Pseudomonas fluorescens* RC536 + *Bacillus subtilis* RC210 + *Bacillus licheniformis* RC502, followed application of farmyard manure and NPK fertilizer, and single inoculation of *Bacillus subtilis* RC210.

According to field trial results, inoculation of rosemary with RC512, RC536, RC16, RC210, RC502, RC512 + RC210 + RC16 and RC536 + RC210 + RC502 increased plant height by 27.8, 1.5, 8.4, 12.4, 31.2, and 21.6% as compared to the control; branch number per plant by %10,2, 6,8, 15,3, 14,2, 18,9, 27,1, and 33,8%; fresh herb yield by 11.2, 2.6, 2.7, 14.1, 10. 7, 30.0, and 23,9%; dry herb yield by 6.6, 3.5, 4.7, 16.7, 8.5, 26.3, and 23.7%; fresh leaf yield by 9.6, 4.7, 5.8, 17.8, 9.5, 29.8, and 24.4%; dry leaf yield by 11.3, 8.1, 6.8, 19.2, 11.0, 28.6, and 26.1%; essential oil ratio by 1.1, 4.2, 7.3, 6.3, 5.3, 10.5, and 7.4%; and essential oil yield by 12.5, 12.9, 8.0, 27.6, 17.1, 42.3, and 35.6%, respectively. NPK and FM applications, however, increased the height of plants up to 32.9 and 14.5%, branch number per plant by 30.3 and 6.7 %, fresh herb yield by 32.7 and 16.4%, dried herb yield by 25.7 and 18.0 %, yield of fresh leaves by 29.6 and 16.2%, yield of dry leaves by 28.1 and 20.1 %, and essential oil ratio by 1.1 and 13.7% and yield of essential oil 29.7 and 36.2%, respectively (Table 1).

Table 1. Effect of mineral fertilizer, farmyard manure, and bacteria-based formulations in single and triple strains combinations on growth, yield parameters of rosemary in the field experiment

Treatments	Plant height (cm)**	Branch number (plant^{-1})	Fresh herba yield (t/ha)	Dry herba yield (t/ha)	Fresh leaf yield (cm)	Dry leaf yield (t/ha))	Essential oil rate (%)	Essential oil yield (L/ha)
Control	68,93 e	14,16 c	26.19 d	12.64 d	13.03 d	9.26 d	0,95 cd	87.8 e
NPK	91,65 a	18,45 ab	34.75 a	15.89 a	16.89 a	11.86 a	0,96 cd	113.9a-c
FM	78,95 cd	15,12 bc	30.48 c	14.92 a-c	15.14 bc	11.09 ab	1,08 a	119.6 ab
RC512 (1)	88,13 ab	15,61 bc	29.12 c	13.48 b-d	14.28 cd	10.31b-d	0,96 cd	98.8 de
RC536 (2)	69,94 e	15,12 bc	26.88 d	13.09 cd	13.64 cd	10.01b-d	0,99 cd	99.1 d
RC16 (3)	74,74 de	16,17 a-c	26.90 d	13.24 b-d	13.79 cd	9.89 cd	0,96 cd	94.8de
RC210 (4)	77,51 cd	16,32 ab	29.87 c	14.75 ab	15.35 bc	11.04 a-c	1,02bc	112.1bc
RC502 (5)	77,77cd	16,85 a-c	29.00 c	13.72 b-d	14.27 cd	10.28b-d	1,0 b-d	102.8cd
1+3+4	90,45 a	18,0 ab	34.06 a	15.97 a	16.92 a	11.91 a	1,05 ab	124.9 a
2+4+5	83,83 bc	18,96 a	32.47 b	1.563 a	16.21 ab	11.68 a	1,02 bc	119.1ab

*Control: without bacteria inoculation or mineral fertilizers; NPK ((100 kg ha^{-1} N, 100 kg ha^{-1} P and 50 kg ha^{-1} K), FM: farmyard manure (cattle manures 2 t ha^{-1}), and N_2-fixing and P-solubilizing bacteria based bio-fertilizers formulations in single (*Pseudomonas fluorescens* RC512; *Pseudomonas fluorescens* RC536, *Bacillus megaterium* RC16, *Bacillus subtilis* RC210, *Bacillus licheniformis* RC502) and three strains combinations (RC512 + RC210 + RC16; RC536 + RC210 + RC502);

**Different letters within the same column indicate significant differences according to Duncan's Multiple Range Test (*P*≤0.01.

Inorganic fertilizers, farmyard manure, and two triple bacteria combinations significantly affected the growth parameters studied in rosemary compared to the control, depending on the growth parameters assessed. The experiment revealed that the PGPR inoculation, inorganic fertilizers, and farmyard manure were an effective treatment to improve the parameters measured of rosemary, especially with reference to the increase in essential oil yield and fresh and dry weight of both herb and leaf yield. Combined inoculation of multi-trait bacteria consistently gave equal or higher growth and yield parameters than inorganic fertilizers and farmyard manure pots. Of the effective bacteria tested, they consistently gave growth, and total biomass yields equal to chemical fertilizers applied. These results were validated by the work of Çakmakçı and Milton (2019) who also showed a substantial elevation in root weight, propagation of lateral and incidental roots, and affect nutrient uptake, as well as fresh and dry grass and root weight, chlorophyll content, number of lateral roots and branches, and trunk diameter in lemon basil (*Ocimum x citriodorum* Vis) following PGPR inoculations.

In previous similar studies, inoculations of *Pseudomonades* sp., *Bacillus lentus*, and *Azospirillum brasilense* have showed improvement in growth, chlorophyll content and essential oil content, weight of root and stem, and total biomass in *Ocimum basilicum* (Heidari et al., 2011), application of combination of nitrogen-fixing and phosphate solubilizing bacteria + 50% chemical fertilizer increased microbial respiration, number of glandular trichomes, and essential oil yield in *Ocimum basilicum* var. thyrsiflorum (Dehsheikh et al., 2020), inoculation of mycorrhizal fungi *Glomus mosseae* and growth-promoting bacteria *Azospirillum* could have a significant effect on grain yield, biological yield, essential oil yield in *Foeniculum vulgare* Mill (Alipour et al., 2021), Application of biofertilizers also played an important role in increasing the essential oil content, bioactive components, and plant nutrition in *Ocimum basilicum* and *Satureja hortensis* (Khalediyan et al., 2021), inoculation of *Bacillus subtilis* and *Bacillus megaterium* regulated and enhanced the yield and essential oil content in *Origanum onites* (Şen and Duran, 2023), and application of phosphate-solubilizing bacteria mitigated the adverse effects of drought stress and increased essential oil content in *Calendula officinalis* under drought stress (Azizi et al., 2024). Inoculations roots of sage seedlings with *P. fluorescens* bacterium and arbuscular mycorrhizal fungi improved the growth, quantity and quality yields of the essential oil (Samani et al., 2019).

Conclusion

Positive effects of this selected mixed biofertilizer formulation, farmyard manure, mineral fertilizers on fresh and dry herbage and leave yield, essential oil ratio and yield, plant height and branch number of rosemary plants showed the beneficial role of these of the use of bacterial formulations and mineral fertilizer or farmyard manure. All treatments tested increased 1.8 cineole, camphor, and camphene of rosemary significantly compared to the control; however, verbenone increased with all applications, except single *B. licheniformis* RC502 inoculation. All the treatments, except for RC512, RC16 and RC502, enhanced borneol content as compared to the control. The use of multi-featured effective free-living bacterial multiple consortia in rosemary is an important area of study to promote growth and yield and to develop substitute strategies for the effective management of plant nutrients. The experiment revealed that the bacterial consortia and farmyard manure, and NPK supply were effective treatments to improve the parameters measured of rosemary.

Acknowledgement

This study, given a brief summary, is a part of the study financially supported by the University Students Research Projects Support Program (2209/A) provided by the Scientific and Technological Research Council of Turkey (TUBITAK). The authors would like to thank TÜBİTAK for their generous support.

Statement of Conflict of Interest

The authors should declare that they are no conflict of interest.

Authors' Contributions

M.Ö and R.Ç designed and analyzed the research, M.Ö. and R.Ç. studies arranged. R.Ç. worked on the preparation of M.Ö. pictures and tables. All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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Potential and Challenges of Microorganisms as Promising Food Sources of the Future

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ABSTRACT: The most important challenges to be faced in the coming years for the development of new, sustainable and robust food production technologies are climate change, population growth and resource depletion. With the increase in the world population, the global food demand is also increasing, production cannot meet the demand and at the same time, increasing environmental concerns require changes in the traditional food supply system. At present, the food industry still faces high resource and energy consumption and pollution, which have caused enormous pressure on the ecological environment, and raised new requirements for future foods. Current and future challenges include emerging microorganisms and their toxins in food products; food allergens; co-optimization between safety and quality; improved nutrient availability for certain ages, characteristics and lifestyles; alternative protein sources; processes that consume less water and energy; environmental, social and economic concerns; and global warming. The discovery and development of microbial protein sources is highly important in the context of increasing concerns about food security, resource conservation, environmental sustainability and public health. Using cellular agriculture techniques, the development of a sustainable and resilient food system can be promoted by developing cheaper and environmentally friendly alternative protein sources by recycling agricultural industry waste resources. To make future foods safer, nutritious, tastier and sustainable, plant-based food, food additive manufacturing, substitute and single-cell protein, synthetic biology, precision fermentation and innovations in food technology are attracting widespread attention. In this review, the potential, challenges and recent developments in the application of microorganisms as promising food production sources of the future, the use of waste and food by-products for the production of food and its components, and future perspectives are evaluated.

Keywords: Cellular agriculture, Single-cell protein, Microorganism, Fermentation, Bacterial biomass, Microalgae

INTRODUCTION

Population growth and urbanization, competition for natural resources, extreme weather events, decrease in agricultural productivity, food insecurity, structural changes in economic systems, advanced food production systems, food losses and waste, and sustainable development efforts are the topics emphasized by FAO (FAO, 2017; Calicioglu et al., 2019). Trends for future agriculture and food systems are important to aid food security and sustainable solutions. The most important challenges to be faced in the coming years for the development of new, sustainable and robust food production technologies are climate change, population growth and resource depletion. With the increase in the world population, the global food demand is also increasing, production cannot meet the demand and at the same time, increasing environmental concerns require changes in the traditional food supply system. At present, the food industry still faces high resource and energy consumption and pollution, which have caused enormous pressure on the ecological environment, and raised new requirements for future foods.

Current and future challenges include emerging microorganisms and their toxins in food products; food allergens; co-optimization between safety and quality; improved nutrient availability for certain ages, characteristics and lifestyles; alternative protein sources; processes that consume less water and energy; environmental, social and economic concerns; and global warming. To make future foods safer, nutritious, tastier and sustainable, plant-based food, food additive manufacturing, substitute and single-cell protein, synthetic biology, precision fermentation and innovations in food technology are attracting widespread attention.

Although production has increased to a certain extent as a result of efforts to increase production capacity, efficiency and productivity to meet food needs; current production systems have caused serious environmental pollution due to greenhouse gas emissions, deforestation, extraction of biological fossil fuels and eutrophication (Willett et al., 2019; Anser et al., 2021); they have also led to many problems such as pollution and degradation of soils, nitrogen and phosphorus pollution, loss of biodiversity and global habitat, destruction of habitat, making agricultural areas less durable, endangering human health, decreasing farm incomes and shrinking agricultural lands (Çakmakçı et al., 2023a). Moreover, as a result of excessive amounts of nitrogenous fertilizers used to promote plant growth (Çakmakçı, 2019; Lim et al., 2021), ammonia emissions (Xu et al., 2019), soil acidification, nitrogen oxides, nitrate pollution in water and environmental problems are increasing (Çakmakçı, 2016; Ward et al., 2018) and the chemical pesticides used cause pollution in food, feed, water and soil (Sørensen et al., 2021). In addition, although animal husbandry is an important sector of food and many countries' economies today, the sustainability of meeting the ever-increasing demand for meat and dairy products through traditional means is debatable due to the increasing need for quality feed and the low efficiency of the feed's conversion to protein (Alberti et al., 2022; Newman et al., 2023; Rasool et al., 2023).

Agro-based industries produce significant amounts of waste, which in turn disrupts the sustainability of the ecosystem. Therefore, integrated technologies for waste management and the development of new protein sources are necessary. Therefore, cellular agriculture has emerged as an alternative biotechnology that allows the production of food or food components by cell cultures in bioreactors (Rischer et al., 2020; Woern ve Grossmann, 2023). Especially due to protein scarcity worldwide, interest in microbial proteins obtained from food and agricultural wastes, especially fruit residues, as relatively cheap and safe protein sources is increasing. Single cell proteins (SCP) used as protein supplements refer to dead, dried microbial cells or total protein obtained from pure and mixed microbial cultures of algae, yeast, bacteria, filamentous fungi, single-cell algae, cyanobacteria grown on different carbon sources (Reihani et al., 2019; Lähteenmäki-Uutela et al., 2021; Thiviya et al., 2022a). Using cellular agriculture techniques, the development of a sustainable and resilient food system can be promoted by developing cheaper and environmentally friendly alternative protein sources by recycling agricultural industry waste resources.

Cellular Agriculture and Single Cell Proteins

Cellular agriculture is a new field of biotechnology that aims to find alternatives to the agricultural production of various foods and their components. An important area of cellular agriculture is the production of SCP using microorganisms and microalgae as food and feed with high protein content (Nyyssölä et al., 2022). As a branch of cellular agriculture, the use of microorganisms for the harvesting of SCP or microbial protein (MP) is gaining more and more attention. Recent advances in biotechnology and fermentation technology have led to significant breakthroughs in microbial protein synthesis, increasing efficiency and scalability. Single cell proteins are biomass or protein extracts obtained from a single or mixed culture of microorganisms.

Some advantages of using microorganisms for single-cell protein production are that production is not affected by seasonal and climatic changes; growth rates are rapid under optimum conditions; genetics can be easily modified; protein has high nutritional value compared to other agricultural foods; it is possible to use low-value agro-industrial residues and by-products as substrates; and small, decentralized land area is required for continuous fermentation processes (Gundupalli et al., 2024).

Microbial protein production, high efficiency due to rapid development rate in substrate conversion, can use cheap and abundant agricultural waste as carbon and energy source for development and biomass production and can help reduce environmental impact caused by improper waste management (Mensah et al., 2017). Using microorganisms for SCP production for food purposes has advantages such as rapid growth, lower area requirement, lower water requirement, and independent production from climate or season compared to plant and animal proteins; however, it requires a growth medium under controlled conditions such as temperature, oxygen, light and continuous mixing (Sharif et al., 2021; Bertasini et al., 2022; Salazar-López et al., 2023). Dry SCP produced from agricultural waste is considered as a new opportunity to meet the increasing protein demands for both humans and animals (Kumar et al., 2024).

While it is possible to produce new types of food and food components through microbial fermentation, alternative proteins and animal tissues such as artificial meat can be produced in bioreactors using stem cells, albeit on a very small scale, as a result of developments in synthetic biology techniques, stem cell biology and tissue engineering (Rubio et al., 2020; Zhang et al., 2020). In addition to protein content, SCP contains fat, carbohydrates, nucleic acids, fatty acids, vitamins and minerals and is rich in certain essential amino acids such as lysine, threonine and methionine. To meet the demands for food security and healthy nutrition, the use of biosynthesis technologies and industrial-scale bioreactors to grow microbial cells and the importance of certain food raw materials accumulated by microorganisms will increase (Yang et al., 2022a).. Although skin, fish, egg, milk and seafood proteins have been successfully produced with cellular cultivation (agriculture, farming) techniques, which are indeed promoted as a new forward-looking solution, artificial meat production is still in its early stages and is still in its research phase (Hassoun et al., 2024).

Microbial Proteins

Microbial proteins, commonly known as SCP, are commonly obtained from microalgae, fungi, yeasts or bacteria. Microbial SCP has a protein content of 30-80% on a dry mass basis, depending on the substrate and microorganisms used. Algae have the highest protein content of 60-70% of the sources used for SCP production, followed by bacteria with 30-80%, yeast with 30-50% and protists with 10-20% (Bertasini et al., 2022). Bacteria such as *Methylophilus methylotrophus*, *Rhodopseudomonas palustris* and *Haloarcula* sp. produce 50-80% protein, fungi such as *Aspergillus niger* and *Fusarium venenatum* contain up to 63% protein (Helmy et al., 2024), microalgae such as *Chlorella sorokiniana* and *Arthrospira platensis* can produce up to 70% protein of cell biomass, and yeasts such as *Saccharomyces cerevisiae* and *Candida tropicalis* have superior nutritional quality as good protein sources (Jach et al., 2022).

The rapid growth power of microorganisms with high protein content can be used in biomass cultivation to produce large amounts of protein (Bajić et al., 2023). Synthetic biology technology, which is based on the design, transformation, and even re-synthesis of microorganisms for desired targets and the interdisciplinary integration for the design of living systems (Huang ve Nikel, 2019),, is expected to increase the production capacity of the food industry by creating new species and technologies and reduce pollution and energy consumption(Shi et al., 2022).

It is envisaged that in the future, the food industry will change the way food is produced through the integration of food technology, biotechnology and information technologies, and that the food of the future will be produced in an efficient, environmentally friendly and sustainable way, largely in industrial workshops (Wang and Zhang, 2024).. In the food production chain, the use of microorganisms in cell factories for preservation, development of desired properties, formation of flavor and production of valuable compounds, natural preservation methods for the reduction of chemical preservatives and the development of microbial combinations for fermenting plant-based raw materials are required (Bachmann and Neves, 2019).

In the future, food production must overcome challenges such as water and resource scarcity, environmental impact, temperature changes, food safety, reliability, scarcity and waste, and solve them at low cost (Çakmakçı and Çakmakçı, 2023), while discovering and characterizing new microorganisms with multiple health-beneficial properties and adapting them to new food formulations (Albayrak and Duran, 2022). In particular, it is of great importance to evaluate microbial sources to determine the probiotic potential of new fermented foods that have not been investigated and investigated sufficiently and to develop new dairy or non-dairy probiotic foods. In the future, rapid production of food components such as proteins, lipids and vitamins by microorganisms with environmentally friendly methods through synthetic biology technologies may be a promising alternative. In addition, microbial biomass can provide not only proteins and lipids but also many vitamins such as biotin, folic acid, cyanocobalamin, niacin, pantothenic acid, pyridoxine, ascorbic acid, pantothenic acid, riboflavin, α-tocopherol, β-carotene and thiamine. In the food industry, SCP substitutes, texturizers, flavor enhancers, flavoring agents, vitamin carriers, micronutrient carriers and emulsifiers are widely used to increase the nutritional value of baked goods, soups, ready meals and many other food products (Thiviya et al., 2022; Kumar et al., 2024).

Despite many important developments, it remains unclear how the SCP production sector will evolve (Bajić et al., 2023). It has been reported that today microbial proteins are not used as raw materials but rather as supplementary components, commercial bacterial and fungal production systems support global food-feed supply chains, use food waste to a limited extent because they require pretreatment, are in their infancy, and in some cases are more costly than traditional protein systems (Sobhi et al., 2023). Although SCP currently has a small market share, it is anticipated that it may become an important alternative in the future due to the increasing global protein demand and the increasing need for sustainable food production (Jain et al., 2023). SCP has been commercialized, but research is ongoing on optimization of fermentation conditions, various potential substrates, search for different carbon sources and examination of various microorganisms.

Microorganisms Producing Single Cell Proteins

Some microorganism species, bacteria such as *Cellulomonas, Alcaligenes, Brevibacterium, Lactobacillus* and *Rhodopseudomonas;* algae such as *Spirulina* and *Chlorella*; fungi such as *Aspergillus, Trichoderma, Fusarium*, and *Rhizopusare*; and yeasts such as *Candida, Saccharomyces, Rhodotorula,* and *Rhodosporidium*, are commonly used in SCP production (Thiviya et al., 2022; Kumar et al., 2024). Additionally, cyanobacteria such as *Spirulina* sp., *Arthrospira platensis* and *Aphanizomenon flos-aquae*; Algae such as *Chlorella luteoviridis, C. pyrenoidosa, C. vulgaris, Odontella aurita* and *Tetraselmis chuii*; Yeasts such as *Saccharomyces cerevisiae, Yarrowia lipolytica* and bacteria such as *Clostridium butyricum* are microorganisms accepted for use in food in the European Union Countries (Lähteenmäki-Uutela et al., 2021).

Bacteria

Bacteria are suitable for producing microbial proteins due to their ability to grow rapidly and multiply on a variety of raw materials, from carbohydrates to hydrocarbons and petrochemicals. Among different sources, bacterial single cell proteins are considered sustainable due to their high protein content (reaching up to 80% on a dry weight basis), amino acid content similar to soybean, vitamins, phospholipids and other substances (Gundupalli et al., 2024). Microbial protein producing bacteria include *Brevibacterium, Cellulomonas, Alcaligenes, Rhodopseudomonas* and *Lactobacillus* species, with *Clostridium butyricum* being the most widely accepted species (Kumar et al., 2024). Other bacteria used for SCP include: *Aeromonas hydrophylla, Acinetobacter calcaoceticus, Alcaligenes eutrophus, Methanomonas methanica, Methylococcus capsulatus, Rhodobacter capsulatus, Rhodobacter sphaeroides, Rhodocyclus gelatinosus, Bacillus* sp., *Cellulomonas* sp., *Methylomonas* sp., *Mycobacterium* sp., *Nocardia* sp., *Pseudomonas* sp., *Rhodopseudomonas* sp., *Brevibacterium* sp., *Methilomonas* sp. ve *Methylophilus* sp. (Bajpai, 2017a; Bratosin et al., 2021; Zhang et al., 2024).

Bacterial populations can double in as little as 2 hours, and *Bacillus* sp., *Cellulomonas* sp., *Clostridium* sp., *Sphingobium* sp., and *Rhodococcus jostii* can be used to degrade lignocellulosic biomass (Zhang et al., 2024). According to recent studies, it has been reported that *Bacillus subtilis* (71%), *Rhodopseudomonas palustris* (72-74%) and *Rhodopseudomonas spalustris* (74%) strains with high protein rates are also advantageous in terms of lipids and vitamins (Bratosin et al., 2021). It has also been reported that gas fermenting bacteria for protein production, gaseous hydrogen oxidizing and methane oxidizing bacteria, can be an important alternative that can increase the dry matter cell mass to a protein yield of over 70% without the need for land and organic substrates (Nyyssölä et al., 2022; Woern ve Grossmann, 2023).

Yeast

Yeast is an ideal strain for microbial protein production owing to its rapid growth rate, high cell density, and simple production equipment. However, limitations, such as low cell wall digestibility and high nucleic acid content, have hindered the further development of yeast-fermented proteins (Vong et al., 2017). Biotechnological applications of yeasts, a heterogeneous group of eukaryotic fungi, are currently limited to a select number of species, such as *Candida utilis*, *Kluyveromyces marxianus*, *Yarrowia lipolytica* and *Pichia pastoris*, among which *Saccharomyces cerevisiae* is dominant (Bajić et al., 2022). Among yeasts, species belonging to the genera *Candida*, *Saccharomyces*, *Rhodosporidium* and *Rhodotorula* contain approximately 40–60% protein in dry mass (Kumar et al., 2024). Yeast and fungi are the most accepted and widely used microorganisms for SCP production due to their long-standing use in traditional fermentation (Riesute et al., 2021).

Fungi

Mushroom protein requires less water and land, accounting for only 10% of the carbon emissions associated with meat production, and if mushroom proteins account for 20% of global beef consumption by 2050, annual deforestation and related carbon dioxide emissions could be reduced by 56% (Wu et al., 2024). Mushroom proteins are beneficial for muscle growth and lowering cholesterol (van der Heijden et al., 2023) and have the advantage of high protein digestibility values compared to ground meat, pea, soy and insect protein (Wu et al., 2024). *Fusarium*, a filamentous fungus widely used in microbial protein fermentation, produces mycelial proteins with a savory flavor and meaty texture compared to those of single-cell proteins, such as yeast and bacteria, and can be used as nutritional substitutes (van der Heijden et al., 2023; Wu et al., 20224). The most well-known fungi as SCP producers are *Fusarium venenatum*, *Rhizopus oryzae*, *Aspergillus flavus*, *A. niger*, *A. ochraceus*, *A. oryzae*, *Cladosporium cladosporioides, Monascus ruber, Penicillium citrinum* and *Trichoderma viride* (Valentino et al., 2016; Ritala et al., 2017; Ibarruri et al., 2021; Bajić et al., 2023). However, it has been emphasized that *Penicillium, Fusarium, Alternaria* and *Aspergillus* species may have harmful effects and the possibility of mycotoxin formation during production should be taken into consideration (Perincherry et al., 2019; Kumar et al., 2024).

Algae

Algae are increasingly used in industrial areas due to their rapid growth rate, easy cultivation, prevalence, survival in harsh conditions and contain high-value compounds. Algae are preferred because they are abundant in nature, do not require land, can improve wastewater and produce biomass, can maximize sustainable biochemical and biomass production at low cost and with less energy, and are rich in high-value bioactive substances. Microalgae attract wide attention as a promising food source in terms of food safety and nutrition, as well as their controllable production costs and environmental friendliness (Gao et al., 2024). Microalgae can be found in deep seas, in extreme temperatures, pH and difficult nutritional environments (Montuori et al., 2023; Rasheed et al., 2022; Zou et al., 2022), and they are noted for their rapid reproduction and widespread distribution Gao et al., 2024), as well as being rich in protein, amino acids, fiber, lipids, fatty acids, minerals and various other nutrients (Sandgruber et al. 2023). As a renewable raw material source, microalgae convert waste into value-added products, can be used in bioremediation processes, and have been reported to produce and accumulate carbohydrates, proteins, lipids and fatty acids (López-Pacheco et al., 2023). Although microalgae are rich in essential nutrients such as carbohydrates, protein, fat, minerals, vitamins, and dietary fiber required for humans, they are also rich in various bioactive substances such as bioactive peptides, antioxidant, carotenoids, phenolics, amino acids (Gao et al., 2024).

In addition, studies have shown that microalgae can use the pollutants in waste for growth (Wang et al., 2024), the growth effect is better at high CO_2 concentrations (Vlaskin et al., 2023) and will play an indispensable and important role in pollution control and climate change amelioration (Joun et al., 2023; Nair et al., 2023; Nishshanka et al., 2023). Microalgae have great potential as a biomass source even at low nutrient concentrations in small areas compared to other crops. *Chlamydomonas reinhardtii* produced carbohydrates under low nitrogen, while *Chlorella vulgaris* produced higher lipid content under low phosphorus conditions, and both species showed a better effect on the accumulation of fatty acid methyl esters at low nitrogen (López-Pacheco et al., 2023).

Future Developments and Challenges

Incorporating gas fermentation into the protein supply chain requires identifying strains with optimal growth kinetics from various gas-fermenting bacterial species. Although microbial proteins appear promising, it is known that coordinated efforts and interdisciplinary approaches are required to ensure the sustainability, quality and safety of microbial protein products; there are still obstacles to overcome in areas such as customer acceptability and industrial scalability (Dalbanjan et al., 2024). The strain or strains selected to produce SCP should be easy to grow and grow under industrial fermentation conditions, be resistant to environmental changes, maintain optimum biochemical and physiological properties during the fermentation process and remain stable in metabolism, have a high protein content and allow the accumulation of large amounts of microbial protein in a short time (Zhang et al., 2024).

Research is needed on the isolation and characterization of productive strains for industrial use, as well as extensive research to overcome the cultivation barrier for hydrogenotrophic cultivation, the nutritional barrier regarding protein quality, and the socioeconomic barriers including approval as a novel food by the food authority and acceptance and adoption by consumers. Substrate, fermentation conditions, bacterial strain and post-fermentation processing affect the chemical composition of bacterial biomass (Zhu et al., 2022). Optimum fermentation conditions, inexpensive substrates and a variety of microorganisms need to be investigated. Mixed microorganism cultures have been suggested to increase microbial biomass yield and improve protein quality (Yadav et al., 2014). However, it is important to consider the interactions between strains in mixed cultures. The resilience of food systems requires strategies to feed urban populations, as well as attention to the sustainability and security of food, water, nutrition and biodiversity (Keith et al., 2023; Knorr and Augustin 2024).

Food security, sustainable food production, and nutrition improvement along with resource depletion, energy crisis, environmental pollution, and climate change have long been widely discussed. In addition, increasing production costs, green production requirements and the effort to find alternative products are becoming increasingly important along with consumer demands. With food security challenges, it is critical to address food production sustainably for future generations. In this respect, microorganisms stand out as resources that will close the gap in food production. As the world population increases, the demand for environmentally friendly, safe and sustainable products derived from bio-based resources is increasing. As the increasing pressure on arable land reduces agricultural land, innovative protein supply chains are required that can significantly reduce the need for arable land and at the same time have a low environmental impact.

Statement of Conflict of Interest

The authors) should declare that they are no conflict of interest.

Authors' Contributions

Conceptualization, R.Ç. and S.Ç.; investigation, S.Ç. and R.Ç.; writing-original draft preparation, R.Ç. and S.Ç.; writing—review and editing, S.Ç. and R.Ç.; visualization, S.Ç. All authors contributed equally to this work. All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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Pistachios: Human Health Perspective

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ABSTRACT: In recent years, there has been intense interest in fruits that are grown healthily and contain important substances for health in the world. Each fruit group contains different substances that are important for human health. Berries are especially rich in anthocyanins, while nuts stand out in terms of their fatty acid composition. It would not be wrong to use the term antioxidant properties in general for all fruits because they contain substances that have antioxidant effects in different amounts. In recent years, there has been an increasing interest in nuts from a human health perspective as well. These fruits, which are widely consumed in the Mediterranean diet, are gradually increasing their volume in the market. Nuts such as almonds, hazelnuts, cashews, macadamia nuts, walnuts and pistachios are nutrient-dense foods and among them pistachios has unique composition. In general, pistachios contain healthy monounsaturated (MUFA) and polyunsaturated (PUFA) fatty acid profiles; protein, soluble and insoluble fibers; vitamins E and K; folate; thiamine; minerals such as magnesium, copper, potassium and selenium; and contains substances such as xanthophyll carotenoids, antioxidants and phytosterol compounds that have known benefits for human health.

Keywords: Nuts, Human Health, Composition, Fatty Acids

INTRODUCTION

Among the horticultural plants, which are very important in agricultural production, there are fruits, vegetables, flowers and grapes. However, it is possible to examine fruits under different groups. The main groups are berries, stone fruits, pome fruits, nuts and citrus fruits. When many fruits are evaluated on a product basis, they are of great importance in terms of human nutrition and health. Many fruits provide various vitamins (especially vitamins A and C), antioxidants, carotenoids and secondary metabolites, especially minerals. However, the consumed products are also abundant sources of protein and carbohydrates (Halvorsen et al., 2006).

One of the main features of fruits containing different groups is that they are considered nutraceutical. On the other hand, fruits are especially rich in fiber. Another feature of fruits is that they are a great source of vitamins and minerals. Fruits are also very rich in phenolic substances, anthocyanins and flavonoids, which are extremely important for human health. All these substances are called antioxidant substances in fruits. A diet rich in different fruit groups can reduce a person's risk of diabetes, weight control, intestinal diseases, sexual disorders, cancer, inflammation, heart disease and other diseases. Many studies have shown that fruits are very effective in preventing human diseases. Fruits are known to be good providers of phytochemicals necessary to ward off degenerative diseases such as cancer and cardiovascular diseases. They have a number of antioxidants that can be used to neutralize reactive oxygen species (ROS).

The total production of horticultural crops in the year 2022 was 8 billion tons (t), which at the time contributed toward 37% of the total agricultural gross domestic product (GDP) globally. In the year 2023, fruits, vegetables, tubers and roots, nuts, and spices were cultivated in ~274 million ha of agricultural land worldwide, producing a total of ~4.7 billion t of produce (Figure 1) (FAOSTAT, 2024).

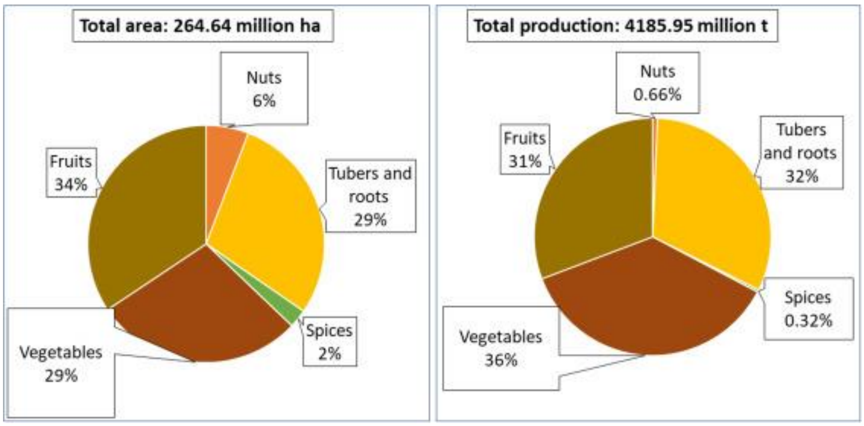

Figure 1. Horticultural production in the world

Pistachios and Human Health

Pistachios, which have an important place among nuts, are highly recommended by health experts due to the high bioactive substances contained in their fruits. In addition to their aromatic taste, pistachio fruits are also very rich in healthy oils, including mono- and poly-unsaturated fatty acids and low saturated fatty acids (Tables 1-3). Compared to other nuts, pistachio fruits attract attention because they contain the highest concentrations of potassium, γ-tocopherol, phytosterols and xanthophyll carotenoids, and they are also an important source of healthy nutrition (Dreher, 2012; Liu et al., 2014; Bulló et al., 2015).

On the other hand, in a very detailed study conducted on many fruit species, pistachio fruits were listed among the 50 foods with the highest antioxidant polyphenols (Halvorsen et al., 2006). Grace et al. (2016) examined pistachios in detail in terms of phytochemical content and according to the results they obtained, they revealed that especially fatty acids, phytosterols and tocopherols were abundant in lipophilic extracts obtained from both the shell and the seed of pistachios. On the other hand, these lipophilic fractions significantly reduced lipid accumulation in mature fat cells. Mandalari et al. (2013) reported in a very detailed study conducted on pistachios that xanthophyll carotenoids, namely lutein and zeaxanthin, which they found only in hazelnuts in hard shells, were found in significant amounts in pistachios. The researchers also revealed that the pistachios they examined contained significant amounts of tocopherol and phenolic compounds. The phenolic compounds, especially anthocyanins, gallic acid, catechin and quercetin, which are abundant in pistachios, are the main water-soluble extracts and are of great importance for human health. These are compounds containing one or more aromatic rings and hydroxyl groups, including phenolic acids, flavonoids, stilbenes, coumarins and tannins (Liu, 2004).

Pistachios, which have an important place among fruit species and offer a profitable investment opportunity to growers, provide various health benefits to people with the consumption of their fruits, as they are an excellent source of many important bioactive compounds (West et al., 2012; Hernández-Alonso et al., 2014; Ribiero et al., 2017; Dos Santos et al., 2020). Various phenolics, especially those found in pistachios, are effective in stopping the formation of active oxygen species and provide significant protective effects against the oxidation of some indispensable biological macromolecules. Studies have shown that the consumption of pistachio fruits is associated with a decrease in the risk of mortality, total cancer, and all-cause mortality (Seifaddinipour et al., 2020; Naghshi et al., 2021).

In bioaccessibility studies conducted on pistachio fruits, it has been revealed that some bioactive compounds, especially polyphenols and xanthophylls, show rapid accessibility in simulated human digestion and their benefits for human health have been demonstrated (Mandalari et al., 2013). In recent years, increasing health-related studies on pistachio fruits show a significant negative relationship between the consumption of pistachio fruits and cancer and other chronic disease risk factors (Canudas et al., 2019; Naghshi et al., 2021). Studies have also revealed that the phytochemicals contained in pistachio fruits potentially exhibit enhanced antioxidant activity and reduce oxidative stress markers in healthy individuals (Kocyigit and Keles, 2006). Fabani et al. (2013) revealed that these phytochemicals, which are common in pistachio fruits, take part in the antioxidant defense system by preventing the production of some pro-oxidants, scavenging free radicals and reducing reactive oxygen intermediates.

Previous studies had reported that pistachios were rich in both non-polar and polar bioactive compounds (Yang et al., 2009; Mandalari et al., 2013; Stuetz et al., 2017). Yuan et al. (2022) reported that pistachios are rich for total phenolics, flavonoids, vitamin E and carotenoids and antioxidant activity, cellular antioxidant activity and antiproliferative activity.

Table 1. Oil, triacylglycerol, sterol and energy values of different nuts (Miraliakbari and Shahidi, 2008)

Nuts	Oil (%)	Triacylglycerol	Sterol	Energy kcal
Almonds	53.0	98.0	0.25	581
Walnuts	72.5	97.1	0.28	618
Pistachio	54.1	95.8	0.21	557
Cashew	45.0	96.0	-	553
Brazil nuts	68.9	96.6	0.19	656
Pine nut	75.1	97.1	0.16	629
Pecans	73.4	96.3	0.28	691
Macadamia	71.0	-	-	718
Hazelnuts	61.9	97.6	0.22	629

Table 2. Total fat, SFA, MUFA, PUFA, 18:2n-6 and 18:3n-3 values of different nuts (Kim et al., 2017)

Nuts	Total fat	SFA	MUFA	PUFA	18:2n-6	18:3n-3
Almonds	50.6	3.9	32.2	12.2	12.2	0.00
Walnuts	65.2	6.1	8.9	47.2	38.1	9.08
Pistachio	44.4	5.4	23.3	13.5	13.2	0.25
Cashew	46.4	9.2	27.3	7.8	7.7	0.15
Brazil nuts	66.4	15.1	24.5	20.6	20.5	0.05
Pine nut	68.4	4.9	18.8	34.1	33.2	0.16
Pecans	72.0	6.2	40.8	21.6	20.6	1.00
Macadamia	75.8	12.1	58.9	1.5	1.3	0.21
Hazelnuts	60.8	4.5	45.7	7.9	7.8	0.09

Table 3. Total phenol, flavonoids, proanthocyanidins, stilbenes, carotenoids and phytatesof different nuts (Kim et al., 2017).

Nuts	Total phenol (mg GAE/100 g)	Flavonoids (mg/100 g)	Proanthocyanidins (mg/100 g)	Stilbenes (mg/100 g)	Carotenoids (mg/100 g)	Phytates (mg/100 g)
Almonds	261	25.01	184.10	ND	0.002	2542
Walnuts	1602	0.54	67.25	ND	0.021	2070
Pistachio	703	136.45	252.71	0.80	22.83	1562
Cashew	242	1.12	8.70	ND	0.031	697
Brazil nuts	197	0.85	0-10	ND	-	190
Hazelnuts	447	13.21	500.66	ND	0.106	1285
Macademia	233	137.90	0-10	ND	ND	470
Pecans	1588	2713.49	494.05	ND	0.055	851

Figure 1 indicate pistachio processing: from harvest to consumer. As indicated in Figure 1, pistachio nuts (closed and open shell) illustrating their unique colors due to the presence of bioactive compounds, mainly lutein (yellow), anthocyanins (red) and chlorophyll (green) (Mandalari et al., 2022).

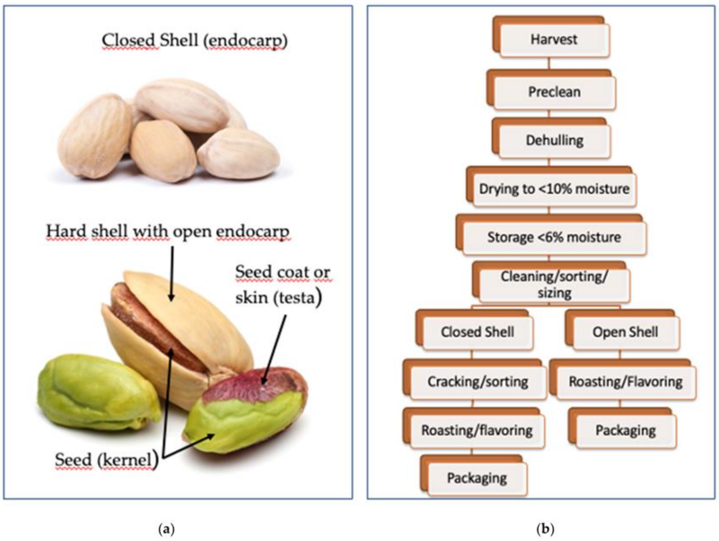

Figure 1. (a) Pistachio nuts (closed and open shell) illustrating their unique colors due to the presence of bioactive compounds, mainly lutein (yellow), anthocyanins (red) and chlorophyll (green); (b) pistachio processing: from harvest to consumer (Mandalari et al., 2022).

Pradhan et al. (2021) indicated that pistachio consumption and health benefits could be explain as;

-Cardiovascular disease:Reduced the risk of CVD through better blood lipid profile and imparting antioxidant activity),

-Obesity:Main mode of weight control of pistachios through, increased satiation, satiety signals and lower metabolizable energy),

-Diabetics:Fibre, healthy fats, low available carbohydrates and carotenoid content of pistachios are the important nutrients involved in glucose metabolism,

-Cancer: Presence of phytochemicals such as flavonoids and quercetin and kaempferol and their antioxidant, antimicrobial, enzyme inhibitory and radical scavenging effects to control cancer.

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Directions for Creating Sustainable Economic Development of Food Security in the Country

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ABSTRACT: Providing the country's population with food products is important for the country as well as one of the socio-economic problems, the solution of which is made up of national, economic, social, demographic and environmental factors. In this regard, the socio-economic system at the country level is directly related to food security, therefore ensuring food security is based on the mobilization of resources available in the country. A reliable food supply is essential for the stability of a country's economic and social stability. In this regard, the state of Azerbaijan implements multifaceted measures in the direction of reliable supply of food products to the population, implements large-scale state programs aimed at the development of the agricultural sector, on which food security directly depends. Currently, the reliable supply of food products to the country's population is one of the main directions of economic policy. The article clarified a number of issues, including the essence of food security, its specific features, as well as the basis of the economic rise of food supply in the transition to a sustainable development model, as well as the stability of economic and social relations with the formation of a market economy in the country.

Keywords: Food Security, Agricultural Sector, Food Supply, Sustainable Development, Internal Food Market, Level of Self-Sufficiency, etc.

INTRODUCTION

The basis of the policy of development of the agricultural sector, which provides reliable food supply to the country's population and provides employment to a large part of the population, was laid in the mid-90s. Among the CIS countries, the fastest land reforms were carried out by Azerbaijan, assistance mechanisms for agricultural producers were created, and important projects in this field were started to be implemented together with international organizations, including the World Bank and the UN Food Organization (FAO). In 2001, the food safety program of the Republic of Azerbaijan was approved by the decree of the head of the country, and as a result of the works carried out within the program, the production of agricultural and food products increased significantly. Later, as a result of the rapid economic development in Azerbaijan, measures were taken to further develop the agricultural sector. The development of the agricultural sector is one of the main directions of the president's economic diversification strategy. Thus, in terms of the employment of approximately 1.5 million people of the country's population in the agricultural sector, the development of this sector is of special importance both in terms of the development of the non-oil sector and the reduction of unemployment and poverty. [2]

In general, hundreds of decrees, orders, laws, decisions and other normative-legal documents were adopted on the implementation of reforms in the agrarian sector and its further deepening, the formation of property relations and entrepreneurship, the formation of new property relations in the agrarian section and the creation of various types of economic subjects, at the same time , the directions of the state protection of the agrarian division and the legal bases of the state regulation of the agrarian market were created. As a result of implemented agrarian reforms, adopted legal and regulatory documents, comprehensive support of agricultural producers by the state, and targeted measures to ensure food security by meeting the growing demand for food products of the population, especially cereals and legumes, potatoes, vegetables and melons dynamic development has been achieved regularly in the production of livestock products [11, p.256]

The conducted studies show that the dynamics of the gross domestic product (GDP) in the last 10 years (2012-2022) show that the country's economy has grown more than twice. During this period, the GDP per capita increased approximately 2.3 times. It should be noted that in Kazakhstan, which is considered to be the second strongest economy of the CIS, the relevant indicator has increased almost 6 times. As it can be seen, Azerbaijan surpassed other Caucasian countries in terms of the growth rate of the economy by almost two times, and also took the first place in the CIS. In addition, during the mentioned period, factors determining economic growth have also been diverted. So, if the reason for economic growth in previous years was strong production in the oil sector, in 2018-2022, the non-oil sector played a leading role in the growth of GDP. The analysis of the data shows that our republic's efforts in diversifying the economy by effectively using oil revenues have yielded successful results. In other words, over the past 20 years, the dependence of economic growth on the oil factor has been reduced to a minimum, and a production environment more adapted to market conditions has been formed, as a result of which the dynamism of economic growth and the reduction of dependence on oil have been ensured. [7]

Ensuring food security in the country is based on the establishment of regional units distinguished by the creation and management of sustainable economic development. Sustainable and complex creation of food products should be achieved during globalization. Rather, the sustainable development of food products is important in terms of providing the country with food products.

The concept of sustainable development of the country's food supply shows the provision of quality food products to the population on the scale of economic and social problems. As we know, the model of the idea of "sustainable development" was adopted by the UN World Commission on Environment and Development, which requires the creation of an effective management mechanism for the protection of food products - a complex of various structural areas of the agricultural economy based on new technologies. Also, in addition to showing the basis of the economic rise of food supply in the transition to a sustainable development model, it also ensures the stability of economic and social relations with the formation of a market economy in the country.

The development of agriculture occupies a leading place in the state's poverty alleviation and socio-economic development programs. Implementation of tasks provided for in documents such as the State Program for Poverty Reduction and Economic Development of the Republic of Azerbaijan in 2003-2005, the State Program for the Development of Small and Medium Enterprises in the Republic of Azerbaijan (2002-2005); The socio-economic development of the regions of the Republic of Azerbaijan State Programs and other documents, including the provision of financial and technical support to farmers, the development of entrepreneurship in the regions, the special weight of the local population in the implementation of infrastructure projects has increased. The program of socio-economic development in the Republic of Azerbaijan in 2008-2015, the State Program of the socio-economic development of the regions of the Republic of Azerbaijan in 2019-2023, the "State Program for the Development of Social Services in the Republic of Azerbaijan for 2023-2026" are primarily of the region aimed at ensuring food security and eliminating unemployment. Solving these problems is the basis of the development strategy of the agrarian sector and is closely related to the agrarian sector. [1-2-3-4]

Currently, one of the main priority issues in the republic is to reduce the dependence of the economy on oil and to ensure that the economic development is directed in other directions. A number of decrees and orders of the state have been approved and are being successfully implemented for the systematic and consistent implementation of measures related to the diversification of the economy. At the same time, in terms of ensuring food security and the formation of a reliable food supply system, these state programs, which are successfully implemented in order to ensure the full and efficient use of the economic potential in the regions of the country, the improvement of the socio-economic situation and the balanced development of the economy, contribute to the comprehensive development of the regions, and including the restoration and expansion of infrastructure areas, the creation of new production and processing enterprises, socio-cultural facilities, the opening of new workplaces, and the further improvement of the population's standard of living.

As we mentioned, meeting the population's demand for food products has always been at the forefront of the hierarchy of needs throughout history. From this point of view, food security is considered to be the main principle of food supply of the country's population at the macro level. Ensuring food security is one of the main problems facing every country, and at the same time, this issue is also important from political, economic, social and other aspects. As it is known, insufficient provision of food security endangers the country's economic sovereignty and poses a serious threat to its existence. From this point of view, it is important to ensure the production of sufficient food products in the country, to form a food market where there is no fair monopoly, and at the same time, the interests of producers and consumers are optimally satisfied. The normal functioning of the domestic food market depends on the presence of sufficient domestic production, regulation of imports, and the level of income of the population, etc. depends on factors.

Material and Method

The normal operation of the domestic food market allows optimal solution of the issue of food security. It can be concluded that there is a close connection between the domestic food market and food security. Therefore, the good provision of food security indicates the normal functioning of the food market, and the normal functioning of the food market is also the harbinger of the good provision of food security. The assessment of the reliable supply of food products to the population is the same as the assessment of food security. This is determined using the following indicators:[7]

- the possibility of physical acquisition of food - the possibility of obtaining high-quality and safe food in the market of food products, anywhere in the country, at any time;

- the possibility of economic acquisition of food - the possibility of obtaining quality food products at prices that correspond to the interests of all groups of the population and their income level;

- availability of food that is safe for consumption - the content of the food meets the appropriate quality standards and protection of the domestic food market from low-quality food products.

Absence of one of these factors does not allow full payment of food security. At the same time, maintaining these indicators at a normal level is one of the most necessary issues. Of course, meeting the demand for food products at the expense of local production is one of the main issues.

In recent years, a serious increase in the production of food products has been observed in our republic. Increased food production improves food security. The conducted studies show that as a result of the purposeful economic policy implemented in our country, the provision of food security is getting stronger. The dynamics of production of basic food products can be seen from the table below.

Table 1. Production of basic food products in the Republic of Azerbaijan, per person (kg)

Commodities	**2018**	**2019**	**2020**	**2021**	**2022**	**% in 2022 compared to 2018**	**% in 2022 compared to 2021**
Grain (net weight)	329	348	318	327	305	92,7	93,2
Potato	92	101	104	106	106	115,2	100
Vegetables	155	173	174	181	181	116,7	100
Vegetables for food	41	45	45	46	46	112,2	100
Sugar beet (for processing)	28	22	23	18	21	75	116,6
Fruits, berries	103	111	114	120	124	120,3	103,3
Meat (cut weight)	34	34	35	36	36	105,8	100
Milk	212	217	220	222	224	105,6	100,1
Fish	171	184	191	184	200	116,9	108,6
Eggs, pcs	6,3	6,4	6,1	5,9	5,9	93,6	100

Source: The table was compiled by the author based on the data of the State Statistics Committee of Azerbaijan.

Studies show that the increase in the production of most food products in recent years has led to an increase in per capita food production. So, compared to 2018, in 2022, grain production per person will decrease by 92.7 percent, fish production by 93.6 percent, sugar beet production for processing by 4.8 percent, vegetable production by 16.7 percent, potato production by 15 percent. ,2 percent, the production of melon plants for food increased by 12.1 percent, the production of fruits and berries by 20.3 percent, the production of cut-weight meat by 5.3 percent, the production of milk by 5.6 percent, and the production of eggs by 16.9 percent. Compared to 2021, in 2022, grain production per person decreased by 93.2 percent, potato production by approximately 1 percent, sugar beet production for processing by 16.3 percent, fruit and berry production by 3.3 percent, meat production by 1 percent, milk production increased by 0.1 percent, egg production by 8.6 percent, and melon production for food increased by 16.6 percent. The increase in the production of food products per person acts as one of the main factors of creating an abundance of products in the domestic agricultural market and raising the standard of living of the population.

The conducted studies show that as the standard of living of the population increases, changes occur in the consumption of food products and the structure of their consumption. Thus, the way people look at the concept of quality is changing, new demands are emerging, and the demand for non-food products is increasing. Deterioration of the standard of living of the population increases the consumption of necessary food products. Sometimes, the increase in their prices also stimulates the demand for these types of food products. For example, according to the observations of the 19th century British statistician Robert Giffen, who studied the consumption structure of the Icelandic population, the serious increase in the price of bread was not due to a decrease in the demand for it, but rather a sharp increase. The reason for this was that the increase in the price of food products resulted in the simplification of the food ration by the low-income population, giving preference to relatively cheaper and more caloric food - bread. This has led to an increase in the demand for bread [6, p. 529–533.]

The realities of Azerbaijan's development model show that the replacement of closed economic development realities with an open economy model has opened wide prospects for sustainable development. That is why the raw material base of the food sector, which is considered the most closed area of economic development, is relevant in the scientific and practical sphere. In the strategy of providing the population with quality food products and raw materials for the food-industrial complex, the organization and management of agriculture based on new technologies is consistently implemented by the state. [8, p. 41]

However, the increase in the level of economic development of our country is manifested in the increase in the standard of living of the population, the logical result of which is the improvement of the standard of living of the population. The increase in the standard of living of the population is reflected in the growing share of non-food products in the consumption of food and non-food products. In recent years, positive changes in this direction have been felt in our country.

The increase in the standard of living of the population is reflected in a number of indicators. One of them is the minimum wage indicator. Thus, this indicator was 250 manats in 2019, 300 manats in 2022, and 345 manats in 2023. The increase in the level of economic development of our country has led to positive changes in the dynamics of a number of indicators. This increase continues every year. Another indicator of the living standard of the population is the average monthly salary in the country. According to the information provided by the State Statistics Committee, the average monthly nominal salary in the country in 2020 was 707.7 manats, while in 2022 it was 840 manats. The highest wages were observed in the mining industry, while the lowest wages were observed in agriculture. According to economic regions, the highest salary is in Absheron. The main reason for this is the fact that the mining industry is mainly located in this region, the capital is located here, and the relationship between supply and demand in the labor market.[5]

As we know, the minimum living wage approved for the country also plays a role in determining the need criterion for determining the minimum amount of wages, allowances, pensions, other payments and targeted state social assistance. Also, let's note that the living wage for 2023 is 246 manats for the country, 261 manats for the working population, 199 manats for pensioners, and 220 manats for children.

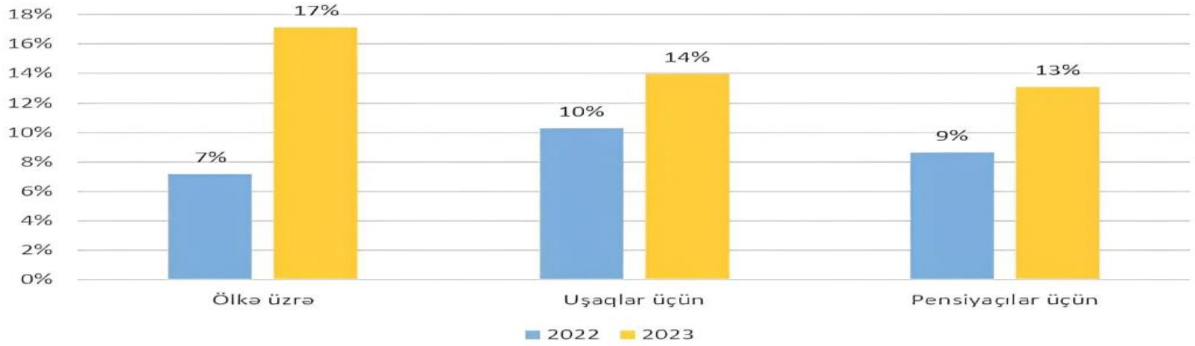

Figure 1. Growth rate of living wage.

As we can see from the picture, the growth rate of the living wage in 2023 compared to 2022 increased by 17 percent for the country, 14 percent for children, and 13 percent for pensioners.

Results and Discussion

Thus, let's note that the main elements of food security include the physical and economic access of every citizen to quality food, the economic independence of the country's national food system, i.e. independence from exports of basic food products, reliability, i.e. the food system's seasonal, weather and it implies protection from risks related to other factors, stability, that is, the development of the national food system in the mode of production expansion.

By examining the internal food market and the factors affecting it, it can be concluded that this market is formed and operates under the influence of various factors. Although economic factors are considered the main factors of the domestic food market and this market is mainly formed under the influence of supply and demand, there are other factors that influence it. One of these factors is the social factor. The standard of living of the population, minimum living wage, consumer basket, minimum wage, average monthly nominal wage, etc. included in social factors. At the same time, environmental, demographic, political, etc. factors affect the food market. factors also affect. Investigating and correctly assessing the impact of these factors is important in terms of preventing unpleasant events that may occur in the domestic food market, and implementing adequate regulatory measures before it's too late.

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Contribution to Dactylogyrid Fauna (Platyhelminthes, Monogenea) of some Introduced Fishes from the Lake Ohrid, N. Macedonia

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ABSTRACT: The fish fauna of Lake Ohrid is represented by 17 autochthonous species from four families: Salmonidae (2), Cyprinidae (12), Cobitidae (1), Nemacheilidae (1) and Anguillidae (1) and six allochthonous species (belonging to four families). A special feature of Lake Ohrid is its high degree of endemism. This also applies to the fish. There are seven endemic fish species in the lake. The stone moroko *(Pseudorasbora parva)* and the European bitterling *(Rhodeus amarus)* are among the fish species introduced into Lake Ohrid. The problem with the introduction of fish and other animal species from other regions of the world is that almost completely unknown species of parasites are introduced with them. Data on non-native fish parasites are important to assess the health status and their overall impact on native fish populations. The introduction of non-native species can have a significant impact on native species populations and the ecosystem, but can also have socio-economic consequences caused by major damage to a country`s fisheries and aquaculture. Invasive species can contribute to the life cycle of native parasites. If an invasive species can serve as a suitable (e.g. intermediate, paratenic or definitive) host for native parasites, these parasites can "spill over" to other native hosts, increasing their infection rates in the native host populations in newly invaded habitats. The parasitological survey from the Macedonian part of Lake Ohrid in 2024 showed that two out of eight examined specimens of the stone moroko (25.0%) and two out of four European bitterlings were infested (25.0%). In our case study, the presence of two dactylogyrid species was detected: *Dactylogyrus squameus* in *Pseudorasbora parva* and *Dactylogyrus bicornis* in *Rhodeus amarus.* Both monogenean parasites were detected for the first time in the ichthyoparasitofauna of their hosts from Lake Ohrid and N. Macedonia.

Keywords: *Dactylogyrus*, Stone Moroko, European Bitterling, Lake Ohrid

INTRODUCTION

Lake Ohrid is located in the extreme south-west of Macedonia. With an estimated age of 2-3 milion years, the oligotrophic and karstic Lake Ohrid is the oldest lake system in Europe. It is a transboundary waterbody in the Western Balkans, shared by North Macedonia (2/3) and Albania (1/3). It lies 695 metres above sea level, has a maximum depth of 289 metres (average depth 164 metres), and an area of 358 km^2. One of the most voluminous lakes (~55 km^3) in Europe, with a long residence time of the water (83 years).

Lake Ohrid is the only ancient and long-lived lake in Europe and a biodiversity hotspot of global importance. It is rich in species, but their abundance is low. About 1,200 native species live in the lake, including at least 212 endemic species. The adjusted rate of endemism is estimated at 36%. Endemic biodiversity: 212 known endemic species + 358 km^2 area = most diverse lake in the world and so-called “Museum of living fossils".

The fish fauna of Lake Ohrid is represented by 17 autochthonous species from four families: Salmonidae (2), Cyprinidae (12), Cobitidae (1), Nemacheilidae (1) and Anguillidae (1) and 6 allochthonous species (belonging to four families). A special feature of Lake Ohrid is its high degree of endemism. This also applies to the fish. There are seven endemic fish species in the lake. The stone moroko *(Pseudorasbora parva)* (Fig. 2) and the European bitterling *(Rhodeus amarus)* (Fig. 3) are among the fish species introduced to Lake Ohrid.

Figure 1. Lakes Ohrid & Prespa

Figure 2. *Pseudorasbora parva* from Lake Ohrid

Figure 3. *Rhodeus amarus* from Lake Ohrid

Invasive species impair the functions and services of the ecosystem and have a major economic impact. Fish species are important invaders, with a large number of species having been introduced by human activities outside their original biogeographical region. Predation, habitat degradation, competition for resources, hybridization and disease transmission are considered key factors associated with the introduction of invasive alien fish. The threat of alien pathogens, often associated with other invasive species that serve as reservoirs, is poorly recognised and deserves more attention in risk assessment and management of biological invasions. Pollution from pathogens introduced by invasive fish species remains largely undetected in current monitoring programmes, so the causes of the harmful effects on native species are unknown (Spikmans et al., 2020).

In aquatic ecosystems, fish play a key role in the transmission of parasite to predatory animals. Small fish act as effective mediators between these two levels, because birds and mammals that can feed on tiny planktonic copepods or small snails are rare. The importance of fish as paratenic host species has been confirmed in many ecological studies (Ondračková et al., 2009).

Rhodeus amarus is a widespread and abundant small fish and can therefore be a suitable intermediate host for many parasite species. As *R. amarus* lives in many European countries in different environments such as rivers, backwaters, artificial canals and estuaries (Kozhara et al. 2007), it can be infested by a relatively large number of parasite species.

The Asian cyprinid *Pseudorasbora parva,* which originates from China and Southeast Asia, is considered a major threat to native fish communities and is included in the European Union`s list of invasive alien species of concern. The spread of *P. parva* is considered one of the most impressive examples of fish invasion in the world (Spikmans et al., 2020).

As small and fast-maturing fish with a wide distribution range and high local abundances in various habitats, *Rhodeus amarus* and *Pseudorasbora parva* are natural and common prey for a variety of piscivorous animals such as fish, reptiles, birds and mammals. In addition to their natural role in the food web, they could therefore also play an important role as vectors of a variety of metazoan parasites to their final hosts.

The composition of the parasite community of the European bitterling *(R. amarus)*, the only bitterling species occurring on the European continent, was studied by Davidova (2008, 2011) at 16 different sites in 4 European sea drainages and a total of 41 species of metazoan parasites were identified. Nine parasite species are new records for the European bitterling. Three parasitised species were most abundant: the host-specific monogeneans *Dactylogyrus bicornis* and *Gyrodactylus rhodei* and the generalist larval digenean *Paryphostomum radiatum.*

The parasite community of the European bitterling was characterised by the dominance of generalists and larval parasites that use fish as intermediate hosts and birds as final hosts. The rare occurrence of ectoparasites and adult endoparasitic species reflected the specific diet of the fish host. Host body size was positively correlated with parasite species richness, but variability explained by length was low. The overall prevalence and abundance of each parasite species was relatively low.

Yurishinets & Zaichenko (2015) reported the detection of 55 parasite species in *Pseudorasbora parva* from Ukraine and Bulgaria based on original and literature data. Some parasite species were introduced into non-native water by *P. parva*. Most of these were organisms with a simple life cycle (80%), without changes in the host animal. Overall, the parasite fauna of *P. parva* in the native distribution area was mainly represented by native species with broad host specificity (80%).

Linowska et al. (2019) found 8 parasite species in *P. parva* from Poland and all of them are common parasites in Poland. In the Balkan region, *Dactylogyrus bicornis* was found in *Rhodeus meridionalis* in Greece (Benovics, 2020).

Studies of the parasite fauna of the fish of Lake Ohrid were primarily carried out by Šinžar (1956), who found *Cyatocephalus truncatus* in 2% of the examined belvica (*Acantholingua ochridana*) and *Metechinorhynchus truttae* in the Ohrid trout (*Salmo letnica*).

Stojanovski found no parasites in *Rhodeus amarus* and *Pseudorasbora parva* in his parasitological studies (1997, 2003 and later).

Materials and Methods

Fish material from a total of 8 specimens of the stone moroko (topmouth gudgeon) - *Pseudorasbora parva* (Temminck & Schlegel, 1846) and 4 specimens of the European bitterling - *Rhodeus amarus* (Bloch, 1782) from Lake Ohrid (southwestern N. Macedonia) was subjected to parasitological examinations in 2024. The localities in Lake Ohrid where the studies were conducted were: Ohrid Bay, Gradište and Kališta. Only fresh fish were subjected to routine identification, dissection and observation methods. The cleaned parasites were separated and placed in special fixatives, which were prepared for identification using special staining and clearing techniques (Vasiljkov, 1983; Gussev, 1983). To identify the parasite species, the intestines of the fish were examined with the stereomicroscope "Zeiss Stemi 305" and the microscope "Zeiss Primovert" and the parasites were removed. Identification was based on the morphology of the parasites using reference keys for identification (Bauer, 1985, 1987). The intensity of the infestation was determined by dividing the total number of parasites found by the total number of infested fish.

Results and Discussion

The parasitological survey from the Macedonian part of Lake Ohrid in 2024 showed that 2 out of 8 examined specimens of stone moroko (25.0%) and 2 out of 4 European bitterling (25.0%) were infested (Table 1). In our case study, the presence of 2 dactylogyrid species was detected: *Dactylogyrus squameus* Gussev, 1955 (Fig. 4) in *Pseudorasbora parva* and *Dactylogyrus bicornis* Malewitzkaja, 1941 (Fig. 5) in *Rhodeus amarus*. Both monogenean parasites were detected for the first time in the ichthyoparasitofauna of their hosts from Lake Ohrid and N. Macedonia.

Table 1. Parasite fauna of the stone moroko - *Pseudorasbora parva* and European bitterling - *Rhodeus amarus* from the Lake Ohrid.

Fish species	Parasite species	Prevalence			Intensity of infection
		No. of examined fishes	No. of infected fishes	% of infected fishes	
Pseudorasbora parva	*Dactylogyrus squameus*	8	2	25.0	1.50
Rhodeus amarus	*Dactylogyrus bicornis*	4	2	50.0	2.50
TOTAL		12	4	33.33	2.0

Dactylogyrus squameus was originally described by Gussev (1955) from the gills of *Pseudorasbora parva* from the Amur River and Lake Chanka, Far-East Russia, and later reported from the same host in Heilongjiang, Liaoning, Hubei and Yunnan, China.

The occurrence of *D. squameus* has been confirmed in the irrigation channel of the Lower Dnieper in Ukraine and in the catchment areas of the Lower Morava and Dyje rivers (watershed of the Middle Danube) in the Czech Republic. Previous European records of *D. squameus* include lentic water bodies in the Ticino River in Italy and a fish pond near Kyiv in Ukraine (Ondračková et al., 2023).

Our finding of low prevalence (25.0%) and abundance (1.50) of *D. squameus* in Lake Ohrid is consistent with this report, which shows a random occurrence of the parasite species rather than a frequent infection in both regions (Danube and Dnieper basins), as well as with the infection of the native stone morocco observed in Lake Niushan in China. Similarly, low infection intensity (1–3) was observed at three native sites in Japan despite a higher prevalence (25–100%), suggesting that *D. squameus* infection of the stone morocco with is naturally low and is maintained in the host population for a long time, potentially limiting the probability of co-introduction into new areas.

Dactylogyrus bicornis was one of the most abundant species in the parasite community of the European bitterling *(R. amarus)* in studies by Davidova (2008, 2011) at 16 different sites in 4 European marine areas, where a total of 41 species of metazoan parasites were identified. The overall prevalence and abundance of the individual parasite species was relatively low.

Our finding of low prevalence (50.0%) and abundance (2.50) of *D. bicornis* in Lake Ohrid is consistent with this report.

These results show that *Rhodeus amarus* and especially *Pseudorasbora parva,* which are widespread and abundant small fish and among the most successful freshwater fish invaders in Europe, may therefore be suitable intermediate hosts for many parasite species. They appear to be able to avoid high parasite infections in their non-native range. The fish were less parasitised by their native, co-introduced parasites compared to their native conspecifics, and acquisition of local parasite species was rare. The release of parasites is considered to be one of the factors influencing the successful establishment of non-native species and their subsequent invasiveness, which could also apply to the European bitterling and the stone morocco. The relatively low prevalence and abundance of monogeneans found in our study is also consistent with the generally low infection burden of native species found in a wide range of populations of both species.

The problem with introducing fish species from other regions of the world arises because almost completely unknown species of parasites are introduced with them. Data on non-native fish parasites are important for evaluating the health status and their general impact on native fish populations. The introduction of non-native species can have notable effects on the populations of native species, the ecosystem, but can also result in socio-economic consequences, caused by major damages in fisheries and aquaculture in a country. Therefore, great attention should be taken to avoid introducing any non-native species into the ecosystem.

We expect to find more parasite species in *R. amarus* and *P. parva* in Lake Ohrid in the following investigations, some of which will certainly be new to the parasite fauna of fishes from N. Macedonia. This will help to add to the knowledge and get a more complete picture of the pathology of fish in N Macedonia, but also of the measures that could be taken to prevent the diseases.

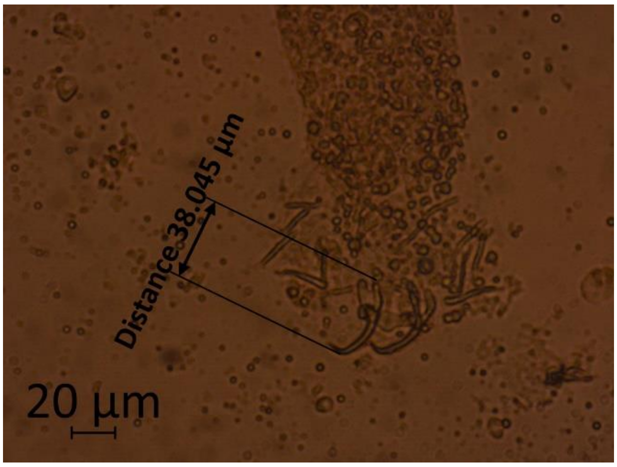

Figure 4. *Dactylogyrus squameus* - adhesive disc (original)

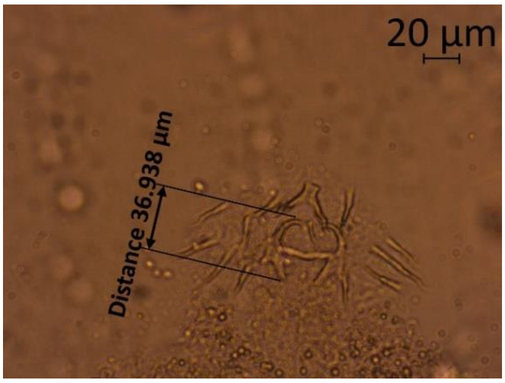

Figure 5. *Dactylogyrus bicornis* - adhesive disc (original)

Acknowledgments

We would like to thank for the grant support of the national project assessment of the health state of fish from lake ohrid through analysis of the composition of fish parasitofauna and histopathology", funded by the ministry of environment and physical planning (Agreement No. 03-95/1 of 22.04.2024).

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Effects of Lobaric Acid on Amino Acid Content of Tomato Seedlings

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ABSTRACT: Tomato (*Solanum lycopersicum L.*) is a vegetable crop widely consumed worldwide. It contains vitamins, minerals, carotenoids, glycoalkaloids, and phytosterols. Lobaric acid (LA) is a secondary metabolite obtained from species such as the Antarctic lichen *Stereocaulon alpinum*. This compound, which attracts attention with its antioxidant and antimicrobial effects, plays essential roles in strengthening plant defense mechanisms, regulating enzyme activities, and increasing photosynthesis efficiency. Moreover, LA has potential applications in agriculture as a plant growth regulator, natural pesticide, and stress tolerance enhancing agent. This study was conducted to evaluate the effects of LA on the amino acid content of tomato seedlings. The study LA was applied at different concentrations (0, 25, 50, and 100 µM) by foliar method and amino acid contents were analyzed. The highest levels of asparagine, serine, glycine, arginine, alanine, tyrosine, and sarcosine amino acids were observed in the 25 µM LA application. While the highest value for glutamate amino acid was recorded in 50 µM LA application, the highest values of aspartate, histidine, threonine, cystine, valine, methionine, tryptophan, phenylalanine, isoleucine, leucine, lysine, hydroxyproline, and proline amino acids were obtained with 100 µM LA application. These findings highlight LA's significant role in modulating amino acid content in tomato seedlings.

Keywords: *Solanum lycopersicum*, Lobaric Acid, Amino Acid, Cystine, Valine

INTRODUCTION

Tomato (*Solanum lycopersicum L.*) is a vegetable with high economic value and high consumption worldwide. Lycopene, beta-carotene, vitamin C, flavonoids, and hydroxycinnamic acid derivatives are some of the necessary elements that are found in these foods, which is why they are regarded to be protective foods (Gerszberg et al., 2015; Alsamir et al., 2021; Pan et al., 2024). Due to the fact that plants spend their whole lives in a sedentary state, it is essential for them to be able to adapt to the stimuli that originate from the outside world and to adequately coordinate their development. As an additional point of interest, the regulation and coordination of metabolism, development, and morphogenesis in higher plants are effectively dependent on chemical signals that are created by the plant itself (Hofmann and Grundler, 2007; Carlos et al., 2021). Rodrigues de Queiroz et al., (2023) reported that the exogenous application of chemicals that have an antioxidant action on plants has been revealed to play significant functions in the plant's defense system.

Lobaric acid (LA), a secondary metabolite, was extracted from the lichen known as Stereocaulon alpnum, which is found in Antarctica. LA is a compound that is abundant in nature and supports many biological functions. This compound is a member of a class of bioactive molecules characterized by the presence of chemicals with anti-inflammatory, antibacterial, and antioxidant properties. Besides, LA is a chemical compound that plays an important role in the regulation of growth and development in plants. In addition to its ability to resist stress factors, it offers antioxidant effects by supporting the functioning of cellular defense mechanisms. Studies show that LA plays an important role in increasing photosynthetic efficiency and adaptation to environmental stress factors such as drought or salinity in plants, as demonstrated, for example, by Paguirigan et al., (2022), Kızıl et al., (2024), Saeed et al., (2024).

Amino acids (aa) are recognized as the molecules that make up proteins. These molecules are also precursors and chemical messengers of many metabolites. Examples of AAs are aspartate, asparagine, serine, serine, glycine, arginine, alanine, tyrosine, sarcosine, histidine, threonine, cystine, valine, methionine, tryptophan, phenylalanine, isoleucine, leucine, lysine, hydroxyproline, and proline (Hernández-Montes et al., 2008; Wang et al., 2023; Dewangan et al., 2023; Kocaman et al., 2024). These aa play vital roles in protein synthesis, growth, and development, stress responses, antioxidant defense, and nitrogen metabolism in plants. Moreover, they detoxify reactive oxygen species (ROS) in plants under stress, facilitate intracellular transport, regulate pH, participate in signal transduction, and regulate defense mechanisms to increase the healthy development of plants and their resistance to environmental stresses (Sharma and Dietz, 2006; Alia et al., 2001; Kumar et al., 2014; Kocaman et al., 2024).

The aim of this study was to investigate the effects of different concentrations (0, 25, 50, and 100 μM) of lobaric acid (LA) on amino acid content of tomato (*Solanum lycopersicum L.)* seedlings by foliar application and to evaluate the possible role of these treatments on seedling development and potential stress tolerance.

Material and Method

Plant Material and Experimental Design

Tomato (*Solanum lycopersicon L.)* was used as plant material. Tomato seeds were obtained from Atatürk University's horticulture department. Tomato seedlings (*Solanum lycopersicon* L cv H2274) were grown in Atatürk University greenhouse at 20-35 ºC and 50-75% relative humidity. Tomato seedlings were transferred to the hydroponic system when they had two true leaflets. The hydroponic system contained nutrient stock solutions A and B (pH: 5.8-6.5) prepared according to Arnon and Hogland (1938). The experimental arrangement was completely randomized. Lobaric acid (LA) at different concentrations (0, 25, 50, and 100 µM) was applied approximately one week later. Lobaric acid was applied as foliar spraying 3 times in total every 5 days. Plants were harvested 5 days after the last application.

Determination of Amino Acids from Plant Leaves

Column separation with phenyl isothiocyanate (PITC) was used to detect amino acids (aa). Firstly, 10 µl of the samples were taken and dissolved in 100 µl buffer solution and then dried under high pressure. Then, five µl of PITC was added to the samples, re-dissolved in buffer solution, and kept for 5 min at room temperature. The samples were then re-dissolved in 40% acetonitrile (0.1 M) and 10% methanol 9:1 (v/v) mixtures, and approximately 15 µl of the samples prepared after these procedures were taken and amino acid determination was carried out by HPLC method (Heinrikson and Meredith, 1984; Saunders et al., 1988; Kocaman et al., 2024).

Statistical Analysis

The statistical analysis was performed using GraphPad Prism 9 software, employing one-way ANOVA within a completely randomized design. The study utilized a 4-Lobaric acid factorial design. To find differences between means at the 0.05 level, Tukey's HSD (honestly significant difference) test was employed. Graphical analysis was conducted with GraphPad Prism 9 software.

Results and Discussion

Bioactive molecules support growth, stress tolerance, and defense mechanisms by regulating amino acid synthesis and accumulation in plants. These molecules support protein synthesis by increasing the activity of enzymes that regulate amino acid metabolism (Franzoni et al., 2019; Hasanuzzaman et al., 2021; Chowdhary and Tank, 2023). Ekinci et al. (2024) reported that amino acids act as signaling molecules in many metabolic processes in plants and are precursors of nucleic acids and proteins.

Figures 1, 2, 3, and 4 show the effect of LA application on tomato seedlings' amino acid content (aspartate, asparagine, serine, glycine, arginine, alanine, tyrosine, sarcosine, histidine, threonine, cystine, valine, methionine, tryptophan, phenylalanine, isoleucine, leucine, lysine, hydroxyproline, and proline).

when aspartate content was evaluated, it was determined that 100 µM LA had the highest effect on aspartate content (~471 pmol µl-1, ****$p < 0.0001$). This effect was found to be statistically significant. On the other hand, the 50 µM LA application had the least effect. The highest glutamate content was obtained from 50 µM LA treatment; this result was statistically significant compared to the control (~473 pmol µl^{-1}, ****$p < 0.0001$) Figure 1.

The highest asparagine, serine, and glycine contents were obtained from 25 uM LA treatment, and these three amino acids were found to be significant in terms of statistical analysis compared to the control group (**$p \leq 0.01$,****$p < 0.0001$). The lowest asparagine, serine, and glycine contents were obtained at 100 uM LA (Figure 1).

The highest histidine content was found in 25 and 100 uM LA (~158, ~161pmol µl^{-1}), and the difference between these treatments and the control was significant (**: $p \leq 0.01$) (Figure 1).

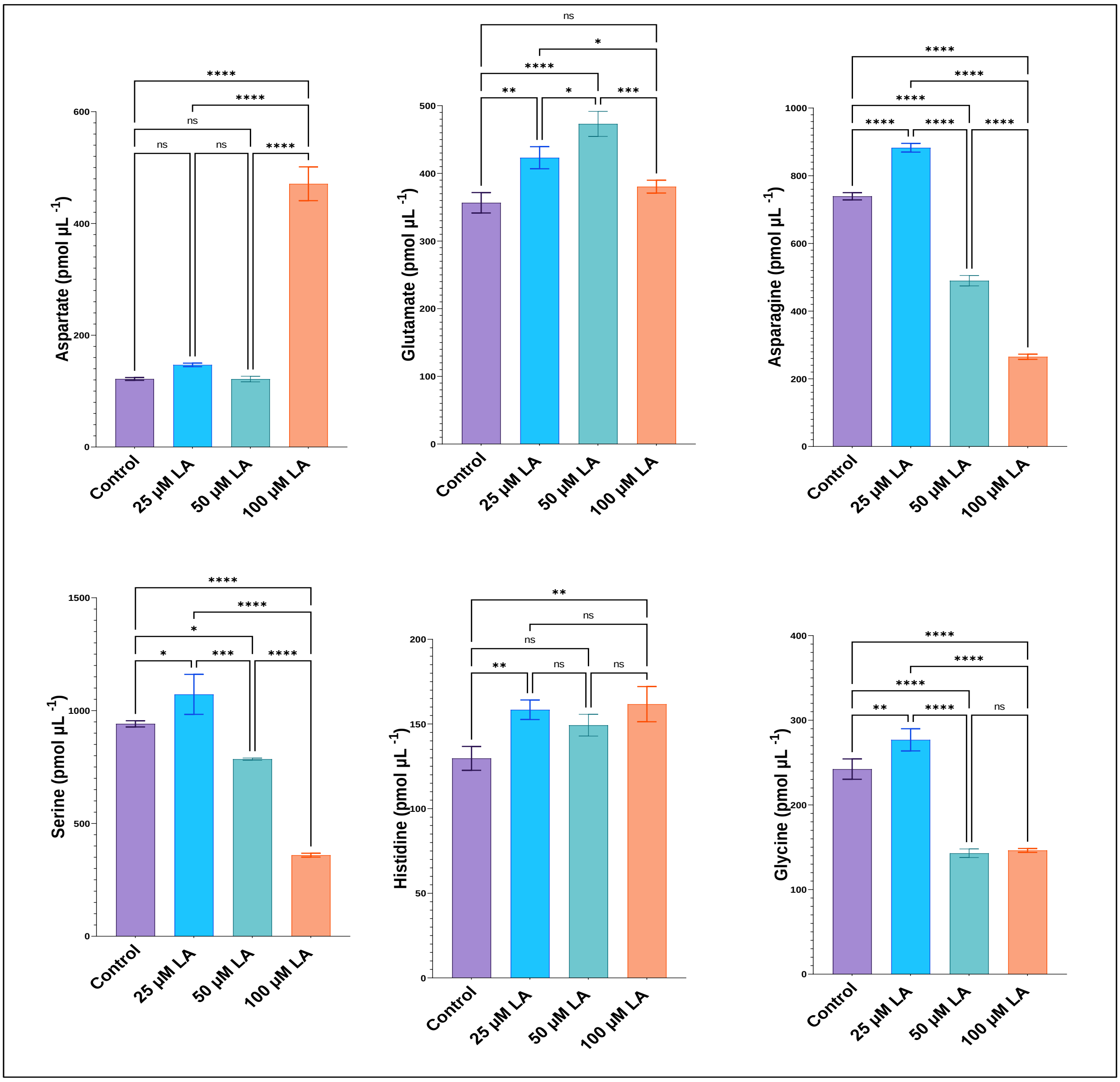

Figure 1. The amino acid content in leaves of tomato according to treatments. (Aspartate, Glutamate, Asparagine, Serine, Histidine, Glycine) (ns: nonsignificant **: $p \leq 0.01$, ***: $p \leq 0.001$ and ****: $p \leq 0.0001$).

A considerable rise in amino acids like threonine, alanine, tyrosine, and tryptophan is assumed to signify an expanded ability for protein synthesis and stress adaption. This is because these amino acids are involved in the production of proteins (Yang et al., 2020; Kocaman, 2023). As a result of this study, among the treatments, 100 µM LA (~1373 pmol μl^{-1}) significantly contributed significantly to increasing the theonine content. The differences between LA and control were significant, while the difference between the other treatments and control was insignificant (****$p < 0.0001$) (Figure 2).

In terms of arginine, alanine, and tyrosine content, the 25 µM LA application had the highest effect, which was statistically significant compared to the control (**$p \leq 0.01$, ***$p \leq 0.001$, and ****$p \leq 0.0001$). In addition, 100 µM LA had the least effect on arginine and tyrosine content, while 50 µM LA had the least effect on alanine content (Figure 2).

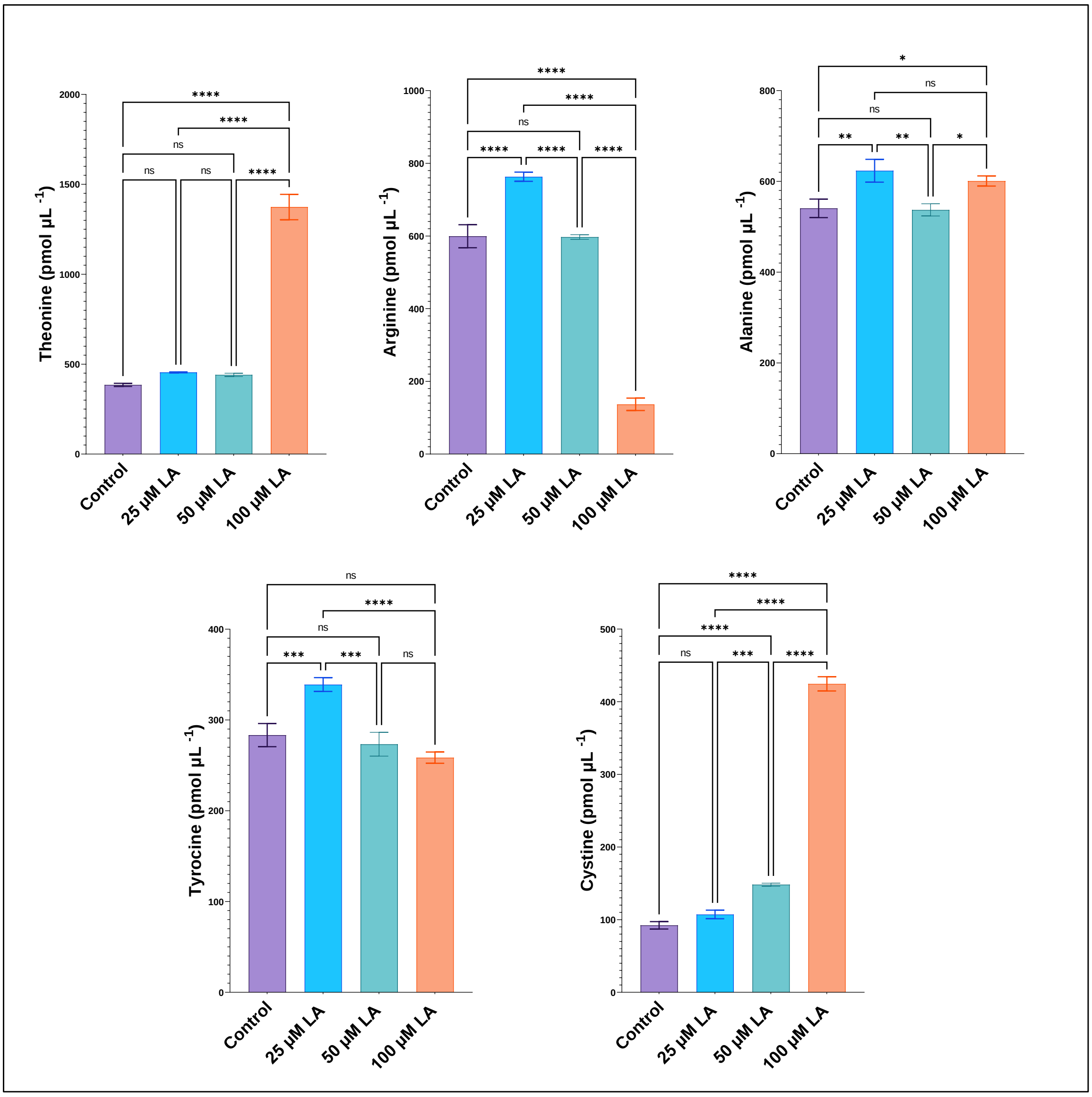

Figure 2. The amino acid content in leaves of tomato according to treatments. (Theonine, Argigine, Alanine, Tyrocine, Cystine) (ns: nonsignificant **: $p \leq 0.01$, ***: $p \leq 0.001$ and ****: $p \leq 0.0001$).

Cystine content was determined to increase in parallel with the increase in the concentration of LA. Moreover, cystine content increased in all applications compared to the control group. The increase in 25 µM LA was statistically nonsignificant (ns), while the increases in 50 and 100 µM LA were statistically significant (****$p \leq 0.0001$) (Figure 2).

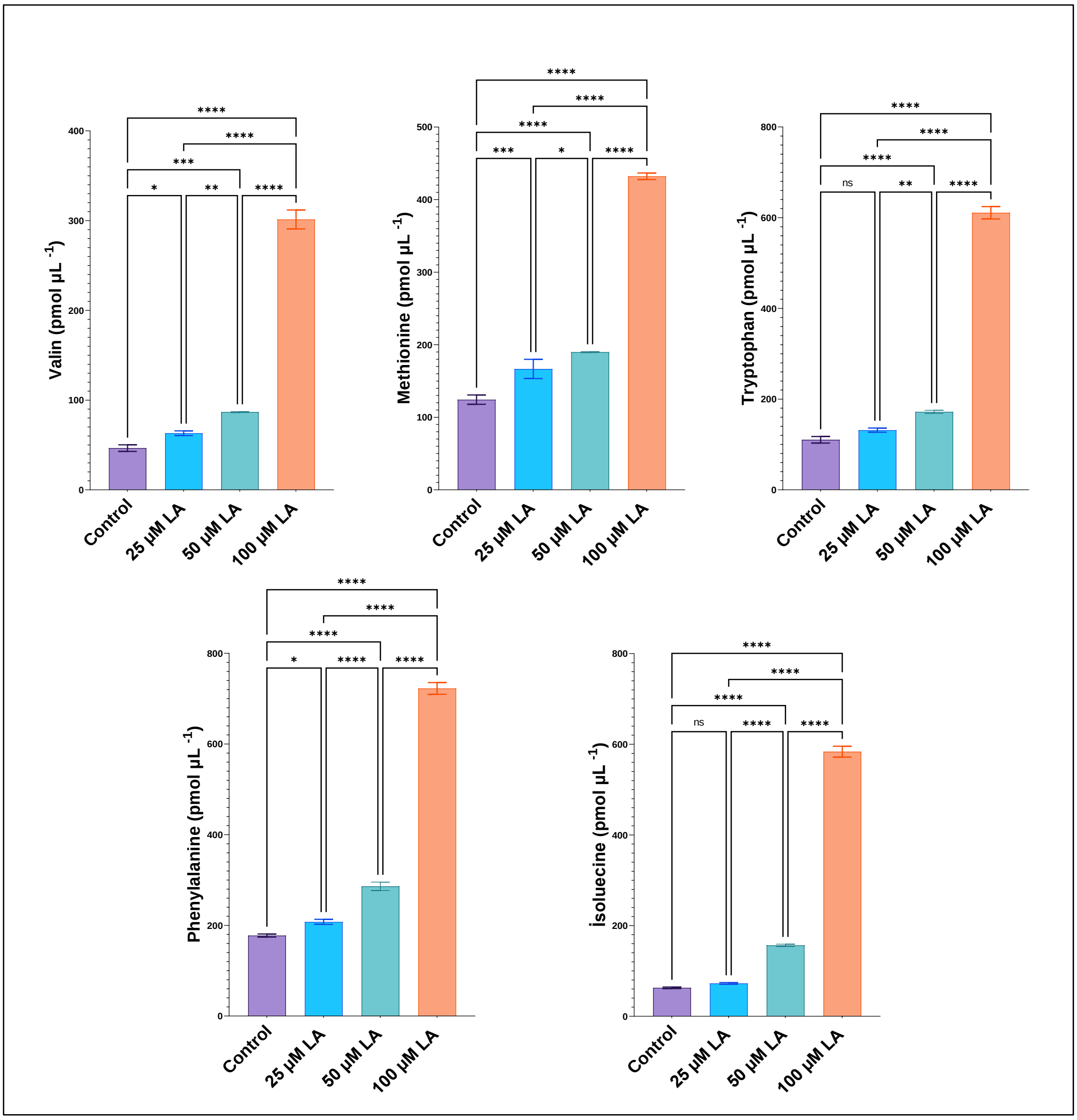

Figure 3. The amino acid content in leaves of tomato according to treatments. (Valin, Methionine, Tryptophan, Phenylalanine, Isoluecine) (ns: nonsignificant **: $p \leq 0.01$, ***: $p \leq 0.001$ and ****: $p \leq 0.0001$).

When the effects of LA applications on valine, methionine, tryptophan, phenylalanine, and isoleucine contents were evaluated, it was determined that all amino acids increased in parallel with the increase in concentration of LA applications. Especially in the 100 µM LA application, the increase was significantly higher and statistically significant compared to the control (****$p \leq 0.0001$) (Figure 3). The observed increase in valine, methionine, tryptophan, phenylalanine, and isoleucine contents with higher concentrations of LA aligns with previous studies highlighting the role of secondary metabolites in enhancing amino acid biosynthesis under stress conditions (Hauck et al., 2010; Vu et al., 2021; Grimm et al., 2021). This suggests that LA may act as a biochemical regulator, similar to other lichen-derived compounds, by modulating key enzymatic pathways involved in amino acid production, as also reported by Zhang et al. (2019).

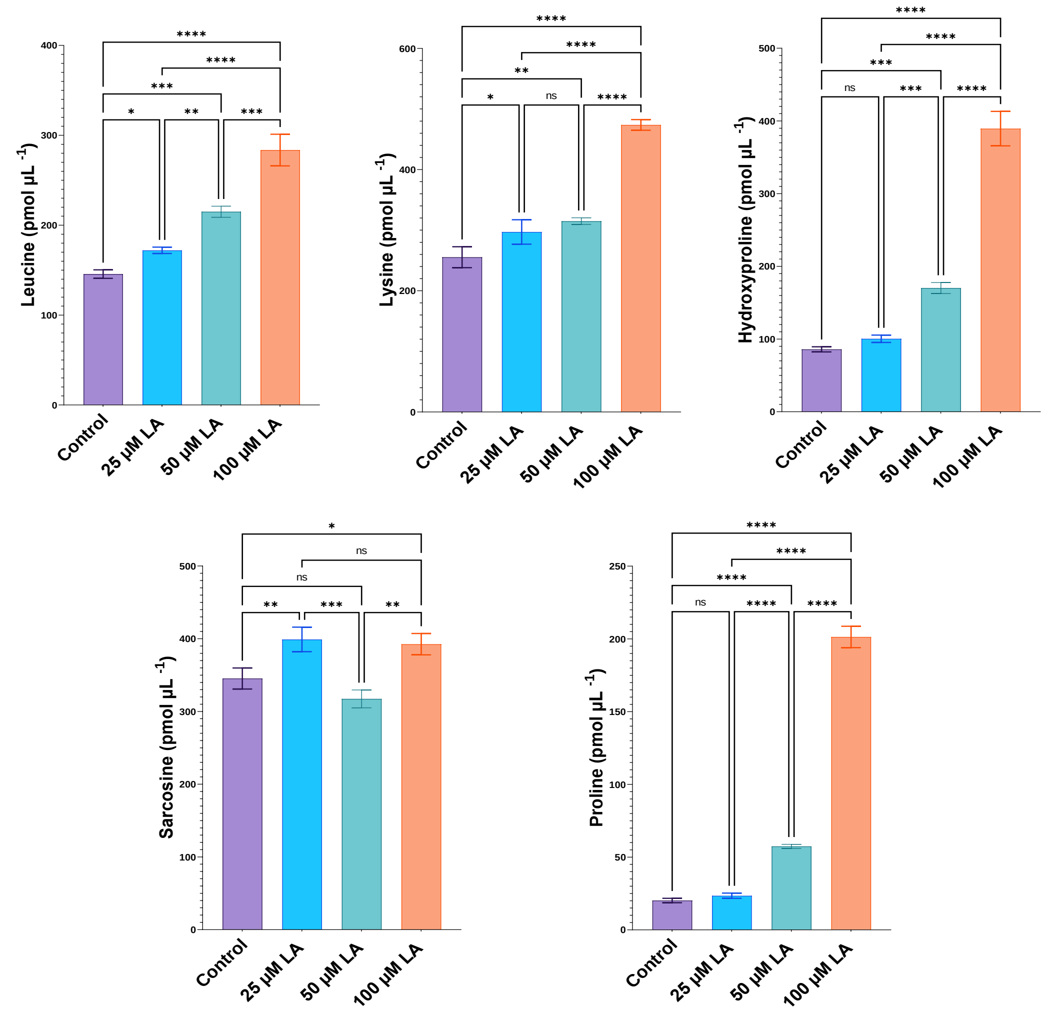

Figure 4. The amino acid content in leaves of tomato according to treatments. (Leucine, Lysine, Hydroxyproline, Sarcosine, Proline) (ns: nonsignificant **: $p \leq 0.01$, ***: $p \leq 0.001$ and ****: $p \leq 0.0001$).

When the effects of LA applications on leucine, lysine, hydroxyproline, and proline contents were evaluated, it was determined that all amino acids increased in parallel with the increase in concentration of LA applications. 100 µM LA application, the increase was significantly higher and statistically significant compared to the control (****$p \leq 0.0001$) (Figure 4).

The highest sarcosine content was determined in 25 µM LA treatment (~399 pmol µl-1). This increase was found to be significant in terms of statistical analysis compared to the control (***$p \leq 0.001$). This increase was followed by 100 µM LA treatment, and the difference between these treatments was not significant. Moreover, the lowest sarcosine content was detected in the 50 µM LA treatment (~317 pmol µl-1). This decrease was nonsignificant (ns) compared to the control group (Figure 4).

The significant increase in leucine, lysine, hydroxyproline, and proline levels observed with 100 µM LA application highlights the dose-dependent efficacy of LA in modulating amino acid metabolism. These findings are consistent with previous studies reporting that secondary metabolites, such as LA, enhance the biosynthesis of specific amino acids by activating stress-responsive pathways and enhancing enzymatic activity (Crozier et el., 2006; Akula and Ravishankar, 2011; Zaynab et al., 2018).

Conclusion

This study demonstrates the significant influence of lobaric acid (LA) on the amino acid composition of tomato seedlings. The results reveal that different concentrations of LA elicit distinct responses, with 25 µM promoting the highest levels of several amino acids, including asparagine, serine, glycine, and alanine. Meanwhile, 50 µM LA showed a notable effect on glutamate levels, and 100 µM LA yielded the highest concentrations of a broader range of amino acids, such as aspartate, histidine, and proline. These findings underscore the potential of LA as a promising agent in agricultural practices, offering applications as a plant growth regulator and stress tolerance enhancer, thereby contributing to improved crop quality and resilience.

Funding

This research was not financially supported by any institution.

Statement of Conflict of Interest

The authors declare no competing interests

Authors' Contributions

Sümeyra UÇAR prepared the manuscript. Esra YAPRAK, Merve YÜCE, and Metin TURAN conducted laboratory experiments and collected data. This manuscript was proofread by Ertan YILDIRIM, Murat AYDIN, and Güleray AĞAR. All authors approved the final form of the manuscript.

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Estimation of Lactation Curves of Morkaraman Sheep Using Nonlinear Models

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ABSTRACT: This study was compared Wood, Dhanoa and Wilmink models in defining the lactation curve in Morkaraman sheep. The animal material of the study consisted of 12 2-year-old Morkaraman sheep. In evaluating the fit of the models, coefficient of determination (R^2), mean square error (MSE) and Durbin Watson (DW) coefficient were used. The coefficient of determination, least square error and Durbin Watson (DW) coefficients for Morkaraman sheep were determined as 0.93, 0.142 and 3.45, respectively, with Wood model, 0.89, 0.242 and 3.67 with Dhanoa model and 0.85, 0.298 and 4.12 with Wilmink model. The Woods model provided a better fit to the lactation data by having the lowest MSE values, the highest R^2 values and the DW coefficients, which means the least number of positive autocorrelated cases. As a result, when the R^2, MSE and DW criteria were examined, it was decided that the Wood model was the most appropriate model to describe the lactation curves of Morkaraman sheep.

Keywords: Lactation Curve, Morkaraman, Nonlinear Models

INTRODUCTION

Milk is a product of vital importance for human nutrition. Although cow milk consumption is quite high in the world, sheep milk is also an important product in the Mediterranean, Middle East and Eastern Europe (Bilgin et al., 2010). In sheep breeding, wool yield and quality were given importance first, and later meat and wool characteristics together. While selection was made for these two characteristics in breeding studies, milk yield was not given much importance. Therefore, there is a great variation in milk yield among sheep breeds, flocks of different breeds, and individuals within flocks. Lactation curves in cattle have been studied intensively for a long time. There are not many studies on sheep yet. Lactation curves are especially useful for making time-dependent decisions. Knowing when an animal reaches its peak yield can help adjust the feeding strategy to meet the animal's needs at various stages of lactation, reduce costs and maintain peak yield for as long as possible (Tozer and Huffaker, 1999; Lomboard, 2006). There are various lactation curve models. The incomplete gamma function or Wood model developed by Wood (1967) is the best known and widely used mathematical model, especially applied to cattle. Most other models are based on the Wood model (Cobby and Le Du, 1978; Wilmink, 1987). They usually include additional parameters to improve fit and have been developed from experimental data (Bilgin et al., 2010; Atoui et al., 2024). These models have been applied to lactation data of dairy cattle, but less frequently to sheep and goats. The aim of this study was to determine the most appropriate mathematical model for estimating lactation curves of 2-year-old Morkaraman sheep using the Wood, Dhanoa and Wilmink models.

Table 1. Mathematical models used in the estimation of lactation curves

Model	**Fonksiyon**
Wood	$Y = at^{b} \exp^{(-ct)}$
Dhanoa	$Y = at^{bc} \exp^{(-ct)}$
Wilmink	$Y = a + bt + c\exp^{(-0.05t)}$

Material and Method

The coefficient of determination (R^2), mean square error (MSE) and Durbin Watson coefficient (DW) are used to determine the most appropriate model. The DW statistic is used as a measure of first-order positive autocorrelation to test whether the residuals are distributed by chance.

$$DW = \frac{\sum_{t=2}^{n} (e_t - e_{t-1})^2}{\sum_{t=1}^{n} e_t^2}$$

In the equation, et is the deviation at time t and et-1 is the deviation at time t-1. The observed DW value is evaluated against the critical values in the table to test for positive autocorrelation. Parameter estimates of lactation curves were estimated using IBM SPSS 20.0 programme.

Results and Discussion

Lactation curves are useful tools for breeders' planning and strategy implementation and can be used to optimise management decisions and selection processes. Lactation curve information makes it possible to estimate total milk production from several test days or a single test day early in the lactation process. Such information helps to make decisions about milk production early in the lactation process. The aim is to identify ewes that reach peak production levels early in lactation and maintain these peaks throughout the entire lactation period. Maintaining a relatively constant milk supply throughout the year is economically important, especially for breeders engaged in seasonal milk production

Local sheep breeds generally have low milk performance. Najari (2005) suggests that the genetic milk performance of local breeds is the result of a long process of natural selection favouring their adaptation to harsh conditions. In such a process, herds may experience reductions in yields such as milk performance, which requires high energy to survive and allow genetic continuity. It is also hypothesised that a high milk performance has a negative genetic correlation with reproductive abilities. Milking, which is rarely practised in pasture-based systems, is practically limited to the peak of the lactation period. However, good milking performance makes a significant contribution to herd outcomes by contributing to offspring growth and hence meat production (Atoui et al., 2024).

In this study, Wood, Dhanoa and Wilmink models were used to predict the lactation curves of Morkaraman sheep, the dominant and widespread native breed of the region. Parameter estimates, coefficients of determination (R^2), mean square error (MSE) and Durbin Watson (DW) coefficients of different models are presented in Table 2.

Table 2. Parameter estimates, R^2 values, mean square error (MSE) and Durbin Watson coefficients (DW) from different models

Model	a	b	c	MSE	R^2	DW
Wood	0.285±0.092	1.733±0.852	0.252±0.087	0.142	0.93	3.45
Dhanoa	0.292±0.047	6.552±2.432	0.252±0.141	0.242	0.89	3.67
Wilmink	1.457±1.895	-0.059±0.067	0.698±2.078	0.298	0.85	4.12

Lactation curves provide useful information about the milk yield of ewes by using data recorded at regular intervals by milking controls. The lowest average LMC was obtained with the Wood model (0.142) and the highest with the Wilmink model (0.298). The lowest coefficient of determination was estimated by Wilmink model (0.85) and the highest by Wood model (0.93).

DW statistic was greater than two in all three models. When compared with the Durbin-Watson critical value table, we see that the DW values we calculated are very significantly ($P<0.01$) different from the table values. This shows that there is no autocorrelation between the yields measured at different times.

In Graph 1, actual milk yield values and lactation curves predicted by different models are presented. As can be seen from Graph 1, all three models gave similar predictions to the actual lactation curve. It was observed that only Wilmink model predicted the initial yield higher than the actual yield, but in the following periods, it gave similar results with the other models.

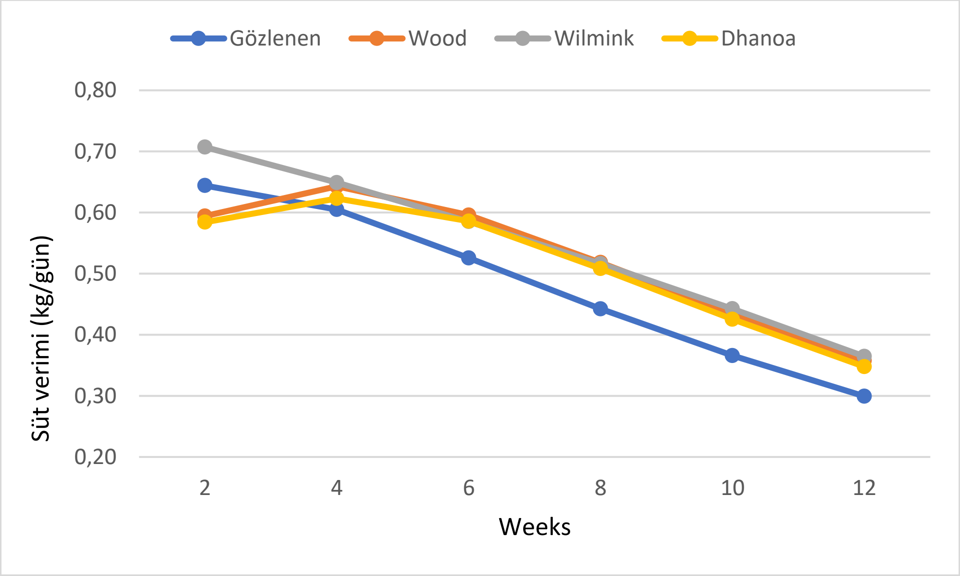

Figure 1. Actual milk yields of Morkaraman ewes and lactation curves estimated by different models

In our study, we tried to determine the most suitable model for lactation milk yield characteristics of Morkaraman ewes by using different lactation curve models. As a result, all models gave similar AQR, R^2 and DW values. However, the Woods model provided a better fit to the lactation data by having the lowest AUC values, the highest R^2 values and the least number of positive autocorrelated cases, which means DW coefficients.

Statement of Conflict of Interest

The author(s) have no conflict of interest.

Authors' Contributions

Ulku Dagdelen, Dogan Turkyilmaz and Nurinisa Esenbuga designed and analyzed the research, Ulku Dagdelen, Dogan Turkyilmaz and Nurinisa Esenbuga studies arranged. Doganb Türkyilmaz worked on the preparation of Ulku Dagdelen and Nurinisa Esenbuga pictures and tables. All authors contributed to the writing of the article, and took part in the process of publication of the article and read and approved it.

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Evaluation of Organic Product Consumption Preferences Using Logistic Regression Analysis: A Case Study of Kırşehir Province

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ABSTRACT: In recent years, organic products have secured a significant position among consumer goods due to the growing emphasis on healthy living and environmental awareness. The accurate analysis of consumer preferences, coupled with the development of effective marketing strategies, has become increasingly critical, thereby rendering consumer profile studies more essential. This study aimed to examine the factors influencing organic product consumption preferences in the province of Kırşehir through logistic regression analysis. The analyses were performed using the enter method and implemented on the Google Colab platform with the Python programming language (Version 3.12). The research utilized data collected via a survey. The survey included questions designed to assess participants' demographic characteristics, organic product consumption habits, and the factors influencing these preferences. The results of the logistic regression analysis indicated that factors such as age, gender, place of residence, household size, awareness of the organic product logo, and preferences for specific organic products were statistically significant in influencing organic product consumption. The results reveal that organic product consumption in Kırşehir is shaped by individual, economic, and social factors. It is thought that these findings can serve as a valuable resource for policymakers in designing strategies to promote organic product consumption and contribute to sustainability initiatives.

Keywords: Kırşehir**,** Logistic Regression Analysis, Organic Consumption

INTRODUCTION

Organic products have become increasingly prominent in consumer preferences, driven by a growing awareness of healthy living and environmental sustainability. Rising concerns about environmental degradation, food safety, and the conservation of natural resources have further fueled global demand for organic products (Kayişoğlu and Türksoy, 2023). These products are cultivated using natural methods, avoiding chemical fertilizers and pesticides. As such, they not only offer consumers a healthier alternative but also represent a production model that is environmentally responsible (Türközü and Karabudak, 2014). Individual, economic, and social factors significantly influence the consumption of organic products, highlighting the necessity of a comprehensive analysis of consumer behavior (Korkmazyürek, 2020). Consumer preferences are part of a dynamic process that shapes purchasing decisions. In niche markets, such as organic products, analyzing these preferences plays a critical role in developing effective marketing strategies. Within this context, factors such as consumers’ demographic characteristics, levels of awareness about organic products, and social influences are emphasized as key determinants of organic product consumption (Çam and Karakaya, 2018). Notably, familiarity with organic product certification logos enhances consumer awareness, thereby increasing the likelihood of choosing organic products (Korkmazyürek, 2020).

This study aims to identify the factors influencing organic product consumption preferences in Kırşehir province. Data were collected through a detailed survey that included questions about organic product consumption habits. The survey also gathered information on participants’ demographic characteristics, knowledge, attitudes, and habits related to organic products. The data were analyzed using logistic regression, a method particularly suitable for evaluating categorical dependent variables. All analyses were conducted using Python programming language (Version 3.12) on the Google Colab platform. Logistic regression was selected for its ability to systematically assess the factors affecting the probability of organic product consumption.

Material and Method

This study was designed to identify the factors influencing preferences for organic product consumption in Kırşehir Province. The data used in the research were collected during a field study conducted in 2022. A survey was developed for data collection, consisting of multiple-choice questions to assess participants' demographic characteristics, knowledge levels regarding organic products, consumption habits, and the factors influencing their preferences for these products. The survey questions were formulated based on a review of the relevant literature and validated for content through expert consultation. Data were gathered from a total of 200 participants. To identify the factors influencing organic product consumption preferences, logistic regression analysis was employed. The dependent variable in this study was defined as participants’ organic product consumption status (consumer/non-consumer). Independent variables included age, gender, education level, place of residence, household size, awareness of organic product logos, and preferences for specific organic products. The selection of these variables was informed by findings from prior studies on organic product consumption (Altuntaş & Aksoy, 2019; Gündoğdu, 2020). Logistic regression analysis is widely utilized to examine the relationship between a binary dependent variable and independent variables, particularly when the dependent variable is dichotomous (Akıllı, 2024). Logistic regression enables the estimation of the factors affecting the likelihood of adopting a specific outcome (e.g., consuming organic products). In this study, the logistic regression model was constructed using the "enter method," which involves simultaneously including all independent variables in the model. The analyses were conducted using Python programming language (Version 3.12), with computations performed on the Google Colab platform. To evaluate the model's fit, the Hosmer-Lemeshow goodness-of-fit test was applied, and the predictive power of the model was assessed. Logistic regression is a multivariate statistical method commonly employed across various fields, including medicine, social sciences, economics, and animal sciences, for modeling and predicting the effects of independent variables on categorical outcomes (Hosmer & Lemeshow, 2013). Logistic regression estimates the probability of the dependent variable belonging to a specific category using a sigmoid function, which is based on the weighted sum of the independent variables.

Logistic regression serves as an extension of multiple regression for cases where the dependent variable is neither continuous nor quantitative. The primary purpose of this method is to predict the categorical values of the dependent variable, specifically estimating the probability that an individual belongs to a particular group (e.g., passing) versus another group (e.g., failing). The predicted values are expressed as probabilities ranging between 0 and 1, which ensures that logistic regression does not produce negative probability estimates. Consequently, all probability values are positive and restricted to the 0–1 interval (Alpar, 2011). Unlike many other statistical methods, logistic regression does not require stringent assumptions such as the normal distribution of independent variables, linear relationships between variables, or homogeneity of variances across groups. This method accommodates a wide range of predictor variables, including continuous, discrete, and binary data. It is particularly effective in situations where the distributions of the dependent and independent variables are expected—or known—to be nonlinear. This flexibility allows logistic regression to produce nonlinear models, thereby broadening its applicability across diverse fields. The theoretical framework of logistic regression is grounded in probabilities, odds (the ratio of the probability of an event occurring to the probability of it not occurring), and the logarithm of odds. Odds play a fundamental role in this method, describing the effect of independent variables on the likelihood of the dependent variable falling into a specific category. This effect is typically expressed using the odds ratio, which measures how a one-unit increase in an independent variable affects the odds of the dependent variable belonging to a particular category. The primary objective of logistic regression is to identify the optimal linear combination of independent variables to estimate the probability of a specific outcome for the dependent variable. This linear combination is transformed using the logit function, which represents the natural logarithm of odds. The logit function, being nonlinear, is employed to calculate the likelihood of the dependent variable falling into a specified category. In this manner, logistic regression provides a robust and versatile tool for categorical data analysis, offering significant practical utility and theoretical insights (Tabachnick and Fidell, 2013; Deniz, 2021; Mertler et al., 2021).

Results and Discussion

In this section, the findings of the logistic regression analysis are presented through numerical and graphical representations. At the initial stage of the analyses, the dataset was examined thoroughly. Following the computation of descriptive statistics, the presence of outliers was investigated. During the evaluation process, a small number of missing data points were identified. Subsequently, exploratory factor analysis was performed to optimize the number of variables. Variables contributing optimally to the explanation of variation were retained for further analysis. The analyses were coded and conducted using the Python programming language (Version 3.12), with the support of libraries such as ‘Statsmodels’ and ‘Scikit-Learn’. In this study, the enter method was employed to conduct logistic regression analysis on organic product consumption. The primary objective was to determine whether the relationship between the dependent variable (organic product consumption) and the independent variables was statistically significant, while also assessing the effect of the independent variables on the dependent variable. The dataset was imported and processed within the Python environment using the Pandas library. The dependent variable in the dataset was defined as a binary variable, whereas the independent variables consisted of all columns except the dependent variable. The classification performance of the model was evaluated through overall accuracy and detailed classification metrics. The confusion matrix, which highlights the classes where the model performs better and those where errors occur, was utilized for performance evaluation and was also visualized for clarity. To assess the overall performance of the model, key metrics such as accuracy, F1 score, sensitivity (recall), and specificity (precision) were calculated. Additionally, the model’s classification ability was detailed using the ROC (Receiver Operating Characteristic) curve, and its overall classification strength was summarized by the AUC (Area Under the Curve) value. Parameter estimates and the effects of variables were examined using logistic regression coefficients and p-values ($p<0.05$). The analyses were conducted using the ‘Statsmodels’ library, and the statistical significance of the variables was tested. Additionally, regression coefficients were visualized using a bar chart to provide a comparative understanding of variable effects. The model's goodness-of-fit was assessed using Cox & Snell R^2 and Nagelkerke R^2 metrics, which indicate the explanatory power of independent variables on the dependent variable. These measures were utilized to provide inferences into the model's ability to capture relationships between variables.

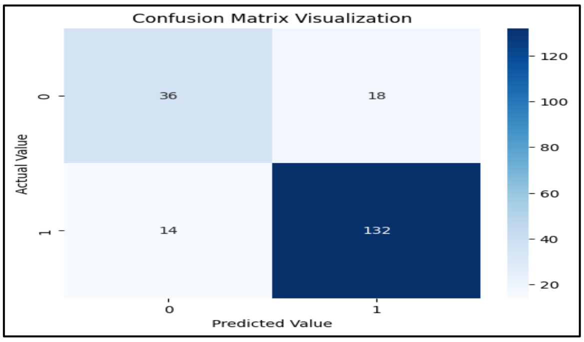

Figure 1. Confusion Matrix

The confusion matrix information is presented in Table 1 and Figure 1. In the analysis conducted using the logistic regression model, the model's correct classification accuracy for the dependent variable was calculated as 84%. The confusion matrix results reveal that, among the 54 observations where the actual value was 0, the model correctly classifies 36 cases, while 18 are misclassified. Similarly, among the 146 observations where the actual value was 1, the model correctly predicts 132 cases, with only 14 being misclassified. In contrast, the recall for the negative class (0) is comparatively lower at 0.67, indicating a greater likelihood of misclassification within this class. The precision values for the negative and positive classes are calculated as 0.72 and 0.88, respectively, with corresponding F1-scores of 0.69 for the negative class and 0.89 for the positive class.

Table 1. Confusion Matrix

Confusion Matrix	Predicted (0)	Predicted (1)
Actual (0)	36	18
Actual (1)	14	132

Parameter estimates and model summary for the logistic regression analysis conducted to examine the factors affecting the probability of consuming organic products are presented in Table 2. In this context, numerical findings regarding coefficients (B), standard errors (S.E.), Wald statistics, significance values (Sig.), probability ratios (Exp(B)) and 95% confidence intervals for Exp(B) are included. In this context, variables that were found to be statistically significant ($p<0.05$) in the prediction of the dependent variable were determined. The coefficient for "Do you recognize the organic farming logo?" variable is positive ($B = 1.3066$, $p = 0.0219$), indicating that individuals who recognize the organic farming logo are more likely to consume organic products. The odds ratio (Exp(B) = 3.6939) suggests that recognizing the logo increases the likelihood of organic product consumption by approximately 3.7 times compared to those who do not recognize it. The 95% confidence interval for the odds ratio (1.208 – 11.295) does not include 1. Internet variable in the context of place of obtaining information about organic products emerges as a significant predictor (B = 0.9677, p = 0.0492), with an odds ratio of 2.632. This indicates that individuals who use the internet are approximately 2.6 times more likely to consume organic products compared to non-users. The confidence interval (1.003 – 6.9067) supports the statistical significance of this relationship.

Table 2. Parameter Estimates and Model Summary

Variable	B	S.E.	Wald	Sig.	Exp(B)	95% C.I. Lower	95% C.I. Upper
const	-2,3	3,633	0,4009	0,5266	0,1002	8,0998	124
Gender	0,3017	0,693	0,1895	0,6632	1,3522	0,3476	5,2604
Age	-0,017	0,0303	0,3383	0,5607	0,9825	0,9258	1,0426
Marital status	0,7329	0,9861	0,5524	0,4573	2,0812	0,3012	14,379
Education level	-0,293	0,3214	0,8315	0,3618	0,7459	0,3973	1,4005
Household size	0,1746	0,2629	0,4413	0,5064	1,1908	0,7112	1,9938
Number of children	0,0566	0,891	0,004	0,9492	1,0583	0,1845	6,0683
Employment status	-0,138	0,2939	0,2215	0,6378	0,8707	0,4894	1,5493
Do you recognize the organic farming logo?	1,3066	0,5702	5,2504	0,0219	3,6939	1,208	11,295
Internet	0,9677	0,4922	3,8655	0,0492	2,632	1,003	6,9067
Television	0,1041	0,55	0,0358	0,8497	1,1097	0,3776	3,2615
Willingness to pay more for organic products	1,4421	0,5209	7,6621	0,0056	4,2295	1,5234	11,742
Price	-0,049	0,1633	0,0904	0,7635	0,952	0,6912	1,3112
Nutritional value	0,1572	0,1668	0,8889	0,3457	1,1703	0,8439	1,6228
My child's health	0,254	0,1856	1,8726	0,1711	1,2892	0,896	1,8549
Color, appearance, and packaging	-0,011	0,1659	0,0046	0,9457	0,9887	0,7142	1,3686
Longer shelf life	0,5038	0,1839	7,5052	0,0061	1,655	1,1541	2,3732
Health issues	-0,318	0,1751	3,3118	0,0687	0,727	0,5157	1,0248
Environmental sensitivity	-0,002	0,162	0,0001	0,989	0,9977	0,7262	1,3707
Curiosity	-0,063	0,1311	0,236	0,627	0,9382	0,7255	1,2133
Smell and taste	-0,136	0,1444	0,8985	0,3431	0,8719	0,6569	1,1574
Supermarkets	0,0945	0,6917	0,0186	0,8913	1,0991	0,2832	4,2646
From the manufacturer	1,482	0,531	7,7882	0,0052	4,4018	1,5545	12,464
Grocery store/greengrocer	0,6945	0,6577	1,1149	0,291	2,0027	0,5517	7,2688
Organic shops	-0,063	0,8485	0,0055	0,9405	0,9387	0,1779	4,9524
Health issues.1	0,4025	0,4472	0,8101	0,368	1,4956	0,6224	3,5936
Tasty	1,8283	0,518	12,454	0,0004	6,2237	2,2544	17,181
Curious	1,5381	0,9308	2,7307	0,0984	4,6559	0,7511	28,861

Log-Likelihood: -73.1601, Deviance: 146.3203, Cox & Snell R^2: 0.3527, Nagelkerke R^2: 0.5122, Pseudo R^2: 0.3728, Log-Likelihood: -73.160, LL-Null: -116.65, LLR p-value: 3.168e-08

Willingness to Pay More for Organic Products variable is positively associated with organic product consumption (B = 1.4421, p = 0.0056). The odds ratio (4.2295) indicates that individuals willing to pay more for organic products are approximately 4.2 times more likely to consume them compared to those unwilling to do so. The confidence interval (1.5234 – 11.742) demonstrates the reliability of this effect. Longer shelf life has a positive and significant effect on organic product consumption (B = 0.5038, p = 0.0061). The odds ratio (1.655) suggests that products with a longer shelf life increase the likelihood of consumption by 65.5%. The confidence interval (1.1541 – 2.3732) confirms the statistical significance of this finding. Positive and significant relationship is observed for products obtained directly from manufacturers (B = 1.482, p = 0.0052). The odds ratio (4.4018) suggests that individuals who purchase directly from manufacturers are approximately 4.4 times more likely to consume organic products compared to other purchasing sources. The confidence interval (1.5545 – 12.464) demonstrates the reliability of this result. Taste preference is strongly associated with organic product consumption (B = 1.8283, p = 0.0004). The odds ratio (6.2237) indicates that individuals who perceive organic products as tasty are approximately 6.2 times more likely to consume them. The confidence interval (2.2544 – 17.181) further supports the significance of this effect. The variable representing curiosity was not found to be statistically significant with a probability ratio of 4.6559 (B = 1.5381, p = 0.0984). It was observed that individuals who stated that they were curious about organic product consumption had a higher probability of consuming organic products. Several variables included in the logistic regression model were observed to lack statistical significance at the conventional threshold ($p > 0.05$), indicating limited or inconsistent effects on the likelihood of organic product consumption. Among these, demographic factors such as gender (B = 0.3017, p = 0.6632), age (B = -0.017, p = 0.5607), marital status (B = 0.7329, p = 0.4573), education level (B = -0.293, p = 0.3618), and household size (B = 0.1746, p = 0.5064) did not display statistically significant associations with the dependent variable. Similarly, employment-related variables, including employment status (B = -0.138, p = 0.6378) and price sensitivity (B = -0.049, p = 0.7635), were found to be statistically non-significant. Behavioral and attitudinal variables, such as television exposure (B = 0.1041, p = 0.8497), nutritional value perception (B = 0.1572, p = 0.3457), concern for child health (B = 0.254, p = 0.1711), and environmental sensitivity (B = -0.002, p = 0.989), similarly failed to emerge as significant predictors. When the Model Fit and Performance criteria are examined, the Cox & Snell R^2 value is observed to be 0.3527, indicating that approximately 35.27% of the variation in organic product consumption is explained by the model. The Nagelkerke R^2 value, which is a normalized version of Cox & Snell R^2, is 0.5122, suggesting that the model accounts for approximately 51.22% of the variation. This result indicates a moderately strong model fit. Additionally, the model's log-likelihood is -73.1601, with a corresponding deviance value of 146.3203. When compared to the null model (LL-Null = -116.65), the likelihood ratio test produces a highly significant result (LLR p-value = 3.168e-08), confirming that the inclusion of predictor variables provides a statistically significant improvement over the null model. These findings collectively indicate that the logistic regression model demonstrates good explanatory power and a robust fit to the data.

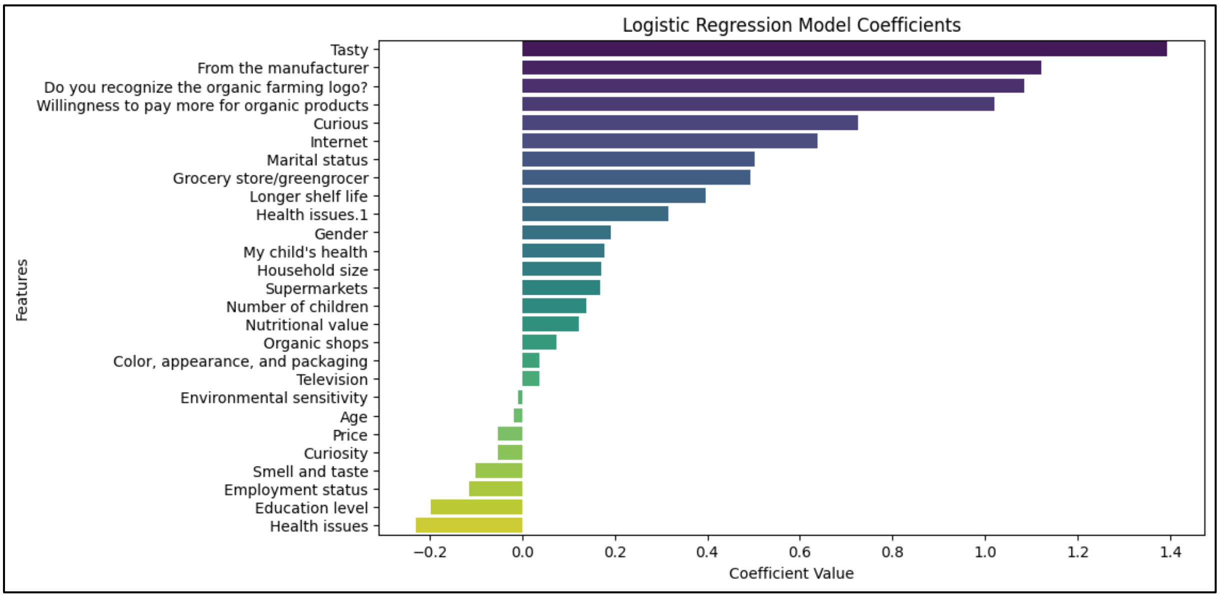

Figure 2. Logistic Regression Coefficients Visualization

The bar chart presented above illustrates the coefficients of the logistic regression model, highlighting both the magnitude and direction of the relationships between each independent variable and the likelihood of organic product consumption. The coefficients represent the effect of a one-unit increase in each predictor variable on the log-odds of the dependent variable, holding all other variables constant. Positive coefficients indicate an increase in the likelihood of consuming organic products, whereas negative coefficients suggest a decrease. The results of the logistic regression analysis indicate that taste perception, direct sourcing from manufacturers, recognition of organic logos, willingness to pay more, and longer shelf life are the most influential predictors of organic product consumption. These findings stated that the importance of product attributes, consumer trust, and awareness in shaping purchasing behaviors. In contrast, demographic and socioeconomic factors, such as gender, age, education level, and employment status, as well as certain attitudinal variables like health concerns and environmental sensitivity, exhibit limited or no explanatory effect in the context of this model.

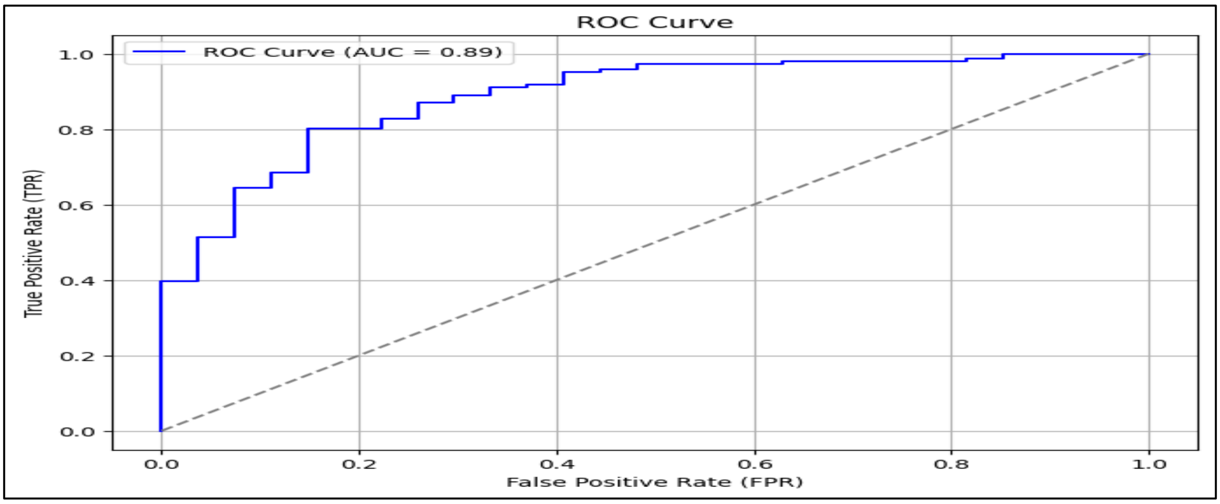

Figure 3. ROC Curve and AUC Score

The ROC curve presented in Figure 3 provides a graphical representation of the logistic regression model's classification performance, illustrating the trade-off between the True Positive Rate (TPR), or sensitivity, and the False Positive Rate (FPR). The ROC curve demonstrates a clear deviation from the diagonal reference line, which represents random classification. The Area Under the Curve (AUC) is reported as 0.89, a value that signifies excellent discrimination. This indicates that the model correctly predicts organic product consumption approximately 89% of the time, underscoring its robustness and high predictive accuracy. Key variables, such as “Tasty,” “From the Manufacturer,” “Recognition of the Organic Farming Logo,” and “Willingness to Pay More for Organic Products,” likely play a substantial role in achieving this high level of model performance. Conversely, non-significant variables, as identified in the parameter estimates, contribute minimally to the model's overall predictive accuracy.

CONCLUSION

This study examines the factors influencing organic product consumption preferences in the province of Kırşehir. The results of the logistic regression analysis reveal that individual awareness, economic motivations, and social tendencies significantly shape organic product consumption. Notably, individuals who recognize the organic farming logo are significantly more likely to consume organic products. Similarly, using the internet as an information source, longer shelf life, taste preferences, and purchasing directly from producers are identified as factors that increase the likelihood of organic product consumption. In contrast, demographic and behavioral variables such as age, gender, marital status, educational level, and price sensitivity do not show statistically significant effects. The results can provide important inferences for policymakers in designing strategies to promote organic product consumption.

Specifically, increasing awareness campaigns, encouraging internet-based information dissemination, and offering products that meet consumers’ taste preferences can promote broader adoption of organic products.

Funding

The research was not supported.

Statement of Conflict of Interest

There is no conflict of interest.

Authors' Contributions

All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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Investigation of Livestock Enterprises Using Clustering Analysis: A Case Study of Tuşba and Gürpınar Districts

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ABSTRACT: Cluster analysis is recognized as one of the multivariate statistical methods extensively employed in the livestock sector to understand, evaluate, and identify differences in the heterogeneous structure of enterprises. This technique is utilized to systematically form groups with similar characteristics by analyzing the natural structure of data. In the present study, hierarchical and non-hierarchical clustering analyses were conducted to examine livestock enterprises operating in the Tuşba and Gürpınar districts of Van Province. The data used in the analyses were collected through surveys, and the K-Means clustering technique was applied as part of the non-hierarchical clustering analysis. All analyses were carried out using the Python programming language (Version 3.12) on the Google Colab platform. The survey was structured to gather detailed information on a range of topics, including demographic and socioeconomic characteristics, livestock activities, utilization of cooperatives and support programs, animal health and vaccination practices, challenges encountered in livestock farming and proposed solutions, as well as the evaluation of livestock products and activities. Through clustering analyses, the data were effectively segmented into distinct groups, resulting in the classification of livestock enterprises into three clusters. The results demonstrate that cluster analysis is an effective tool for understanding the structural differences among livestock enterprises in the Tuşba and Gürpınar districts of Van Province. Furthermore, it is considered that these results may provide significant contributions to local governments and policymakers in their planning and evaluation of strategies targeted at the livestock sector.

Keywords: Cluster Analysis, K-Mean, Livestock Enterprises

INTRODUCTION

The livestock sector holds strategic importance for rural development and economic growth (Ertaş, 2019). Analyzing quantitative data on livestock populations in large-scale cattle farming enterprises reveals significant sources of variation and a predominantly heterogeneous organizational structure. This heterogeneity complicates the classification of enterprises, comparative analyses, and rational planning processes from a methodological perspective. Specifically, statistically modeling the parameters underlying this variation (e.g., farm size, animal breeds, production systems, feeding practices, and environmental factors) can contribute positively to the analysis of structural and functional heterogeneity within cattle farming enterprises. Such modeling also supports the development of practical and sustainable strategies for decision-makers in the livestock sector. In this context, cluster analysis—a multivariate statistical technique—serves as an effective tool for understanding and classifying the structural differences of agricultural enterprises (Seyfioğlu et al., 2023). Fundamentally, cluster analysis involves grouping units with similar characteristics to create homogeneous subgroups (Everitt & Hothorn, 2011). This method facilitates the systematic analysis of demographic, economic, and technical data in the livestock sector, thereby aiding policymakers in strategic decision-making. Moreover, grouping livestock enterprises not only enables more efficient resource allocation but also clarifies structural problems within the sector.

The literature contains numerous clustering studies in the agricultural sector. For instance, Seyfioğlu et al. (2023) examined the mechanization levels and technical specifications of pesticide equipment in agricultural enterprises in Ankara Province. Data from 381 enterprises were analyzed using cluster analysis, and enterprises were subsequently grouped. Similarly, Değirmenci et al. (2017) evaluated 20 irrigation associations in the Lower Seyhan Plain through cluster analysis using performance indicators such as irrigation rates for the first and second crops, annual maintenance-repair rates, and average water fees. The analysis identified three groups of irrigation associations, demonstrating significant variation through dendrogram visualizations. The study concluded that water fees and maintenance-repair rates significantly influence the success of irrigation associations. Likewise, Tümer et al. (2010) employed cluster analysis to examine the socio-economic characteristics of farmers in Tokat Province, identifying three homogeneous groups of farmers with similar attributes. The study underscored the importance of grouping farmers by their characteristics for designing effective agricultural policies. Additionally, Sarı and Külekçi (2016) used an ordinal logit model to investigate factors affecting the agricultural organization of enterprises in Erzurum Province. Surveys were conducted with 139 farmers from 15 villages across the districts of Aziziye, Aşkale, Çat, Horasan, and İspir. The analysis revealed that factors such as the distance to urban centers, education level of farmers, access to agricultural subsidies, livestock ownership, farming experience, and newspaper readership significantly influenced agricultural organization. The study recommended promoting cooperatives, distributing subsidies through organizations, and providing training programs to enhance agricultural organization.

The present study aims to analyze livestock enterprises in the Tuşba and Gürpınar districts of Van Province using two different clustering techniques. The research examines variables pertaining to the demographic and socio-economic characteristics of enterprises, their livestock activities, challenges faced, and proposed solutions. The data were analyzed using both hierarchical and non-hierarchical clustering methods. All analyses were conducted on the Google Colab platform using Python programming language (Version 3.12).

Material and Method

The data used in this study were collected through a comprehensive survey designed for enterprises, developed based on an extensive literature review. The survey form included detailed information on various aspects, such as the demographic and socio-economic characteristics of the enterprises, livestock activities, the use of cooperative and support programs, animal health and vaccination practices, challenges encountered in the sector, and proposed solutions to these challenges. The survey was conducted face-to-face in 2023, yielding data from a total of 160 enterprises. The collected data were analyzed using cluster analysis, a multivariate statistical method. The analyses were carried out on the Google Colab platform using the Python programming language (Version 3.12). During the data processing and analysis phase, basic statistical techniques were initially applied to calculate descriptive statistics, and missing data were checked and addressed.

The first method applied in the study was hierarchical clustering analysis, a clustering technique that groups observations into a hierarchical structure based on their similarities or differences and visualizes relationships between observations through a dendrogram, a tree-like structure. Hierarchical clustering is particularly advantageous in cases where the number of clusters is not predetermined, as it facilitates the exploration and understanding of the natural structure of the data (Everitt & Hothorn, 2011; Yıldırım et al., 2020). The visualization capabilities of this method are especially beneficial for complex and heterogeneous datasets, allowing researchers to better comprehend the structure of the dataset (Rencher, 2002).

In hierarchical clustering, data are organized naturally throughout the clustering process, eliminating the need to predefine the number of clusters (Ward, 1963). Dendrograms provide a clear depiction of relationships within the data, making it possible to understand similarities and differences between various clusters (Hastie et al., 2009). A dendrogram is a hierarchical tree structure consisting of layers, each representing a cluster (Jain & Dubes, 1988). This visualization tool allows researchers to evaluate the clustering process in detail by revealing which observations are grouped into clusters at each stage. Two main approaches exist within hierarchical clustering. The first is the agglomerative approach, in which each observation begins as an individual cluster. The algorithm iteratively combines two or more smaller clusters using a proximity matrix, merging them step by step into larger groups. This process continues until all observations are grouped into a single cluster, with the number of clusters gradually decreasing throughout (Rencher, 2002). The second approach is the divisive algorithm, which is the inverse of the agglomerative approach. This method starts with all observations grouped in a single cluster and progressively divides them into smaller sub-clusters. The divisive hierarchical method begins with one cluster containing n observations and, at each step, splits one cluster into two sub-groups. The process continues until n clusters, each containing a single observation, are formed (Jain & Dubes, 1988). In this study, Euclidean distance was employed as the distance metric for hierarchical clustering analysis, and the Ward method was used as the linkage method (Ward, 1963). Hierarchical clustering is a widely used method and has been the focus of scientific research in various fields, particularly in livestock science. In the livestock sector, hierarchical clustering is employed to analyze structural differences among enterprises, classify them based on common characteristics, and establish a knowledge-based foundation for sectoral planning.

The K-Means clustering technique, on the other hand, aims to group observations into a predetermined number of clusters. This method assigns each observation to the nearest cluster center, thereby forming clusters while maximizing within-cluster similarity. K-Means is particularly favored in applied research due to its efficiency and speed in clustering, especially when handling large datasets (Ahmed et al., 2020). The K-Means technique is widely applied across various disciplines to classify datasets, perform segmentation, and analyze relationships among observations. It serves as an effective tool for exploring the natural structure of data and supporting decision-making processes, particularly in livestock science and other fields (Ikotun et al., 2021). The method is especially useful for datasets with heterogeneous structures, as it effectively identifies differences between groups (Rencher, 2002). The K-Means algorithm determines k centroid points to represent clusters and seeks to minimize an objective function based on the squared error criterion (Akıllı, 2023). During this process, the cluster centers and associated data points are identified, with each data point assigned to the nearest cluster center (Alpar, 2011; Tatlıdil, 1996). The algorithm focuses on minimizing squared error while maximizing similarity within clusters by appropriately assigning data points to cluster centers (Ding & He, 2004; Faraoun & Boukelif, 2007; Akıllı, 2023). The K-Means algorithm is specifically designed to partition data points into a predefined number (k) of clusters. Among its key advantages are its low computational cost, which allows for fast and efficient results with large-scale datasets, its mathematical simplicity, which facilitates implementation in various software and programming environments, and its effectiveness when working with continuous (quantitative) data, making it adaptable across a wide range of applications

(Sarıman, 2011). The algorithm operates through the following steps: First, a cluster number between 1 and k is assigned to the data components. This phase, referred to as initialization, involves determining the number of clusters (k) based on the researcher's judgment. Then, cluster centers are calculated, and data points are assigned to their nearest centroids. Subsequently, the objective function (J) is calculated to evaluate clustering performance. Next, the positions of the cluster centers are updated. This iterative process is repeated from the second step until no further changes occur in the cluster centers or predefined stopping criteria are met. Through this iterative refinement, the final clusters are obtained (Akıllı, 2023).

Results and Discussion

In this section of the study, numerical and graphical representations of the analysis findings are provided. During the initial phase of the analyses, descriptive statistical methods were employed to examine the data frame in detail, and the presence of outliers was investigated. A small number of missing data points were identified during the evaluation process. To avoid introducing bias in the results, these missing values were imputed based on the mean values of the respective variables. Data standardization was performed using the "StandardScaler" module in the Python programming language (Version 3.12), ensuring that all variables were normalized to have a mean of 0 and a variance of 1. For the hierarchical clustering analysis conducted in this study, distances between observations were calculated using the Ward method, and clustering was carried out with the help of the linkage function. A dendrogram visualization was generated from the resulting linkage matrix, facilitating the determination of the optimal number of clusters. To quantitatively evaluate the performance of the clustering analysis, the Silhouette Score and Dunn Index were computed. Furthermore, the Principal Component Analysis (PCA) method was employed to reduce the dimensionality of the data to two dimensions, enabling a visual representation of the cluster distributions. The outputs derived from the hierarchical clustering analysis were saved in Excel format, and the results were documented in the analysis report. Additionally, a histogram was generated to visualize the clusters containing agricultural enterprises, clearly illustrating the distribution of the number of observations across clusters.

Figure 1 presents the dendrogram derived from the hierarchical clustering analysis based on the Ward method, applied to enterprises engaged in livestock activities in the Tuşba and Gürpınar districts. The visual analysis identifies two main clusters, with observations assigned accordingly. The variables used in the analysis encompass multidimensional information, including the demographic and socio-economic characteristics of the enterprises, livestock activities, the utilization of cooperatives and support programs, animal health and vaccination practices, challenges encountered in livestock farming, proposed solutions, and the evaluation of livestock products. The blue linkage line at the top of the dendrogram indicates a relatively high distance between the two main clusters, signifying distinct differences between them. The sub-branching within the clusters reflects the degree of similarity among enterprises. Shorter linkage lines within the orange and green clusters suggest that enterprises in two groups share more similar characteristics. The dendrogram visualization demonstrates that livestock enterprises in the Tuşba and Gürpınar districts are grouped into two main clusters, hierarchically structured based on their similarities and differences. Figure 2(a) depicts the results of the clustering analysis, visualized in two dimensions using the Principal Component Analysis (PCA) method. PCA was utilized to summarize the structure of the data in a multidimensional space, with operations performed on the first (PC1) and second (PC2) components. Figure 2(a) reveals that the analyzed observations are divided into two main clusters. Observations in the first cluster (blue) are concentrated in the upper-left region, representing a homogeneous group of enterprises with similar characteristics. Observations in the second cluster (orange) are distributed across the lower-right and upper-right regions, indicating a broader distribution and greater variance, reflective of a more heterogeneous structure. The separation between the two clusters obtained from the hierarchical clustering analysis is likely attributed to differences in socio-economic, demographic, or activity-based characteristics of the observations. Along the first component (PC1), the clusters show clear distinctions, while variation along the second component (PC2) is spread across a wider range. To further illustrate the clustering results, a cluster distribution chart displaying the number of observations in each cluster is presented in Figure 2(b).

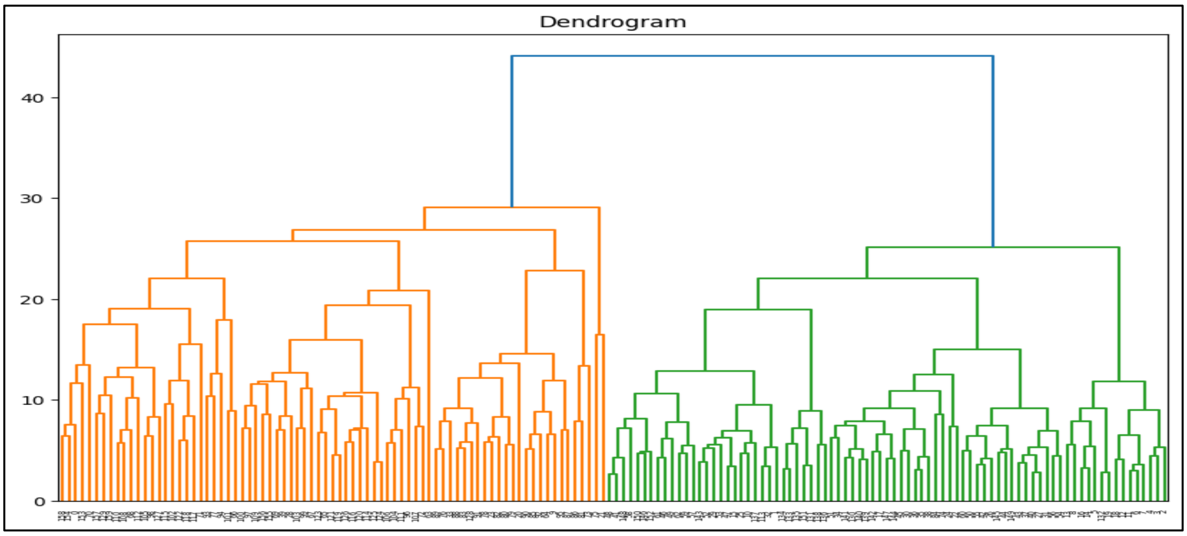
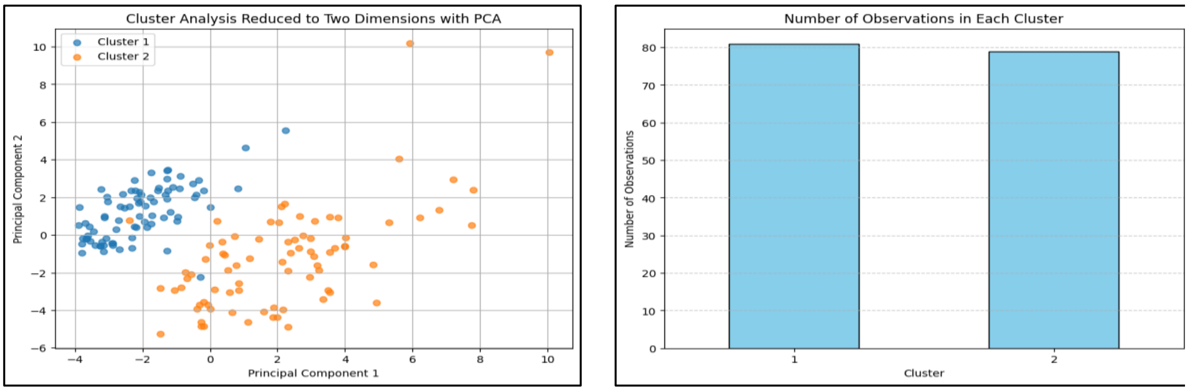


Figure 1. Dendrogram



(a) (b)

Figure 2. Cluster Analysis Reduces to Two Dimensions with PCA(a), Number of Obs. in Each Clusters(b)

Figure 3 visually presents the results of the hierarchical clustering analysis evaluated using Silhouette analysis. This method assesses the appropriateness of assigning observations to clusters. The average Silhouette score, calculated as 0.123, indicates that while the separation between clusters is weak, it falls within an acceptable range. However, this value also suggests some ambiguity in the assignment of observations to clusters. The first cluster, depicted in blue, shows that the majority of observations exhibit a positive Silhouette coefficient, reflecting higher internal consistency within this cluster and suggesting that the observations are well-suited to their assigned group. In contrast, the second cluster, shown in orange, has Silhouette coefficients concentrated around negative and near-zero values. This finding indicates lower internal consistency within the cluster and suggests that some observations are positioned near the boundary between the two clusters. The Dunn Index for the hierarchical clustering analysis was calculated as 0.237, which reflects limited homogeneity within each cluster.

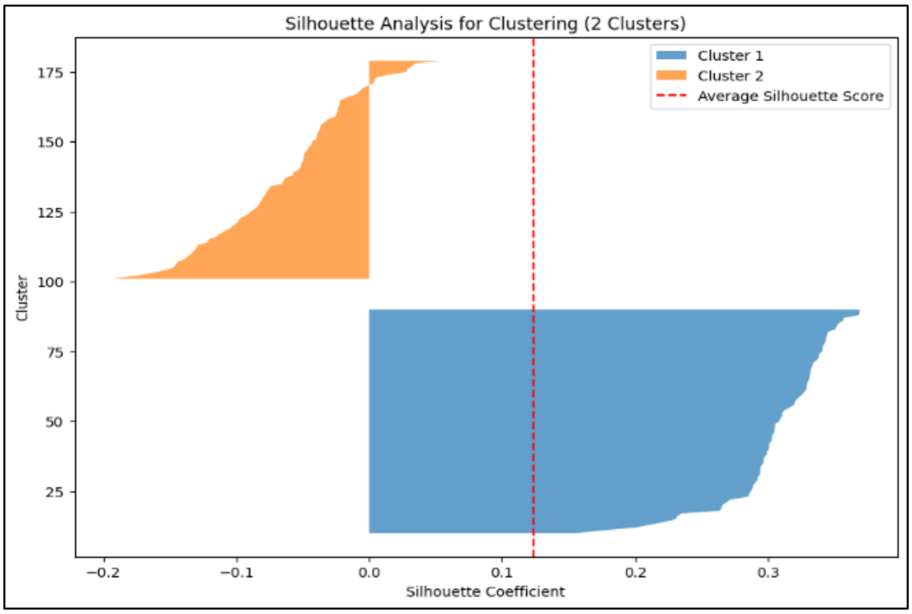
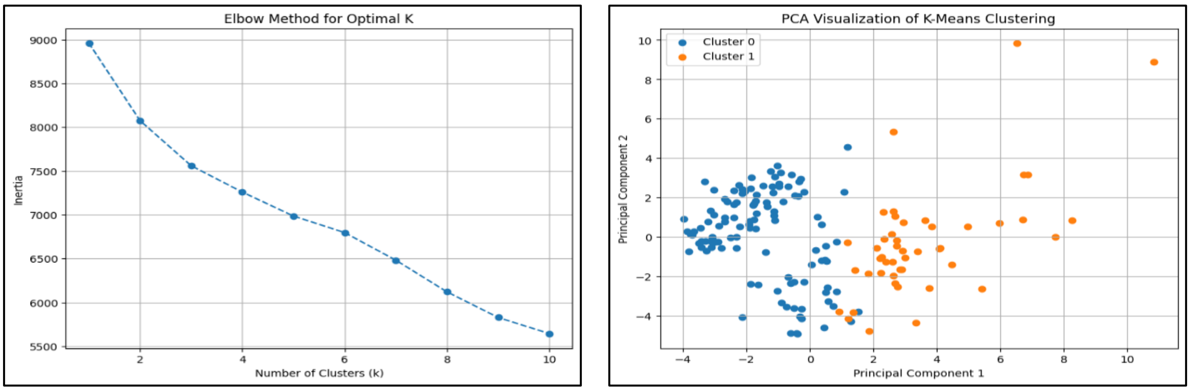


Figure 3. Silhouette Analysis for Clustering



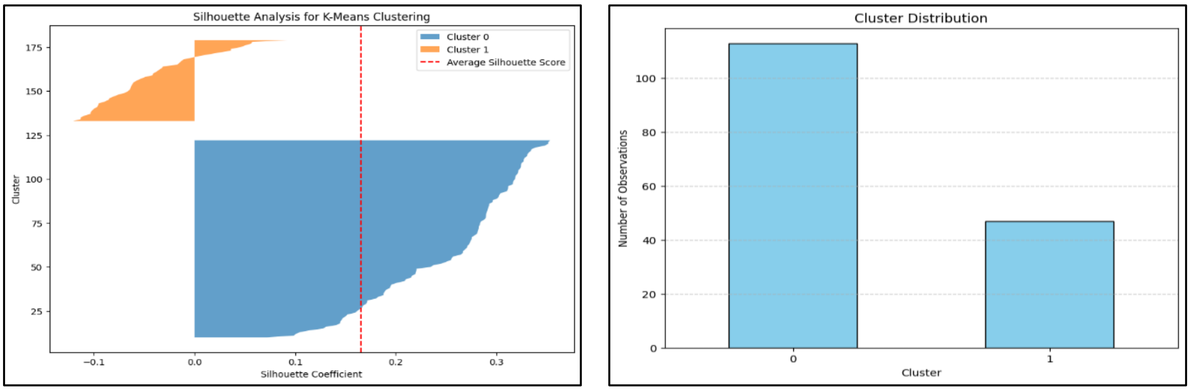
(a) (b)

Figure 4. Elbow Method for Optimal k (a), PCA Visualization of K-Mean Clustering (b)

The second clustering technique employed in this study was the K-Means algorithm. The optimal number of clusters was determined to be two. To assess the differences between clusters, the Mann-Whitney U test was conducted. Mann Whitney U statistics and p-values were calculated for each variable to identify statistically significant differences between the two clusters.

Figure 4(a) presents a visualization created using the Elbow Method to determine the optimal number of clusters for the K-Means clustering algorithm. The horizontal axis represents the number of clusters (k), while the vertical axis shows the distortion (the total intra-cluster distance). As the number of clusters increases, the distortion value decreases, indicating improved intra-cluster consistency. However, after a certain point, the rate of decrease slows, forming an "elbow" in the curve. Based on the clear findings of the Elbow Method, the optimal number of clusters is determined to be two (k=2). Figure 4(b) presents the results of the K-Means clustering analysis, with the clusters projected onto two dimensions using the Principal Component Analysis (PCA) method. The visualization shows that the observations are divided into two clusters (Cluster 0 and Cluster 1). Observations in Cluster 0 (depicted in blue) are primarily concentrated on the negative side of the PC1 axis, suggesting that enterprises within this cluster share similar characteristics and exhibit high intra-cluster consistency. In contrast, Cluster 1 (depicted in orange) is distributed more broadly across the positive side of the PC1 axis and along the PC2 axis. This pattern reflects greater intra-cluster variance, indicating that the enterprises within this cluster are more heterogeneous. The separation between the clusters along the PC1 axis underscores the primary source of variation between the groups, while the PC2 axis contributes less to the differentiation. The results reveal the presence of statistically significant differences among the analyzed observations. In this context, the results can provide a data source for understanding the relationships between variables derived from livestock enterprises.

Figure 5(a) illustrates the results of the Silhouette analysis for the K-Means clustering. The graph demonstrates that the observations are distributed across two clusters, consistent with the results of the K-Means clustering analysis. The average Silhouette score obtained in this study is 0.166, indicating weak but acceptable separation between the clusters. This suggests the absence of well-defined boundaries among the observations. As can be seen in the Figure 5(a), Cluster 0 (the larger cluster, depicted in blue) performs better in terms of the Silhouette coefficient compared to Cluster 1. The majority of observations in Cluster 0 exhibit positive Silhouette values, reflecting moderate internal consistency and cohesion within this group. In contrast, the Silhouette values for Cluster 1 (depicted in orange) are generally low, with many values close to zero. This indicates limited internal cohesion within the cluster, suggesting that some observations may lie near the boundary of the two clusters. The Dunn Index, calculated as 0.268, further supports these findings. While this value indicates that the separation between clusters is acceptable, it also points to a need for improved intra-cluster homogeneity to strengthen the internal structure of the clusters. Overall, the results suggest that while the clustering achieves a basic level of separation, further refinement could enhance the consistency and clarity of the grouping.



(a) (b)

Figure 5. Sillhouette Analysis for K-Means Clustering (a), Cluster Distribution (b)

Figure 5(b) illustrates the cluster distribution derived from the K-Means clustering analysis. According to the figure, Cluster 0 is the largest cluster, comprising 113 observations, whereas Cluster 1 consists of 47 observations. This distribution highlights that Cluster 0 represents the dominant group in terms of the number of observations, while Cluster 1 forms a smaller subgroup. The observed data distribution across the two clusters suggests the presence of distinct groupings based on the variables included in the analysis. Cluster 0 likely reflects enterprises with more common or shared characteristics, whereas Cluster 1 may represent enterprises with more specific or divergent traits.

Table 1: Farmer Demographic and Socioeconomic Characteristics

Variables	Cluster 1	Cluster 2	p-Value
Farmer's Age	46,52±1,107	47,85±1,66	0,658
Educational Status	2,902±0,085	3,085±0,113	0,21
Social Security	2,424±0,126	2,595±0,186	0,423
Cooperative Membership	1,911±0,026	1,744±0,064	0,005

Cooperative Membership emerges as the most significant indicator of variability between clusters (p = 0.005), suggesting statistically meaningful differences in mean values between Cluster 1 and Cluster 2. Specifically, Cluster 1 exhibits a higher mean (1.911 ± 0.026) compared to Cluster 2 (1.744 ± 0.064). This notable difference may reflect a greater tendency for farmers in Cluster 1 to participate in cooperatives, potentially due to access to collective resources or economic incentives that encourage such involvement. In contrast, variables such as Farmer's Age (p = 0.658), Educational Status (p = 0.21), and Social Security (p = 0.423) do not demonstrate statistically significant differences between clusters (p > 0.05). The absence of significant variation in these demographic characteristics—apart from Cooperative Membership—suggests that the two clusters are relatively similar in terms of age, education, and social security coverage. These findings offer valuable inferences for policymakers seeking to enhance cooperative-based initiatives, as cooperatives are well-known to improve resource mobilization, capacity building, and economic resilience among farmers.

Table 2: Animal Inventory

Variables	Cluster 1	Cluster 2	p-Value
Breeding Ewe	141,5±7,297	312,4±18,73	0,000
Ram	6,566±0,847	19,31±3,943	0,000
Female Lamb	60,52±3,45	123,3±9,462	0,000
Male Lamb	53,79±3,201	112,7±9,271	0,000
Female Yearling Sheep	20,09±1,814	40,17±10,49	0,145
Male Yearling Sheep	12,07±2,781	4,808±2,285	0,000
Breeding Doe	9,849±1,17	35,1±5,29	0,000
Buck	0,831±0,11	2,744±0,489	0,000
Female Kid	4,159±0,506	13,91±2,056	0,000
Male Kid	3,469±0,429	11,4±1,903	0,000
Female Yearling Goat	0,637±0,176	2,468±1,354	0,970
Male Yearling Goat	0,247±0,063	0,34±0,228	0,353
Cattle	1,389±0,693	11,1±3,057	0,000
Calf	0,53±0,329	3,085±0,882	0,000

The results of the Mann Whitney u test reveal significant differences between the two clusters in terms of livestock distribution. Statistically significant differences (p<0.05) were observed in the variables of breeding ewe, ram, female lamb, male lamb, male yearling sheep, breeding doe, buck, female kid, male kid, cattle, and calf, with Cluster 2 demonstrating notably higher values across these animal types. For instance, the number of breeding ewes in Cluster 2 was recorded as 312.4 ± 18.73, compared to 141.5 ± 7.297 in cluster 1. Similarly, the values for ram, female lamb, and male lamb were significantly higher in Cluster 2. In contrast, male yearling sheep showed higher values in cluster 1 compared to Cluster 2. On the other hand, no statistically significant differences (p>0.05) were found for female yearling sheep, female yearling goat, and male yearling goat, indicating a relatively uniform distribution of these categories across the two clusters. These results suggest that the clusters are not homogeneous in terms of livestock composition, with specific animal types exhibiting concentrated distributions, particularly in Cluster 2.

Table 3: Reasons for Livestock Breeding

Variables	Cluster 1	Cluster 2	p-Value
Reason for Small Ruminant Breeding - Habit	3,3±0,046	3,425±0,104	0,077
Reason for Small Ruminant Breeding - Sole Income Source	1,522±0,08	1,808±0,159	0,171
Reason for Small Ruminant Breeding - Additional Income	3,407±0,08	2,574±0,154	0,000
Reason for Small Ruminant Breeding - Household Needs	1,778±0,058	2,148±0,125	0,006

As can be seen in Table 3, the results of the Mann Whitney u test for the reasons behind small ruminant breeding reveal both statistically significant and non-significant differences between the two clusters. Statistically significant differences (p<0.05) were observed for "additional income" and "household needs", while no significant differences were found for "habit" and "sole income source". "Additional income" was significantly higher in Cluster 1 (3.407 ± 0.08) compared to Cluster 2 (2.574 ± 0.154), indicating that breeders in Cluster 1 place a greater emphasis on additional income as a motivation. Similarly, "household needs" was reported at higher levels in Cluster 2 (2.148 ± 0.125) compared to Cluster 1 (1.778 ± 0.058), suggesting that meeting household needs is a more prominent motivation for breeders in Cluster 2. In contrast, "habit" showed no statistically significant difference between the clusters (p=0.077), with mean values of 3.3 ± 0.046 in Cluster 1 and 3.425 ± 0.104 in Cluster 2. Similarly, "sole income source" did not exhibit a significant difference (p=0.171), with mean values of 1.522 ± 0.08 for Cluster 1 and 1.808 ± 0.159 for Cluster 2.

Table 4: Animal Feeding Practices

Variables	Cluster 1	Cluster 2	p-Value
Roughage Type	3,292±0,115	3,382±0,15	0,727
Roughage Source	2,849±0,045	2,617±0,107	0,021
Concentrate Feed Type	2,026±0,104	1,808±0,147	0,234
Concentrate Feed Source	2,566±0,069	2,851±0,08	0,055
Adding Salt/Minerals to Feed	1,07±0,024	1,319±0,068	0,000
Supplementary Feeding	1,353±0,045	1,51±0,073	0,067
Pasture	5,716±0,166	5,361±0,264	0,136
Highland Grazing	0,433±0,105	0,765±0,172	0,005

Table 4 shows the findings of the Mann Whitney U analysis on variables related to Animal Feeding Practices. Statistically significant differences (p<0.05) were observed for "Roughage Source", "Adding Salt/Minerals to Feed", and "Highland Grazing", while the remaining variables did not exhibit significant differences. Specifically, "Roughage Source" was significantly higher in Cluster 1 (2.849 ± 0.045) compared to Cluster 2 (2.617 ± 0.107). Similarly, "Adding Salt/Minerals to Feed" was reported at significantly higher levels in Cluster 2 (1.319 ± 0.068) compared to Cluster 1 (1.07 ± 0.024), suggesting that breeders in Cluster 2 are more inclined to supplement feed with salt or minerals. Additionally, "Highland Grazing" showed a statistically significant difference (p=0.005), with higher values in Cluster 2 (0.765 ± 0.172) compared to Cluster 1 (0.433 ± 0.105).

Table 5: Breeding Management

Variables	Cluster 1	Cluster 2	p-Value
Breeding Ram/Buck Source	1,318±0,057	1,553±0,124	0,154
Duration of Ram in the Flock	1,637±0,045	1,914±0,041	0,000
Duration of Buck in the Flock	1,699±0,043	1,936±0,036	0,001
Breeding Ram Usage Duration	3,699±0,115	2,723±0,138	0,000
Breeding Ewe Usage Duration	5,584±0,101	5,425±0,257	0,953
Breeding Buck Usage Duration	2,053±0,177	2,021±0,17	0,730
Breeding Doe Usage Duration	3,23±0,256	4,127±0,339	0,128
Breeding Selection Criteria	3,194±0,098	2,404±0,186	0,001

According to given results in table 5, statistically significant differences (p<0.05) were observed for "duration of ram in the flock", "duration of buck in the flock", "breeding ram usage duration", and "breeding selection criteria", while the remaining variables did not exhibit significant differences. The "duration of ram in the flock" was significantly higher in Cluster 2 (1.914 ± 0.041) compared to Cluster 1 (1.637 ± 0.045), indicating longer utilization of rams in Cluster 2. Similarly, the "duration of buck in the flock" was also significantly longer in Cluster

2 (1.936 ± 0.036) compared to Cluster 1 (1.699 ± 0.043). The "breeding ram usage duration" demonstrated a statistically significant difference, being higher in cluster 1 (3.699 ± 0.115) compared to Cluster 2 (2.723 ± 0.138). Conversely, the "breeding selection criteria" was significantly higher in cluster 1 (3.194 ± 0.098) compared to Cluster 2 (2.404 ± 0.186), suggesting that Cluster 1 places greater emphasis on selection criteria for breeding purposes. On the other hand, no statistically significant differences were observed for "breeding ram/buck source" (p=0.154), "breeding ewe usage duration" (p=0.953), "breeding buck usage duration" (p=0.730), and "breeding doe usage duration" (p=0.128), indicating similar practices across the two clusters for these variables.

Table 6: Health and Veterinary Services

Variables	Cluster 1	Cluster 2	p-Value
Veterinary Check-up	1,61±0,046	1,404±0,072	0,017
Vaccination Practice	1,238±0,04	1,574±0,072	0,000
Milk Usage After Vaccination	1,61±0,046	1,276±0,065	0,000
Enterotoxemia	0,185±0,036	0,489±0,073	0,000
Sheep Pox	0,008±0,008	0,34±0,069	0,000
Brucellosis	0,442±0,046	0,34±0,069	0,235
External Parasites	0,858±0,032	0,404±0,072	0,000
Respiratory Diseases	0,858±0,032	0,659±0,069	0,004
Milk Usage After Medication	2,415±0,092	1,723±0,144	0,000

Health and veterinary services results were given in Table 6. Statistically significant differences (p<0.05) were observed for "veterinary check-up", "vaccination practice", "milk usage after vaccination", "enterotoxemia", "sheep pox", "external parasites", "respiratory diseases", and "milk usage after medication", while "brucellosis" did not show a significant difference between the clusters. Specifically, "veterinary check-up" values were significantly higher in Cluster 1 (1.61 ± 0.046) compared to Cluster 2 (1.404 ± 0.072), indicating more frequent veterinary visits in Cluster 1. Conversely, "vaccination practice" was significantly higher in Cluster 2 (1.574 ± 0.072) compared to Cluster 1 (1.238 ± 0.04), reflecting a greater focus on vaccination practices in Cluster 2. For "milk usage after vaccination", Cluster 2 exhibited significantly lower values (1.276 ± 0.065) compared to Cluster 1 (1.61 ± 0.046), suggesting stricter restrictions on milk usage post-vaccination in Cluster 2. Similarly, "milk usage after medication" was significantly lower in Cluster 2 (1.723 ± 0.144) compared to Cluster 1 (2.415 ± 0.092), indicating more cautious milk management following medication in Cluster 2. Regarding disease prevalence, "enterotoxemia" was significantly more prevalent in Cluster 2 (0.489 ± 0.073) compared to Cluster 1 (0.185 ± 0.036). Similarly, "sheep pox" showed significantly higher prevalence in Cluster 2 (0.34 ± 0.069) compared to Cluster 1 (0.008 ± 0.008). In contrast, "external parasites" were significantly more prevalent in Cluster 1 (0.858 ± 0.032) compared to Cluster 2 (0.404 ± 0.072). "Respiratory diseases" also showed significantly higher values in Cluster 1 (0.858 ± 0.032) compared to Cluster 2 (0.659 ± 0.069). On the other hand, "brucellosis" did not show a statistically significant difference between the clusters (p=0.235), with values of 0.442 ± 0.046 in Cluster 1 and 0.34 ± 0.069 in Cluster 2.

Table 7: Production and Mortality Rates

Variables	Cluster 1	Cluster 2	p-Value
Number of Lambs per Season	110,8±6,779	220,7±17,73	0,000
Number of Kids per Season	7,424±0,916	26,89±4,137	0,000
Number of Dead Lambs	6,46±0,614	21,42±2,664	0,000
Number of Dead Kids	0,92±0,138	3,021±0,361	0,000

Production and mortality rates results are presented in Table 7. The Mann Whitney u test reveals statistically significant differences (p<0.05) between the two clusters for all analyzed variables, including "number of lambs per season", "number of kids per season", "number of dead lambs", and "number of dead kids", indicating notable disparities in production and mortality rates. The "number of lambs per season" was significantly higher in Cluster 2 (220.7 ± 17.73) compared to Cluster 1 (110.8 ± 6.779), show greater lamb production in Cluster 2. Similarly, the "number of kids per season" was significantly higher in Cluster 2 (26.89 ± 4.137) compared to Cluster 1 (7.424 ± 0.916), state a higher kid production rate in Cluster 2. However, mortality rates were also significantly elevated in Cluster 2. The "number of dead lambs" was recorded as 21.42 ± 2.664 in Cluster 2, compared to 6.46 ± 0.614 in Cluster 1, indicating markedly higher lamb mortality in Cluster 2. Similarly, the "number of dead kids" was significantly greater in Cluster 2 (3.021 ± 0.361) compared to Cluster 1 (0.92 ± 0.138), underscoring higher kid mortality rates in Cluster 2.

Table 8: Shelter, Record Keeping, and Manure Management

Variables	Cluster 1	Cluster 2	p-Value
Record Keeping	1,867±0,032	1,297±0,067	0,000
Shelter Type	2,194±0,041	1,957±0,029	0,001
Manure Utilization	1,823±0,036	1,404±0,072	0,000

The Mann Whitney U analysis results for record keeping, shelter type, and manure utilization are presented in Table 8. The Mann-Whitney U test reveals statistically significant differences between the two clusters for all three variables: "Record Keeping", "Shelter Type", and "Manure Utilization", indicating notable variations in these management practices (p<0.05). "Record Keeping" was significantly higher in Cluster 1 (1.867 ± 0.032) compared to Cluster 2 (1.297 ± 0.067), suggesting that Cluster 1 places greater emphasis on maintaining systematic records. Similarly, "Shelter Type" exhibited a statistically significant difference, with Cluster 1 showing higher values (2.194 ± 0.041) compared to Cluster 2 (1.957 ± 0.029), indicating that more developed or structured shelter types can be employed in Cluster 1.

CONCLUSION

In this study, hierarchical and non-hierarchical clustering analyses were conducted to examine livestock enterprises operating in the Tuşba and Gürpınar districts of Van Province for analyzing and understanding the heterogeneous structures of livestock enterprises. By employing both hierarchical and non-hierarchical clustering methods livestock enterprises in the Tuşba and Gürpınar districts of Van Province were systematically clustered into two distinct structures. The results reveal significant inter-cluster variability across critical dimensions, including feeding and nutrition strategies, animal health and disease management practices, productivity parameters, and socioeconomic characteristics. The clustering results can offer practical implications for policymakers and local governments. Also, the identification of clusters with shared characteristics can enables the formulation of targeted strategies to address specific challenges, enhance resource use efficiency, and improve productivity. From a statistical methodology perspective, this study highlights the utility of advanced computational tools in agricultural research. The use of Python programming on the Google Colab platform enabled the clustering analyses to be executed with precision and reproducibility, illustrating the applicability of modern data science techniques for managing large-scale and complex datasets. It is thought that the research findings and methodological process will shed light on researchers who will work on this subject in the future.

Funding

The research was not supported.

Statement of Conflict of Interest

There is no conflict of interest.

Authors' Contributions

All authors contributed to the writing of the article and took part in the process of publication of the article and read and approved it.

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International Conference on
Food, Agriculture and Animal Sciences
19-22 December 2024, Erzurum, TÜRKİYE
ICOFAAS

Effects of Reproductive Management on Profitability of Dairy Production

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ABSTRACT: Profitability of dairy farms is influenced by multiple factors, including feed costs, milk prices, labor efficiency, herd health and reproductive efficiency . Among these, reproductive management is a key determinant of long-term profitability. Efficiency of reproductive practices directly influence key production parameters, such as milk yield, calving intervals, herd size, days open, conception rates, sustainable replacement rate and overall herd health, which are all crucial components of economic success in dairy farming. Inadequate reproductive management can lead to increased culling rates, prolonged calving intervals, and lower milk yields, which in turn reduce overall farm profitability. Developments in reproductive technologies have revolutionized dairy farm management and significantly influenced farm profitability. These technologies enable more precise breeding, improve conception rates, and help optimize herd genetics, all of which directly impact production and economic outcomes. This review examines the relationship between reproductive management and profitability in dairy production, exploring how breeding strategies, fertility control, health management, and technological innovations can impact reproductive performance, milk production efficiency and ultimately, the financial outcomes for dairy farmers.

Keywords: Reproductive Management, Dairy, Profitability

INTRODUCTION

Although milk is the main product of the dairy industry, it has been well documented that the economics or profitability of the industry is influenced directly and indirectly by reproductive performance of the industry. Beside milk sales, cows replaced and replacement heifers are important income sources and all influenced by reproductive performance. Reproductive programs affect number of services and rearing expenses during open period, dry period and lactation and therefore, feed cost, labor and veterinary expenses. (Giordano, J. 2019). Milk production starts upon calving, makes a peak within weeks and then decreases slowly. Extended lactation due to higher number of open days causes lactation to extend, and therefore, towards the end of longer lactation average milk production decreases compared to cows having shorter lactation period. Reproductive performance of cows is determined by the ability of a cow to conceive after mating or artificial insemination, the ability to maintain this pregnancy, and also number of calves weaned. Results of a great number of the studies showing that genetically high milk yield in modern cattle breeding has caused serious declines in fertility. There is a multi-faceted relationship between fertility and milk yield. Selection for high milk production generally leads to a decrease in fertility. This may be related to the negative effects of metabolic high performance on reproductive functions. Inadequate fertility may extend the lactation cycle and cause a decrease in total milk yield. In this case, it is important to balance both milk yield and fertility for a healthy reproductive cycle. Therefore, it is important to know the sources of variation in income of a herd imposed by reproductive management and to make decisions for determining reproductive management and also the level of herd performance (Giordano, J. 2019).

Effects of Extended Calving Intervals on Profitability

The feed intake and milk production of cows during lactation are not completely compatible with each other. The feed consumption in the early and late stages of lactation differ as well as the increase and decrease rates of milk production differ and results in different conversion rates of feed to milk. Dry matter intake reaches its maximum level a few weeks after peak milk yield. The rate of decrease in feed intake after peak is slower than .the rate of decrease in milk yield. For this reason, the ratio for value of milk produced to feed costs is high in the early part of lactation but as lactation progresses the ratio decreases. Therefore, the timing of pregnancy in each lactation determines the amount of time cows spend in the most productive period of the lactation curve throughout their lives, which affects their profitability and overall profitability (Giordano, J. 2019). Since gestation period does not change very much, the reason for extended calving period is mainly due to extended service period which is the period from calving to conception. Krpálková et al. (2013) reported that in a 21 day period only one percent of increase in pregnancy rate resulted in economic gain of 14.6 EUR per cow/year. They also concluded that poor fertility caused cows to have longer period with less efficiently produced milk. Roche et al. (2013) reported that increasing the calving interval from 12 to 14 months resulted in an 8–10% decrease in total annual milk production.

Beside decreased average milk production and increased feed cost per liter milk, longer calving intervals increase the costs of breeding and maintenance on farms. Due to more inseminations to achieve pregnancy, additional costs such as artificial insemination, veterinary services and hormone treatments also negatively affects the profitability (Lucy, 2001).

Animals with fertility problems are often disposed of early and replaced with new breeders. This results in both a high capital cost per animal and losses in milk production during the replacement period. Diskin and Kenny (2014) reported that early removal of cattle with poor reproductive performance from herds can result in a 15-20% loss of income on the farm economy. Other than extended voluntary open days, the reason for extended calving period is usually repeat breeding; that results in increased on farm labor costs, beside veterinary and synchronization costs. Sometimes labor for visual heat detection may be costlier than an estrus synchronization program, and this depends on availability of farm labor, facilities, herd size etc.

Although many studies showed that due to low reproductive performance through extended service period profitability decreased, Arbel et al. (2001) reported contradictory results. The investigators showed that the negative relationship between reproductive performance and profitability may differ high yielding and low yielding cows. The study investigated effects of calving interval on profitability at two different time, day 154 (extended) and day 93 (control) postpartum. First insemination was performed on primiparous cows and at day 124 and day 71 on multiparous cows. They reported that either primiparous or multiparous cows were more profitable when lactation was extended with a 60 day delay with respect to the usual voluntary waiting period.

Relation Between Milk Yield, Reproduction and Profitability

High milk yield in dairy cattle is one of the main goals of modern farms. Within the last century dairy cows milk yield has been increased incredibly and still continuous to increase. However, this goal can create a conflict with reproductive performance. High milk yield often leads to metabolic stress and energy balance problems, which negatively affects reproductive performance.

While high milk yield in dairy cattle provides a great economic advantage, a decrease in reproductive performance may limit this benefit. Genetic programs that select for high milk yield may cause metabolic stress, negative energy balance and fertility problems mainly by insemination failures and therefore extending the calving interval. Several studies have been showed the negative relationship between milk yield and pregnancy rate.

High milk yield challenges the metabolic balance of cows and leads to energy imbalances that negatively affect reproductive performance. A study by Roche et al. (2013) showed that ovarian functions were suppressed in cows with high negative energy balance in the early lactation. Genetic programs that select for high milk yield may have indirect effects on fertility. Berry and Diskin (2015) stated that genotypes that provide high milk yield are generally associated with low fertility. Considering fertility traits along with milk yield in genetic improvement programs is critical to maintaining this balance. Although high milk yields increase total income, a decrease in fertility can increase costs. A decrease in pregnancy rates increases insemination costs and negatively affects renewal rates. Dobson and Smith (2000) reported that high milk yields increase total farm costs by 15-20%.

Conclusion

It is well established that reproductive performance of dairy cattle is a major determinant of profitability of dairy operations and affects major sources of income such as total milk sales, number of cows replaced, number of replacement heifers born. Reproductive performance also affects sources of cost such as rearing costs, opportunity cost of delayed lactation, feed, labor and veterinary inputs, lactation length, dry period length, days in rearing number of services to conceive. Cows with poor fertility have longer lactation period. Towards the longer lactation periods these cow produce milk less efficiently, reducing net return and increasing culling risk of the cows.

Long calving intervals cause serious economic losses in the dairy industry. In order to prevent these losses, effective reproductive management strategies, genetic improvement and nutritional optimization are needed. For long-term economic success, it is important to keep the calving interval at optimum levels. Best reproductive management tolls depends on farms condition (herd size, labor available etc.) A high reproductive performance is essential for profitability of dairy farms. Profitability of higher milk production may occur only if the cow does not have fertility, longevity, and health problems. Declining fertility is the most common reason for culling in the high-producing herds. Culling due to low reproductive performance can reduced by improved estrous detection, efficient synchronization of reproductive programs. Factors including but not limited to genetics, animal health, proper housing, nutrition, competent farm staff, increasing herd size, heat detection, higher milk production, managental problems and heat stress (global warming and climate change) increasingly getting more importance on reproductive performance and therefore profitability of the dairy farms. Although many researchers suggested a shorter calving interval for a profitable production, detailed investigation showed that this may depend on also level cows milk yield, and extended calving interval was more profitable for high producers and shorter calving intervals was more profitable in low yielding cows.

Specially in the early stages of lactation, negative energy balance has tremendous effects reproductive performance through its effects on ovulation and fertility, metabolic diseases or metabolic stress like ketosis, hypocalcemia and therefore profitability. The relationship between high milk yield and reproductive performance in dairy cattle is a complex issue that must be carefully managed from both biological and economic perspectives. Effective management of the conflict between milk yield and fertility is critical to ensure the sustainability of dairy farming.

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Effects of Phytoestrogens on Farm Animal Reproduction

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ABSTRACT: Phytoestrogens are the natural chemical compounds found in plants, especially in soy, alfalfa and other legumes, that are similar to the hormone estrogen. These compounds are structurally similar to the hormone estrogen and in some cases can affect the reproductive processes of animals by acting on their endogenous estrogen systems. In agriculture, especially in feeds, food additives, and plant-based supplements, the effects of phytoestrogens on farm animal reproduction have been increasingly investigated in recent years. The effects of phytoestrogens on the reproductive health of farm animals have been addressed in various studies in recent years and many opinions have emerged about the positive and negative effects of these compounds. This article examines the potential effects of phytoestrogens on reproductive health and performance in farm animals, and discusses findings on the possible consequences of these compounds on hormonal regulation, fertility, and general health. In addition, the adverse effects of phytoestrogen use on the reproductive systems of animals and proposed strategies for managing these effects is discussed.

Keywords: Pyhtoestrogens, Farm Animals, Reproduction

INTRODUCTION

Phytoestrogens are natural non-steroidal phenolic compounds found in more than 300 plants and most of them are consumable plants. They are non-essential secondary plant metabolites related with plant defense. The level of these compounds increases when plants applied with pesticides or other biotic or environmental stressors. These compounds are abundant in animal diets, mostly in legumes (soybean, alfalfa, clover etc.) and have similar chemical structure with 17-β estradiol or estrogen. They can be found at concentrations thousand of times higher than physiologic level of E2 and can mimic or block the effects of the estrogen by binding to its receptors. Therefore, phytoestrogens affect hormonal balance in animals and humans. Especially in pastures where phytoestrogen-rich forage plants such as clover are abundant, it is not possible to control animals which plants to be consumed. Considering that they also consume these estrogenic compounds in various amounts, it has been reported by many studies that the reproductive performance of these animals is affected. Especially sheep have a higher chance of consuming phytoestrogen-containing plants than cattle due to their grazing characteristics. However, since other farm animal species such as cattle and poultry also have the potential to consume feedstuffs containing these compounds, both in pasture and in feed provided on the farm, it should be taken into consideration that these species are also likely to be affected by these compounds in various ways. Although this review examines studies on the effects of phytoestrogens on the reproductive performance of farm animals, there are many studies investigating the effects of phytoestrogens on human health. Many potential health benefits in humans were reported; such as easing menopause symptoms, supporting bone health, improving heart health and reducing the risk of cancer. However, it was suggested that the effects can vary from person to person and large amounts may have adverse effects; in certain conditions such as hormone-sensitive cancers, caution has been advised.

Sources of Phytoestrogens

Phytoestrogens are plant-based compounds and livestock exposure to phytoestrogens occurs mainly through grazing or feed supplements. They are found commonly in legumes, such as soybean, clover and alfalfa are very important animal feeds and contains large amounts of these compounds.

Chemical Structures and Classification of Phytoestrogens

More than 100 phytoestrogens were determined and are categorized into three primary classes; isoflavones, coumestans, and Lignans. isoflavones (e.g., genistein, daidzein) are predominantly found in soybeans. Coumestans (e.g., coumestrol) are found in clover and alfalfa, and lignans are present in flaxseed and cereal grains.

These chemical compounds have a very similar structure of 17 beta estradiol which is the most potent estrogen and also a potent synthetic estrogen (diethylstilbesterol) along with the antiestrogen tamoxifen, and the well-known phytoestrogens, coumestrol, equol, genistein and daidzein (Figure 1). All these chemical structures have a common phenolic group which is shown in big circle in Figure 1. The phenolic group is essential for a chemical to bind the estrogen receptor. Although all of these compounds can bind the receptor, some like estradiol 17 beta activate the receptor, some others, for example tamoxifen which is a potent syntetic anti-estrogen, may bind the receptor, but do not activate it. Therefore, it competes for the receptor by blocking it. Since there are so many phytoestrogens and affinity of each of these molecules to estrogen receptors differs, their estrogenic effects differ. When plants or their extracts are used in studies with animals or cells the result may be divergent due to variation in the content of the plants.

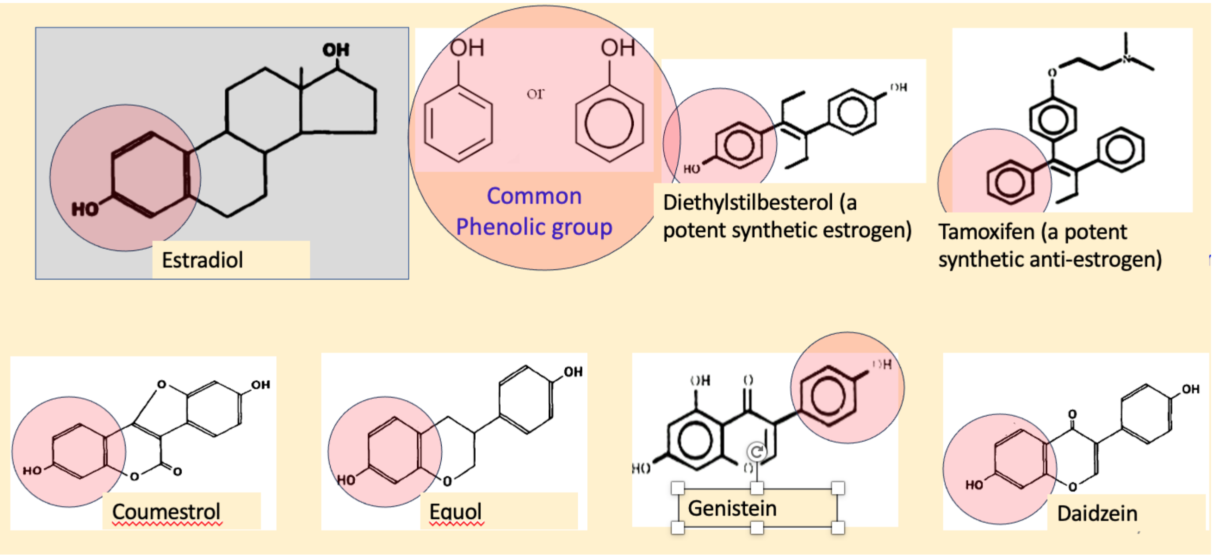

Figure 1. Chemical structure of estradiol, diethylbesterol (a potent syntethic estrogen), tamoxifen (a potent syntethic anti-estrogen), coumestrol, equol, genistein and daidzein. A common phenolic group are existed in structure of these compounds.

These compounds act as agonists or antagonists of estrogen receptors (ER-α and ER-β), depending on concentration and hormonal milieu. Isoflavones are the most extensively studied due to their prevalence in agricultural feed products. The structural similarity of these compounds to 17β-estradiol underpins their ability to bind to estrogen receptors and exert estrogenic or anti-estrogenic effects.

Biochemical Mechanism of Phytoestrogens

Due to common phenolic group of these compounds can compete for estrogen receptors and occupy the receptor. The weak estrogenic compound can activate estrogen receptor, on the other hand, antiestrogens blocks (antiestrogen) the receptor Another mechanism of action of phytoestrogens is inhibition of aromatase, the enzyme required for estrogen biosynthesis. The secretory function of the corpus luteum is impaired through increasing oxytocin and also decreasing prostaglandin E2 (PGE2) in luteal cells is another way of affecting reproductive functions. Progesterone is produced mainly by corpus luteum and needed for preparation of uterus for pregnancy and maintenance of pregnancy by preventing uterus contractions.

Phytoestrogens also affect the hypothalamic–pituitary–gonadal (HPG) axis. They cause a decrease in the release of luteinizing hormone (LH), inhibition to the response of gonadotropins on granulosa cells, interfere with the endogenous feedback of 17β-estradiol, increase prostaglandin F2α (PGF2α) secretion from the endometrium, affect the development and maturation of ovarian follicles (Wyse et al., 2024).

Phytoestrogens exhibit a higher affinity for estrogen receptor β (Erβ) than for Erα. Nikoliç et al. (2017) reported that compared to estrogen, relative activity of different phytoestrogens could be as low as 1/495 (coumestrol), 1/1190 (genistein) 1/1639 (equol) 1/7692 (daidzein), and 1/166667 (formononetin). The effects of phytoestrogens on reproduction are dose-dependent. At low to moderate doses, they may improve reproductive performance by enhancing hormonal balance. At high doses they may lead to adverse effects such as anovulation and embryonic loss.

Effest of Phytoestrogens on Reproduction of Farm Animals

Clover disease was named after the outbreak of infertility in sheep grazing pastures rich in clover in 1940s. Later studies with different species or breeds revealed adverse and beneficial effects of phytoestrogens. Reported adverse effects are; reduced reproductive efficiency, silent heath, lower conception rates, increased embryonic loss (Wyse et al., 2024), decreased reproductive hormones (estrogen, progesterone, testosterone lutenizing hormone), suppression of follicular development, alteration in genital tracts (ovarian cysts), blocked spermatogenesis, decreased sperm count (Whitten and Naftolin 1998)

Similar pregnancy rates were reported when 0.8 vs 0.3 % of BW soybeans were fed 6 months before their first service or by constand feeding 2.5 kg/day of soybeans to heifers. Decreased pregnancy rates were reported upon feeding 61.5 % clover for five months to Holstein heifers compared to 92.3 %; fed corn silage fed for five months to Holstein heifers.

Hormonal changes were observed in lactating cows consumed alfalfa or red clover for 60 days. In cows consumed alfalfa or red clover, estrogen, progesterone and lutenizing hormone decreased. Serum progesterone levels decreased throughout the estrous cycle in cows fed 2.5 kg of soybeans for 21 d. Improvement in scrotal growth and semen quality in Angus bulls fed diet with 10 % of soybeans from weaning to pre-puberty. Angus cows grazed legume and ryegrass pasture had reduced oocyte development, reduced progesterone production and increased early embryonic loss.

Ewes consumed alfalfa ad libitum for 10 months increased concentration of prostaglandins in serum, alterations in the genital tract (43%), cysts in the endometrium, increased glandular activity and para ovarian cysts were observed. Ewes fed clover prior to lambing to first estrus had shorter estrus duration (20 h) vs. (34 h in control ewes fed corn. Mustonen et al. (2014) reported that fecundity of the ewes was similar when red clover was feed with high phytoestrogen concentration.

On the other hand, some beneficial effects of phytoestrogens were reported especially in males, and birds; improved reproductive parameters; increased testicular weight, increased semen volume, increased libido, increased oviduct development, increased eggshell thickness, increased hatchability of egg, improved growth rate in lambs. I a study with lambs fed ad libitum with alfalfa or subterranean clover had no alterations in fertility, fecundity, and the development of the reproductive system, and calving interval but had higher weight at puberty (Pace et al.,2006).

Rams fed 1.1 kg/d of alfalfa contaminated with fungus decreased sperm concentration. Fungal infestations may increase the synthesis of phytoestrogenic substances. Rams fed alfalfa or soybeans daily for 90 d, no difference in sperm volume, color, motility, concentration and progressive motility. The infertility caused by PEs was temporary and get normal within 1 month after removal from the estrogenic feed. When ewes exposed to PEs for long periods infertility may become is permanent. Feeding ewes with berseem clover during seasonal anestrus disrupted behavioral estrus, decreased luteal progesterone synthesis and fecundity (Hashem et al., 2018).

A study by Moreno et al. (2020) highlighted that while goats showed lower sensitivity to isoflavones, chronic exposure could still result in cumulative fertility issues over multiple breeding cycles.

Pregnant does fed a diet of 18 % of soybean meal during gestation males reached puberty earlier but no difference found in reproductive organs, semen quality and sexual behavior Male rabbits fed 30 % of clover hay and supplemented with isoflavones had increase in semen volume and and libido. Male rabbits fed diet rich in soybeans and flaxseed increased abnormalities in spermatozoa, decreased libido. Pregnant does fed commercial feed with 18 % of soybean their offspring had normal morphology of the reproductive organs.

Laying hens fed diets supplemented with flax seeds or fenugreek, E2 and LH concentrations increased, shell thickness increased at the end of the egg laying cycle When laying hens were fed a diet supplemented with daidzein, shell thickness and oviduct weight increased. Laying hens fed supplemented diets with daidzein did not change egg quality or fertility or hatchability of eggs increased

Conclusion

Phytoestrogens are a diverse group of molecules and when digested estrogenic and non-estrogenic compounds form. In ruminant, it is more difficult to understand the whole mechanism due to microbial digestion and a huge variety of microbes. The effects of the phytoestrogens are on; impaired ovarian function, reproductive endocrine, development of reproductive organ and metabolism (steroidal effects). The diverse effects of PEs on reproduction of farm animals based on; type and amount of PEs/plant consumed, mode of administration (in feed/extracts), time and the level of exposure, processing of the plant , adaptation of the rumen microbes to degrade the ingested metabolites, season of the year , species, animals age (sexual maturity) and sex of animals (Moralez et al. 2022). The adverse effects of phytoestrogenic metabolites may alter reproductive system specifically at certain time of development and fertilization causing infertility and immune system suppression. Although large number of animal studies have been conducted with phytoestrogens, despite limitations, there is increasingly more interest on human health affected through edible plants consumed by human (Wocławek-Potocka et al.,2013).

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In Planta Transformation Techniques: Bridging The Gap Between Innovation and Application

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ABSTRACT: Plant transformation represents a crucial yet challenging aspect of advancing plant science, addressing fundamental and practical barriers. The inherent recalcitrance of many key crops to genetic transformation continues to hinder scientific progress, particularly in underutilized species essential for global food security. Over recent decades, a variety of stable transformation techniques, collectively termed “in planta,” have emerged as innovative alternatives. These methods bypass complex tissue culture steps, emphasizing genotype independence, simplicity, cost-efficiency, and versatility across experimental environments. This article underscores the transformative potential of in planta methodologies in plant biotechnology, fostering equitable advancements in research and unlocking genetic innovation in both model and minor crops.

Keywords: *In Planta,* Plant transformation, Bridge, Innovation, Application

INTRODUCTION

The ability to genetically transform plants has been a cornerstone of modern plant biology, enabling researchers to study gene function, engineer traits, and improve crop resilience. Traditionally, transformation techniques have relied heavily on in vitro tissue culture, a process that involves regeneration of plants from callus tissues or explants under controlled conditions. While effective, these methods are often species-specific, labor-intensive, and prone to somaclonal variation, which can introduce unintended genetic changes (Tzira and Citovsky, 2006).

In planta transformation offers an alternative approach by directly introducing genetic material into intact plant tissues or reproductive structures. This eliminates or minimizes the need for tissue culture, making the process simpler, faster, and more cost-effective. Techniques under this category include the transformation of germline, embryo, meristem, vegetative tissues and some novel systems (Belanger et al. 2024).

The emergence of genome-editing technologies such as CRISPR-Cas9 has further highlighted the importance of efficient transformation systems. *In planta* transformation offers a streamlined platform for delivering gene-editing reagents directly into plants, facilitating precise genetic modifications across diverse species. Its simplicity and reduced dependence on specialized infrastructure make it particularly valuable for laboratories in resource-limited settings by reducing technical complexity and broadening the range of amenable species, *in planta* transformation is poised to play a pivotal role in advancing plant biotechnology. It holds significant potential for accelerating crop improvement, enhancing food security, and addressing global challenges in agriculture (Zlobin et al. 2020).

Classification of *In Planta* Transformation Techniques

Germline Transformation

The floral dip method is a cornerstone of in planta transformation, particularly in *Arabidopsis thaliana*. It involves dipping developing floral tissues into a suspension of *Agrobacterium tumefaciens*, facilitating germline transformation. Originally introduced by Bechtold (1993) using vacuum infiltration, the method was later simplified by Clough and Bent (1998) to eliminate vacuum steps, increasing efficiency and ease of use. This streamlined approach typically achieves transformation rates of 0.1–3% (Clough & Bent, 1998; Bechtold et al. 1998; Bent, 2006). Several variations, such as low inoculum density, vacuum infiltration of floral buds, and simplified protocols, have been introduced to refine the technique (Wang et al. 2020; Das & Joshi, 2011; Ali et al. 2022). However, the floral dip method faces two key limitations: It generates hemizygous offspring, requiring screening through the T3 generation to isolate homozygous progeny and it has a narrow range of species applicability, primarily within the Brassicaceae family, with limited success in other families like Linaceae and Solanaceae due to biological and morphological constraints (Desfeux et al. 2000; Bent, 2006; Honda et al. 2021). These constraints arise from factors such as flower morphology, reduced susceptibility to *Agrobacterium*, necrotic reactions, and large floral structures (Bent 2006; Bent 2000) Innovative adaptations, including floral bud injection (e.g., in tomato and sunflower), floral bud painting (e.g., in maize), and floral bud spray (e.g., in wheat), have expanded its utility beyond Brassicaceae (Cosic et al. 2017, Shahid 2016). Despite these advancements, the floral dip method remains limited compared to broader techniques like shoot apical meristem injury. This method has significantly influenced plant molecular biology, but further innovations are required to address its species limitations and improve its broader applicability (Honda et al. 2021). Pollen transformation involves introducing a foreign gene into pollen grains using Agrobacterium tumefaciens or naked DNA. The transformed pollen is then used to fertilize recipient plants in vivo, making it a straightforward and scalable approach due to the abundance and ease of isolation of pollen grains. However, structural barriers such as the outer exine, inner intine, and nucleases released during germination hinder the direct integration of

DNA into pollen (Eapen 2011, Matoušek, & Tupý 1985). To address these challenges, various techniques have been developed, including electroporation, particle bombardment, vacuum infiltration, sonication, Agrobacterium-mediated transformation, and magnetofection. Despite these advances, the success of pollen transformation remains species-specific, with demonstrated efficiencies in tobacco, cotton (*Gossypium hirsutum*), sorghum (*Sorghum bicolor*), petunia (*Petunia x hybrida*), Indian mustard (*Brassica juncea*), and maize (*Zea mays*) (Zhang 2019, Zhao 2017). Certain methods, like the MAGELITR system, incorporate a brief in vitro phase, which can be restrictive for labs lacking micropropagation facilities. Furthermore, techniques such as magnetofection have shown variable success, being less effective in monocots. Despite these limitations, pollen transformation remains a valuable strategy, particularly for species with suitable pollen structures and favorable lab conditions (Sharma 2020).

Embryo Transformation

The pollen-tube pathway is a transformation technique where exogenous DNA is applied to the severed style of a recipient plant. The DNA travels through the growing pollen tube to the ovary, where it integrates into the zygote to produce a transformed embryo (Luo & Wu 1988). This method, first reported in cotton (*Gossypium hirsutum*) in 1983 and rice (*Oryza sativa*) in 1989, avoids the need for regeneration steps and is relatively simple to prepare. Despite these advantages, the technique has faced significant criticism due to poor transformation efficiency and inconsistent results. For example, studies in soybean (*Glycine max*) observed plants with apparent β-glucuronidase (GUS) activity that were not confirmed as transgenic by PCR. Morphological variations seen in the first generation often did not persist in subsequent generations, raising questions about reproducibility and reliability (Shou et al. 2002).

The pollen-tube pathway is now supported by numerous protocols for various crops, including cotton (*Gossypium histiridium*), maize (*Zea mays*), rice (*Oryza sativa*), wheat (*Triticum aestivum*), and at least 24 additional species (Wang et al. 2019). The ovary-drip method delivers exogenous DNA, typically in the form of a minimal linear gene cassette, directly to the ovule after pollination and complete removal of the style. This approach offers higher transformation rates compared to the pollen-tube pathway, achieving a transformation frequency of 3.38% versus 0.86% for the latter. However, the method requires precise manipulation to avoid mechanical damage to the ovule (Yang 2009). The technique has been successfully applied to crops like soybean and maize. A critical factor influencing its efficiency is the handling of the style. While the ovary-drip method shows promise due to its efficiency, its success relies on meticulous technique, limiting its widespread adoption. Pollen-tube agroinjection method combines the principles of the pollen-tube injection pathway with Agrobacterium tumefaciens-mediated transformation. It involves puncturing the carinas of legume flowers and injecting 0.1 mL of an Agrobacterium solution, achieving a transformation rate of 50% in peanut. Despite limited studies, its high efficiency suggests potential as an alternative to the conventional pollen-tube pathway (Zhou et al. 2023). Ovary injection transformation technique injects Agrobacterium directly into the locule of a plant's ovary after pollination, successfully transforming species such as tomato and soybean. Transformation rates in tomato have reached up to 88% using protocols with different incubation periods. In soybean, injecting at specific pod formation stages achieved efficiencies of 6.45–14.2% in plants and up to 35.48% in seeds. A variation involving micro-vibration was developed to enhance DNA integration by ultrasonic stimulation (Zia et al. 2011). Infection of pre-imbibed embryos with Agrobacterium method involves injuring seeds (e.g., pricking, cutting) and then imbibing them in an Agrobacterium solution to infect the embryo. Transformation rates in early protocols were low (0.7% in R0 plants and 0.07% in R1), but the technique has evolved into more effective protocols for various species, including maize and soybean. A variant for Arabidopsis achieved transformation without injuries to pre-imbibed seeds but with low efficiencies (0.0015–0.32%) (Fledmann 1987). Agro-imbibition is a newer, genotype-independent technique in which surface-sterilized seeds are fully imbibed in an Agrobacterium solution and germinated on a nutrient medium or soil. Transformation efficiencies vary widely, from 14.3% in chickpea to 93.8% in rice. While simple and efficient, its adoption is limited by the need for licensing due to multiple patents (Singh et al. 2020). Imbibition of desiccated embryos approach involves rehydrating desiccated zygotic embryos in an Agrobacterium solution. Physiological changes during desiccation, such as cell wall bursting, enhance DNA uptake. Soybean embryos processed using this method achieved transformation rates up to 80% in T0 mutants, and stable transformants were observed in the T3 generation. This method is also compatible with Arabidopsis and other species (Rao et al. 2016).

Meristem Transformation

The shoot apical meristem injury method targets the universal shoot apical meristem, transformable at any plant growth stage. This approach involves wounding the meristem, infecting it with Agrobacterium tumefaciens, and allowing plant growth under in vivo conditions. Transformants are typically screened in the T1 generation. Standardized protocols, such as those for safflower and peanut, report transformation efficiencies of 1.3–5.3% in safflower and 3.3% in peanut. Variations include sonication, electroporation, and vacuum infiltration to improve efficiency (Fletcher et al. 2002, Rohini & Rao 2000, Betchtold, 1993). Vegetative propagules, such as tubers, bulbs, and plantlets, are transformed under in vivo conditions. The cut–dip–budding method achieves efficiencies of 10–47% in sweet potato and 40–50% in Taraxacum kok-saghyz (Mei et al. 2024). The RAPID method injects Agrobacterium into the stem to generate transformants with efficiencies of 28–40% in species like potato and sweet potato. Additional systems target banana suckers, sugarcane setts, and cacti bulbs (Mayvan et al. 2015). Morphogenic regulators, such as WUSCHEL and BABY BOOM, enhance de novo shoot organogenesis. The direct delivery method injects Agrobacterium with these regulators directly into plants, bypassing tissue culture. Transformation rates range from 30–95% in tobacco and up to 13.3% in tomato under in vivo conditions (Lian et al. 2022). Nodal agroinjection method injects Agrobacterium into nodes of cotyledonary branches. Transformation rates of 45.24% were reported in peanut, and the method has been applied to CRISPR-Cas9 knockouts (Han et al. 2023). Direct regeneration of meristems under in vitro conditions technique where embryonic axes and shoot apical meristems are directly transformed under in vitro conditions, achieving efficiencies of 9.84% in soybean and 60% in cotton. This method simplifies medium composition and reduces hormone requirements (Baskaran 2016). Plumular meristem system transforms chickpea and pigeon pea seedlings by decapitating and wounding the shoot apex. Transformation rates reached 44% in chickpea and 72% in pigeon pea in the T1 generation (Ganguly et al. 2018).

Vegetative Tissues

The callus-based transformation system involves wounding seedlings or mature plants and treating the injuries with Agrobacterium tumefaciens. Hormone treatments are often applied to promote callus or adventitious bud formation, and selection markers such as antibiotics or herbicides are used to identify transformants. Maintaining proper humidity, temperature, and darkness—achieved through covering wounds with parafilm, aluminum foil, or plastic—enhances callus development. Darkness, in particular, has been shown to favor callus growth. Proper selection techniques, such as kanamycin treatment, can enhance the regeneration of transformed shoots by suppressing untransformed cells (Pozueta-Romero et al. 2001). This system has been successfully demonstrated in a range of species, including fruit trees (*Citrus sinensis*, *Citrus maxima*, *Dimocarpus longan*), vines (passionfruit), shrubs/trees (poplar, eucalyptus), and annual crops like tomato (Yuan et al. 2022). In patented applications, soybean and coffee have been shown to regenerate new shoots upon decapitation, and species like chili pepper, eggplant, and common bean exhibit strong regeneration and GUS expression abilities. Plants regenerated using this system often undergo direct regeneration simultaneously, which can lead to mosaicism in the transformed plants. While the literature on in vivo callus transformation is less extensive than other strategies, its versatility is evident from applications in indirect de novo shoot induction for species like tomato, chili pepper, and woody trees such as jujube and pomegranate under various conditions, including colchicine mutagenesis (Shi et al. 2015). This approach highlights its adaptability for diverse plant species and demonstrates potential for both transformation and related regeneration protocols.

Novel Systems

Grafting-mediated genome editing utilizes the graft union's phloem vasculature to transfer phloem-mobile RNA sequences from a transgenic rootstock to a non-transgenic scion. This process includes wound healing, callus bridge formation, and vascular development, enabling horizontal gene transfer (Ham et al. 2017). Heritable genome edits by fusing Cas9 and guide RNA (gRNA) sequences to tRNA-like structures, facilitating RNA transport from rootstock to scion in Arabidopsis thaliana and Brassica rapa. The inheritance rates for deletion edits were 1.6% (heterozygous) and 0.1% (homozygous), although these were likely underestimated due to pooled PCR screening (Zhang et al. 2016). To overcome challenges in recalcitrant species, transgenic rootstocks from easily transformable species like *A. thaliana* and *Nicotiana* sp. were suggested, as they are compatible with a broad range of plants.

Virus-Induced Gene Silencing (VIGS) is a transient method for analyzing gene function. However, it is unreliable for generating stable mutations, with heritable effects rarely observed (Senthil-Kumar & Mysore 2011). Virus-Induced Genome Editing (VIGE) emerged to create permanent heritable mutations. VIGE combines genome editing tools (e.g., CRISPR-Cas9) with viral vectors delivered via Agrobacterium transformation methods such as agroinfiltration and agrospray (Abrahamian et al. 2020).

The modified Tobacco rattle virus vector delivered gRNAs to the shoot apical meristem in Cas9-overexpressing tobacco, enabling heritable mutations. This system has been validated with other viruses, including Barley yellow striate mosaic virus and Cotton leaf crumple virus, expanding its versatility (Lei et al. 2022). Both methods highlight innovative approaches for genome editing without extensive reliance on tissue culture, broadening applicability in various plant systems.

Conclusion

The field of in planta transformation is rapidly evolving, bridging gaps in genetic accessibility for diverse plant species. As demonstrated in this review, these techniques not only overcome the constraints of conventional tissue culture methods but also provide a scalable, equitable platform for global scientific innovation. Moving forward, the focus should shift toward optimizing these methodologies for monocots and underrepresented crops, thus addressing critical gaps in agricultural biotechnology. Integrating advances in CRISPR-Cas systems and high-throughput genomic tools with *in planta* approaches holds significant promise, enabling precise, efficient, and sustainable plant improvements. Additionally, the collaborative development of open-source resources, such as the online compendium presented here, exemplifies the collective effort needed to refine and disseminate these transformative techniques. By fostering interdisciplinary research and community engagement, *in planta* transformation can become a cornerstone of next-generation plant science, driving breakthroughs in crop resilience, productivity, and adaptability. This integration of technical innovation with global accessibility marks an important step toward harnessing plant biotechnology for a more sustainable future.

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